

Result No.	Score	Query Match	Length	DB	ID	Description
1	466	72.2	1261	6	AR359850	AR359850 Sequence
2	466	72.2	1261	6	AX039100	AX039100 Sequence
3	466	72.2	1261	9	HSAA23396	AJ743396 Homo sapi
4	465	72.2	5306	9	AB032984	AB032984 Homo sapi
5	462.8	71.8	645	6	AX048004	AX048004 Sequence
6	462.8	71.8	2220	6	AX359849	AX359849 Sequence
7	462.8	71.8	2220	6	AX039099	AX039099 Sequence
8	462.8	71.8	2220	10	RN0243395	AJ243395 Rattus no
9	462.8	71.8	2632	6	AX048005	AX048005 Sequence
10	462.8	71.8	3107	10	AF378093	AF378093 Rattus no
11	462.8	71.8	3108	6	AX047994	AX047984 Sequence
12	462.8	71.8	3236	9	AB097521	AB097521 Macaca fa
13	462.8	71.8	3910	10	BC070899	BC070899 Rattus no
14	461.2	71.5	4025	10	AK173115	AK173115 Mus muscu
15	461.2	71.5	4169	10	BC053919	BC053919 Mus muscu
16	461.2	71.5	4176	10	BC058636	BC058636 Mus muscu
17	460.6	71.4	670	10	AY049036	AY049036 Mus muscu
18	428.4	66.4	606	6	C0728741	C0728741 Sequence
19	367.2	56.9	922	5	BX935227	BX935227 Gallus ga

20	323.8	40.2	912	5	EX931708
21	301	46.7	471	6	BD059018
22	300.4	46.6	1654	5	BC077295
23	165	25.6	127347	2	AP000682
24	165	25.6	144833	2	AC063921
25	165	25.6	149800	2	AC021981
26	165	25.6	172546	2	AC024604
27	165	25.6	174285	2	AC145484
28	165	25.6	178169	9	AP002765
29	165	25.6	178431	2	AP002749
30	165	25.6	181471	9	AC065539
31	162.6	25.2	140307	2	AC135353
32	162.6	25.2	238861	2	AC148331
33	162.4	25.2	214306	2	AC128723
34	158.4	24.6	1335	9	HUMG501A
35	158.4	24.6	1404	9	HUMG501B
36	158.4	24.6	1525	9	EC067122
37	158	24.5	657	4	OC053382
38	158	24.5	657	6	AX048006
39	155.6	24.1	617	6	CQ722293
40	152.2	23.6	1490	6	AX401978
41	152.2	23.6	1490	10	RATSC31B
42	151	23.4	1125	10	MM046681
43	151	23.4	1340	10	MM085786
44	151	23.4	1557	10	BC039140
45	151	23.4	1568	10	BC009652

ALIGNMENTS

RESULT 1				
AR359850				
LOCUS	AR359850	1261 bp	DNA	linear
DEFINITION	Sequence 4 from patent US 6553565.			PAT 17-AUG-2003
ACCESSION	AR359850			
VERSION	AR359850.1	GI:33766660		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 1261)			
TITLE	Healin,P. and Lynam,N.R.			
JOURNAL	Vehicle interior rearview mirror assembly including an			
FEATURES	Patent: US 6593565-A 4 15-JUL-2003;			
Source	Location/Qualifiers			
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	/organism="Unknown"			
ORIGIN	/mol_type="genomic DNA"			

	Query Match	72.2%	Score 466;	DB 6;	Length 1261;
	Best Local Similarity	58.8%;	Pred. No 1,2e-106;		
	Matches 379;	Conservative 145;	Mismatches 121;	Indels 0;	Gaps 0;
Qy	1	ATGCCNCAGTAAACGNYNTTTTCNYYNGCMSNTYNGTYNAINTAYAGGTGTMWSN	60		
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Db	376	ATGGCTCCATTCAATAGATTGTTTCCCTCGGCTCTCTCGGCTATTACTAGGTGCAGT	435		
Qy	61	GTNGYTTTCNGNTGYTGNGAAGTCCCMMSNBARCNGARGGNNGTNCARGNAAYCCN	120		
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Db	436	GTCGTCTCCCTGTGTGTGTGAAGTGCCCTCGAGAACGAGGCCGTGACBAGGCC	495		
		: :			
Qy	121	ATGAARYTNMGNTGYATATNSMTGYATGAARMGNGARGRTNGARGCNACNACNGTNGTN	180		
		: :			
Db	496	ATGAAGCTGGCGTTCATCTCCCTGCATTAAGAAGAGAGGTGGAGGCCACACCAGTGGTG	555		
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Qy	181	GARTGTTTTYAAMNCCNGARGGNGUNARAYTTTTYTNAITNTYVGARTRMGNAAVGN	240		
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Db	556	GAATGTCTTACACBAGCCCCGAGGGCGTAAAGATTTCTTATTATTCAGATATCGAATATGCG	615		
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Qy	241	CAYCARGARGTNGARWNSCCNTTTYCARGMNGNTNCARTGGAAYGGANWSNABARAYYTN	300		

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Db      616 CACACAGAGGTGAGAGCCCTTTACAGGGGCGCTGAGTGAATGACAGCAAGACCTG 675
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Db      676 CAGGAGGTGTCATCTGCTGCTCAACGTCATCTGAACGACTCTGCGCTCTACACCTG 735
Qy      361 AAYGTMSMNGMAGRTTYGARFTTYGARGCNCAYMGNCCNTTYGTNABACNACMNGNTYN 420
Db      736 AATGTGTCGGGAGTTTGAAGGTCATCGGCCCTTTGTGAAGACAGCGGCTG 795
Qy      421 ATNCCNYTMNGNTNACNGARGCNGNGARAGATYTYACMWSNGTNGTMSNGARATN 480
Db      796 ATCCCCCTAAGATCACCGAGAGGCTGAGAGACTTCACTCTGTGTCTCAGAAATC 855
Qy      481 ATGATGTAYATNTYNTGNTNTTYTNAACNYTNTGYTNTYNTATNABATGATNTATYTG 540
Db      856 ATGATGTACATCTTCTGTGCTTCTTCAACCTGTGTGCTCTCATGAGATGATATATYTG 915
Qy      541 TAYMGNAAAGTGMNSAARGCNGARGCNGCNGARAGAAAYGCNWSNGATYATYNTGNCN 600
Db      916 TACAGAAAGTCTCAAAAAGCCGAGAGGACGCCCAAGAAAACCGCTCTGACTACCTTGC 975
Qy      601 ATNCCMWSNGARAAYARAGARAAAYWSNGCNGTNCNGTNGARGAR 645
Db      976 ATCCCATCTGAGAACAGAGAACTCTGCGGTACCACTGAGGAA 1020

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RESULT 2
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 LOCUS Sequence 4 from Patent WO0063367.
 DEFINITION AX039100
 ACCESSION AX039100
 VERSION AX039100.1 GI:11229276

KEYWORDS

Homio sapiens (human)
 Homo sapiens
 Bukariyoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 Cox, P., Dixon, A., Jackson, A. and Morgan, K.
 A novel family of beta sub-unit proteins from a voltage-gated sodi-
 um channel, nucleic acids encoding them and therapeutic or.
 diagnostic uses there of
 Patent: WO 0063367-A 4 26-OCT-2000;
 WARNER-LAMBERT COMPANY (US); Cambridge University Technical
 Services Limited (GB)

FEATURES

source
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 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 72.2%; Score 466; DB 6; Length 1261;
 Best Local Similarity 58.8%; Pred. No. 1.2e-106;
 Matches 379; Conservative 145; Mismatches 121; Indels 0; Gaps 0;

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Qy      1 ATGCCGNCNTTAAVNGNTNTTYCCNYTNGCWSYNTGNTYNTATNTATYGGGTMNSN 60
Db      376 ATGCCGNCCTTCAATAGATGTTTCCCTGCTTCTCTGTGTTACTGAGGTCAAT 435
Qy      61 GNTGTATYTCNGTNTGYTNGARGTNCNWSNGARACNGARCGTNCARBNAAYCCN 120
Db      436 GTCTGCTTCCCTGTGTGTGTGAGAGTCCCTCGAAGACGAGGCGGTGACAGGCAACCC 495
Qy      121 ATGAARYTMMNTGYATNMSTNTGYATGAARMNGARGARCTNGARCNACNACNGTNTN 180
Db      496 ATGAAGTGGCTGCATCTCTCTCATGAAGAGAGAGAGAGGTCAGGCCACACGAGGTG 555
Qy      181 GATGTGTTATYTMNGNCNARAGNGNARAGATTTTATNTATNTATYARTATYMAAYGN 240
Db      556 GAATGTGTTTACAGGCCGAGGCGGTAAAGATTTCTTATTTACAGATATCGAATATGCG 615

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Qy      301 CARGAGTGMNSAATNACNGTNTYNAAYGTNACNYTNAAYGAWNSGNGNTYNTAYACNTGY 360
Db      676 CAGGAGGTGTCATCTGCTGCTCAACGTCATCTGAACGACTCTGCGCTCTACACCTG 735
Qy      361 AAYGTMSMNGMAGRTTYGARFTTYGARGCNCAYMGNCCNTTYGTNABACNACMNGNTYN 420
Db      736 AATGTGTCGGGAGTTTGAAGGTCATCGGCCCTTTGTGAAGACAGCGGCTG 795
Qy      421 ATNCCNYTMNGNTNACNGARGCNGNGARAGATYTYACMWSNGTNGTMSNGARATN 480
Db      796 ATCCCCCTAAGATCACCGAGAGGCTGAGAGACTTCACTCTGTGTCTCAGAAATC 855
Qy      481 ATGATGTAYATNTYNTGNTNTTYTNAACNYTNTGYTNTYNTATNABATGATNTATYTG 540
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Qy      541 TAYMGNAAAGTGMNSAARGCNGARGCNGCNGARAGAAAYGCNWSNGATYATYNTGNCN 600
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Qy      601 ATNCCMWSNGARAAYARAGARAAAYWSNGCNGTNCNGTNGARGAR 645
Db      976 ATCCCATCTGAGAACAGAGAACTCTGCGGTACCACTGAGGAA 1020

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RESULT 3
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 LOCUS HSA243396
 DEFINITION Homo sapiens mRNA for voltage-gated sodium channel beta-3 subunit
 (scn3b gene).
 ACCESSION AJ243396
 VERSION AJ243396.2 GI:7242612
 KEYWORDS scn3b gene; voltage-gated sodium channel beta-3 subunit.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

1 Morgan, K., Stevens, E.B., Shaw, B., Cox, P., Dixon, A.K., Lee, K.,
 Pinnoch, R.D., Hughes, J., Richardson, P.J., Mizuguchi, K. and
 Jackson, A.P.
 beta 3: an additional auxiliary subunit of the voltage-sensitive
 sodium channel that modulates channel gating with distinct kinetics
 Proc. Natl. Acad. Sci. U.S.A. 97 (5), 2308-2313 (2000)

FEATURES

1..1261
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /cissue_type="Brain"

ORIGIN

Query Match 72.2%; Score 466; DB 6; Length 1261;
 Best Local Similarity 58.8%; Pred. No. 1.2e-106;
 Matches 379; Conservative 145; Mismatches 121; Indels 0; Gaps 0;

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Qy      1 ATGCCGNCNTTAAVNGNTNTTYCCNYTNGCWSYNTGNTYNTATNTATYGGGTMNSN 60
Db      376 ATGCCGNCCTTCAATAGATGTTTCCCTGCTTCTCTGTGTTACTGAGGTCAAT 435
Qy      61 GNTGTATYTCNGTNTGYTNGARGTNCNWSNGARACNGARCGTNCARBNAAYCCN 120
Db      436 GTCTGCTTCCCTGTGTGTGTGAGAGTCCCTCGAAGACGAGGCGGTGACAGGCAACCC 495
Qy      121 ATGAARYTMMNTGYATNMSTNTGYATGAARMNGARGARCTNGARCNACNACNGTNTN 180
Db      496 ATGAAGTGGCTGCATCTCTCTCATGAAGAGAGAGAGAGGTCAGGCCACACGAGGTG 555
Qy      181 GATGTGTTATYTMNGNCNARAGNGNARAGATTTTATNTATNTATYARTATYMAAYGN 240
Db      556 GAATGTGTTTACAGGCCGAGGCGGTAAAGATTTCTTATTTACAGATATCGAATATGCG 615

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3' UTR

ORIGIN

Query Match 72.2%; Score 466; DB 9; Length 1261;
Beet local Similarity 58.8%; Pred. No. 1.2e-106;
Matches 379; Conservative 145; Mismatches 121; Indels 0; Gaps 0;

Oy 1 ATGCCNGCNTTAAVMGNVTNTTYTCNTYNGNMSNTNGTNTATNTAATYTGSTNMSN 60
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Oy 61 GTNTGYTTYCCNGNTGYGTNGARGTNCNMNSNGARCNGARCGNGTNCARGANAYCCN 120
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RESULT 4
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LOCUS Homo sapiens mRNA for KIAA1158 protein, partial cds.
DEFINITION AB032984
ACCESSION AB032984.1 GI:6330135
VERSION

KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS	Hiroseawa,M., Nagase,T., Ishikawa,K., Kikuno,R., Nomura,N. and Ohara,O.
TITLE	Characterization of cDNA clones selected by the Genemark analysis from size-fractionated cDNA libraries from human brain
JOURNAL	DNA Res. 6 (5), 329-336 (1999)
MEDLINE	20039618
PUBMED	10574461
REFERENCES	2 (bases 1 to 5306)
AUTHORS	Ohara,O., Nagase,T. and Kikuno,R.
TITLE	Direct Submission
JOURNAL	Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute,
	Laboratory of DNA Technology; 153-3 Yena, Kisarazu, Chiba
	297-0812, Japan (E-mail:cdnaifnc@kazusa.or.jp,
	URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
	Fax:+81-438-52-3914)
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ORIGIN	
Query Match	72.2%; Score 466; DB 9; Length 5306;
Blast Local Similarity	58.8%; Pred. No. 1.8e-106;
Matches 379; Conservative 145; Mismatches 121; Indels 0; Gaps 0;	
Oy	1 ATGCCGCGTYYAAMGNVTNTTCVCNYTGCMNSGTNTGTYTNATNTAVTGGTMSN 60
Dbb	48 ATGCCTGCCTCAATAAGTTGTTCCCTCCTCTCTCTGCTTAICTACTGGSTCACT 107
Oy	61 GTNTGYTTYCCGNTGYGTNGARGTNCNMWSNGARACNGARGCNTNGCARGNAAYCN 120
Dbb	108 GTGCTCTCCCTGTGTGTGTGAAGTCCCTCGAGAAGGAGCGCGTAGAGGCAACC 167
Oy	121 ATGAARTMGNTGYATMNSTYTGAATGARANGABARAGTNGARGCNAACNCGTNGTN 180
Dbb	168 ATGAAGCTGCCTGCATCTCTCGATATAGAGAGAGAGGAGGCGCACCAAGTGGTG 227
Oy	181 GARAGTYYTVAAMNCNGARGGNGANAAGAYTYYTNAATNTAYGARTVMGNAAYGN 240
Dbb	228 GAATGCTTCTACAGGCCCGAGGCGGTAAAGATTCTTATTTACAGATATCGAATGCG 287
Oy	241 CAYCARGAGTNGARMSNCCNTTYCARGGMGNTYCARTGAAVGGNWSNARAGAYTN 300
Dbb	288 CACCAAGAGGAGGAGAGGCCCTTTCAAGGAGGCGCTGACAGTGAATGCAAGAACGCTG 347
Oy	301 CARAYGTMSNATNACNCTYTNAAVGTNAACNTTAAAGAYMSNGNTYNTAVACMTGY 360

Db 348 CAGAGCTGTCACACTGTCCTCAAGCTCACTGGAAGACTCTGGCCCTACACCTGC 407
QY 361 AAYGTWMSNMGNGARTTYGARTTYGARGCNCAVMGNCNTTYGTNAABACNA CMNGNTN 420
Db 408 AATGTCTCAGAGGAGTCTTAAGTTCAGAGCAACAGGCTTTTGTGAAGCACAGAGACTG 420
QY 421 ATNCNVTMMGNTACNCGARGGCGNGNGARGATYTYACNWSNCTNGTMSNGARATN 480
Db 468 ATCCCCCTTAAGATCACCGAGAGGCTGAGAGAGACTTCACTCTGTGTCTCAGAAATC 527
QY 481 ATGATGTAVATNTYNTNGTNTTYTNAACNTYNTGYTYNTAATNGARATGATNTATYTG 540
Db 528 ATGATGTACATCTCTGCTCTCTCTCACTGTGCTCTCACTGAGATGATATATTCG 587
QY 541 TAYMGNAAGTMSNABGNGARGGCGNGCGNCGARABAAVGCNMSNGATYTYNTGNCN 600
Db 588 TACAGAAAGTCTCTTAAGGCGGAGAGGCGACAGCAAGAAATGCGTCTGACTACTTGC 647
QY 601 ATNCNWSNGARAAVYARGARAAVWSNCGNCTNCNGTNGARGAR 645
Db 648 ATCCCTTCAAGAACAGAGAACTCTGCGCTACACTGAGAGAA 692

RESULT 5
AX048004 645 bp DNA linear PAT 15-DEC-2000
LOCUS Sequence 21 from Patent WO0069912.
DEFINITION AX048004
ACCESSION AX048004
VERSION AX048004.1 GI:11876882
KEYWORDS
SOURCE
ORGANISM
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Lepus sp.
Bukaryaota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Lepus.
REFERENCE
AUTHORS
TITLE
JOURNAL
Curtis, R.A.
Gene encoding a sodium channel beta-3 subunit protein
Patent: WO 0069912-A 21 23-NOV-2000;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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ORIGIN

Query Match 71.8%; Score 462.8; DB 6; Length 645;
Best Local Similarity 58.4%; Pred. No. 6,7e-106;
Matches 377; Conservative 145; Mismatches 123; Indels 0; Gaps 0;

QY 1 ATGCCGNCNTTYAAVMGNTNTTYCCNTYNGCNMSNTYNTGNTAATNTATYTGGSN 60
Db 1 ATGCTGCTCTCAACAGATTGCTCCCTAGCTTCTTAATGCTCACTAGGCTGAGA 60
QY 61 GINTGYTTYCNGTNTGYTGNGARGTNCNWSNGARACNGARGCNGTNCARGNAAYCCN 120
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Db 241 CACGAGAAAGTGAGAGCCCTTCAAGGCCGTGAGTGAATGGAGCAAGAGCTG 300
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QY 361 AAYGTWMSNMGNGARTTYGARTTYGARGCNCAVMGNCNTTYGTNAABACNA CMNGNTN 420
Db 361 AATGTCTCAGAGGAGTCTTAAGTTCAGAGCAACAGGCTTTTGTGAAGCACAGAGACTG 420
QY 421 ATNCNVTMMGNTACNCGARGGCGNGNGARGATYTYACNWSNCTNGTMSNGARATN 480
Db 421 ATACCTTTCAGATCACTBAAGGCGGAGAACTTCACTCCGTGTCTCGAAATC 480
QY 481 ATGATGTAVATNTYNTNGTNTTYTNAACNTYNTGYTYNTAATNGARATGATNTATYTG 540
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QY 541 TAYMGNAAGTMSNABGNGARGGCGNGCGNCGARABAAVGCNMSNGATYTYNTGNCN 600
Db 541 TACAGAAAGTCTCTTAAGGCGGAGAGGCGACAGCAAGAAATGCGTCTGACTACTTGC 600
QY 601 ATNCNWSNGARAAVYARGARAAVWSNCGNCTNCNGTNGARGAR 645
Db 601 ATCCCTTCAAGAACAGAGAACTCTGTGTACTGTGAGAGAA 645

RESULT 6
AR359849 2220 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 3 from patent US 6593565.
DEFINITION AR359849
ACCESSION AR359849
VERSION AR359849.1 GI:33766659
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unknown.
Unclassified.
REFERENCE
AUTHORS
TITLE
JOURNAL
Heslin, P. and Lynam, N.R.
Vehicle interior rearview mirror assembly including an
accessory-containing housing
Patent: US 6593565-A 3 15-JUL-2003;
FEATURES
source
1. 2220
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 71.8%; Score 462.8; DB 6; Length 2220;
Best Local Similarity 58.4%; Pred. No. 9,3e-106;
Matches 377; Conservative 145; Mismatches 123; Indels 0; Gaps 0;

QY 1 ATGCCGNCNTTYAAVMGNTNTTYCCNTYNGCNMSNTYNTGNTAATNTATYTGGSN 60
Db 363 ATGCTGCTCTCAACAGATTGCTCCCTAGCTTCTTAATGCTCACTAGGCTGAGA 422
QY 61 GINTGYTTYCNGTNTGYTGNGARGTNCNWSNGARACNGARGCNGTNCARGNAAYCCN 120
Db 423 GTCGCTCTCCCTGTGTGTGAAGTCCCTCGAGACAGAGGCGGTGAGGCAATCCC 482
QY 121 ATGAARTTMGNTGYATNMSNTGYATGAARMGNGARGARGTNGARGCNAACNGTNGTN 180
Db 483 ATGAAGCTGAGTGCACTCTCTCATGAAGAGGAGGAGGTGAGGCGCACACTGTGTG 542
QY 181 GARTGTTTYAVMGNCNCGARGGNGNARGAVTYTYNTAATNTAYGARTYMGNAAYG 240
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QY 361 AAYGTWMSNMGNGARTTYGARTTYGARGCNCAVMGNCNTTYGTNAABACNA CMNGNTN 420

Db 723 AATGTCACAGGAGCTTGAATTCGAGACACAGGCTTTTGTAAGACCAACGAGCTG 782

Qy 421 ATNCNTYTMNGNTNACNGARCGNGCNGARGAATTTACNWSNGTNGTWSNGARATN 480

Db 783 AATACCTTTGCGAGCTCAAGAGAGCGGAGAGACCTTCACTCGGTGCTCGGAAATC 842

Qy 481 ATGATGTAATNTYNTNGTNTTNTTNTNACNTNTNGTNTNTNATNATGATNTATATGY 540

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Qy 541 TAYGNAAAGTNTWSNAARCGNGARCGNGCNGARGAATTTACNWSNGTNTGATNTATYTCN 600

Db 903 TACGAAAGGCTCTCTAAGCGCGGAGAGGACACAGGAAATGCTCTGACTACTCTTCT 962

Qy 601 ATNCNWSNGARAAVAARGAARAAVWSNCGTNCNGTNGARGAR 645

Db 963 ATCCCTTCAGAGAACAGAGAACTGTGTGTAAGTGTGAGAGAA 1007

RESULT 7
AX039099 2220 bp DNA linear PAT 18-NOV-2000

LOCUS
DEFINITION
AX039099 Sequence 3 from Patent WO0063367.

VERSION
AX039099.1 GI:11229275

KEYWORDS
Rattus sp.

SOURCE
ORGANISM
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1
Cox, P., Dixon, A., Jackson, A. and Morgan, K.
A novel family of beta sub-unit proteins from a voltage-gated sodium channel, nucleic acids encoding them and therapeutic or diagnostic uses thereof
Patent: WO 0063367-A 3 26-OCT-2000;
WARNER-LAMBERT COMPANY (US) ; Cambridge University Technical Services Limited (GB)
Location/Qualifiers
1. .2220
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FEATURES
source

ORIGIN
Query Match 71.8%; Score 462.8; DB 6; Length 2220;
Best Local Similarity 58.4%; Pred. No. 9.3e-106;
Matches 377; Conservative 145; Mismatches 123; Indels 0; Gaps 0;

Qy 1 ATGCCGNCNTTYAAVMGNTNTTYCCNTYNGCNMSNTYNTNATNTATYTGCTWSN 60

Db 363 ATGCTGCTCTCAACAGATGCTTCCCTAGCTCTCTAGTCACTACTGAGGTGAGA 422

Qy 61 GTNTGTTTCGNTNGTNGTNGARGTNCNMSNABARACNGTNCARCGNAAYCCN 120

Db 423 GTCTGCTTCCCTGTGTGTGTGAAGTGCCTTCGAGACAGAGCGGTGCAAGGCAATCC 482

Qy 121 ATGAARYTMNGNTGATNTMSNTGYATGAARMNGARGTNGARCGNACNACNGTNGTN 180

Db 483 ATGAAGCTGAGGTGATCTCTGCAATGAAGGAGGAGGAGGCCACCACTGTGTG 542

Qy 181 GARTGCTTYTAYMGNCCNGARCGNGNABARAGATTTTNTATNTATGARTAYMGNAYGN 240

Db 543 GAGTGCTTCTACAGGCTCGAGGCGGTAAAGATTTCTTATATATGATATCGAATGCG 602

Qy 241 CAYCARBARGTNGARWMSNCTTYCARGNGNNTNCARTGAAVCGNWSNABARAGATNT 300

Db 603 CACCAAGAAAGTGAGAGCCCTTCAGAGCGGCTTCGAGTGAAGGAGGACCAAGACTG 662

Qy 301 CARGAAGTMSNATNACNGTNTYNTNAAVGTNA CNTYNTNAAVGA YWSNGNTYNTNAAVACNTGY 360

Db 663 CAGGACGATCACTCACTGTAAGTCACTTTGAATGACTCTGAGCTCTACACATGC 722

Qy 361 AAYGTMSNMGNTARTTYGARTTYGARCNCAIWNCCNTTYGTNAAAPACNMGNTYN 420

Db 723 AATGTCACAGGAGCTTGAATTCGAGACACAGGCTTTTGTAAGACCAACGAGCTG 782

Qy 421 ATNCNTYTMNGNTNACNGARCGNGCNGARBARATTTTCNWSNGTNGTWSNGARATN 480

Db 783 AATACCTTTGCGAGCTCAAGAGAGCGGAGAGACCTTCACTCGGTGCTCGGAAATC 842

Qy 481 ATGATGTAATNTYNTNGTNTTNTTNTNACNTNTNGTNTNTNATNATGATNTATATGY 540

Db 843 ATGATGTAATNTTCTTCTGCTCTTCTCTGCTGTTATGATATGATATCTATTTGC 902

Qy 541 TAYGNAAAGTNTWSNAARCGNGARCGNGCNGARGAATTTACNWSNGTNTGATNTATYTCN 600

Db 903 TACGAAAGGCTCTCTAAGCGCGGAGAGGACACAGGAAATGCTCTGACTACTCTTCT 962

Qy 601 ATNCNWSNGARAAVAARGAARAAVWSNCGTNCNGTNGARGAR 645

Db 963 ATCCCTTCAGAGAACAGAGAACTGTGTGTAAGTGTGAGAGAA 1007

RESULT 8
RNO243395 2220 bp mRNA linear ROD 29-JAN-2003

LOCUS
DEFINITION
RNO243395 Rattus norvegicus mRNA for voltage-gated sodium channel beta-3 subunit.

ACCESSION
AJ243395

VERSION
AJ243395.2 GI:7242802

KEYWORDS
scn3b gene; voltage-gated sodium channel beta-3 subunit.

SOURCE
Rattus norvegicus (Norway rat)

ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1
Morgan, K., Stevens, E.B., Shaw, B., Cox, P., Dixon, A.K., Lee, K., Plimock, R.D., Hughes, D., Richardson, P.J., Mizuguchi, K. and Jackson, A.P.
beta 3: an additional auxiliary subunit of the voltage-sensitive sodium channel that modulates channel gating with distinct kinetics
Proc. Natl. Acad. Sci. U.S.A. 97 (5), 2308-2313 (2000)

2
Morgan, K.
Direct Submission
Submitted (28-JUN-1999) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
Reviewed by (3)
3 (bases 1 to 2220)

REMARK
REFERENCE
Morgan, K.
Direct Submission
Submitted (09-MAR-2000) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
On Mar 14, 2000 this sequence version replaced gi:7161888.

FEATURES
source

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ORIGIN

3'UTR

Query Match 71.8%; Score 462.8; DB 10; Length 2220;
Best Local Similarity 58.4%; Pred. No. 9,3e-106;
Matches 377; Conservative 145; Mismatches 123; Indels 0; Gaps 0;

QY 1 ATGCCGNCNTTAAAYMGNNTTTCCTCCNYTNGCNSNTNGTNTAATNTAATYGGGTMSN 60
DB ATGCCGNCNTTAAAYMGNNTTTCCTCCNYTNGCNSNTNGTNTAATNTAATYGGGTMSN 60
QY 61 GNTGTGTTCCGNTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 120
DB 61 GNTGTGTTCCGNTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 120
QY 423 GTCTGCTTCCCTGT 482
DB 423 GTCTGCTTCCCTGT 482
QY 121 ATGAARYTMNGTGYATMNSNTGYATGAARMNGARGGTNGARGCNAACNGTNGTN 180
DB 483 ATGAAGCTGAGTGATCTCTCGATGAAGAGGAGAGGTGAGGCGACACTGTGTG 542
QY 181 GARTGTTTAAVNGCNGARGNGNAAAGATTTTNTAATNTAATYAGRTAYMGNAAYGN 240
DB 543 GAGTGTGTTCAACAGGCTGAGGCGGTAAAGATTTCTTATATATGATGATCGGAATGCG 602
QY 241 CAYCARGARTNGARMSNCNTTTCARCGMNGNTNCAFTGAAAYGMSNNAARGAYTN 300
DB 603 CACCAAGAGTGAGAGGCCCTTCCAGAGCGGTGTGAGTGAAGTGAAGAGCAAGACCTG 662
QY 301 CARGAYTMSNATNACNGTNTAAYGTNACNYTNAAYGAYMSNGNTNTAATNTAYACNTGY 360
DB 663 CAGGAGTATCCATCACTGTACTCAATGTCACTTTGATGATCTGTGGCCCTTCAACATGC 722
QY 361 AAYGTMSMNGARFTTYGARTTYGARGCNCAYMNCNTTGTNTAARACNACMNGNTYN 420
DB 723 AAGTGTCCAGGAGTTCGAATTCAGAGCACAGAGCCTTTGTGTGAAGACACAGACCTG 782
QY 421 ATNCNVTMNGTNAACNGARGNGCNGARGAYTTCACMNSNGTNGTNGARGATN 480
DB 783 ATACCTTTGGAATCACTGAAGGCGGAGAGAACTTCACTTCCTGTGTGTGTGTGTGTGTGT 842
QY 481 ATGATGTAATNTYNTNGTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTT 540
DB 843 ATGATGTAATNTTCTCTGCTTCTCTCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 902
QY 541 TATMGNAARBTMSNARCGNCGARGCNGCNCARGAARAYGCMNSNGATYATYNTNGN 600
DB 903 TACAGAAAGTCTCTAAGGCCGAGAGGACGACAGAAATATGCTGTCACTACCTTGTCT 962
QY 601 ATNCMNSGARAAYARAGARAAYMSNGCNGTNCNGTNGARGAR 645
DB 963 ATCCCTTCAGAGAACAGAGAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1007

RESULT 9
AX048005 2632 bp DNA linear PAT 15-DEC-2000
LOCUS AX048005
DEFINITION Sequence 22 from Patent WO0069912.
ACCESSION AX048005
VERSION AX048005.1 GI:11876883
KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1
AUTHORS Curtis,R.A.
TITLE Gene encoding a sodium channel beta-3 subunit protein
JOURNAL Patent: WO 0069912-A 22 23-NOV-2000;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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ORIGIN

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Best Local Similarity 58.4%; Pred. No. 9,7e-106;
Matches 377; Conservative 145; Mismatches 123; Indels 0; Gaps 0;

QY 1 ATGCCGNCNTTAAAYMGNNTTTCCTCCNYTNGCNSNTNGTNTAATNTAATYGGGTMSN 60
DB 78 ATGCCGNCNTTAAAYMGNNTTTCCTCCNYTNGCNSNTNGTNTAATNTAATYGGGTMSN 60
QY 61 GNTGTGTTCCGNTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 120
DB 61 GNTGTGTTCCGNTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 120
QY 138 GTCTGCTTCCCTGT 197
DB 138 GTCTGCTTCCCTGT 197
QY 121 ATGAARYTMNGTGYATMNSNTGYATGAARMNGARGGTNGARGCNAACNGTNGTN 180
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DB 258 GAGTGTGTTCAACAGGCTGAGGCGGTAAAGATTTCTTATATGATGATCGGAATGCG 317
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DB 318 CACCAAGAGTGAGAGGCCCTTCCAGAGCGGTGTGAGTGAAGTGAAGAGCAAGACCTG 377
QY 301 CARGAYTMSNATNACNGTNTAAYGTNACNYTNAAYGAYMSNGNTNTAATNTAYACNTGY 360
DB 378 CAGGAGTATCCATCACTGTACTCAATGTCACTTTGATGATCTGTGGCCCTTCAACATGC 437
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DB 438 AAGTGTCCAGGAGTTCGAATTCAGAGCACAGAGCCTTTGTGTGAAGACACAGACCTG 497
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DB 618 TACAGAAAGTCTCTAAGGCCGAGAGGACGACAGAAATATGCTGTCACTACCTTGTCT 677
QY 601 ATNCMNSGARAAYARAGARAAYMSNGCNGTNCNGTNGARGAR 645
DB 678 ATCCCTTCAGAGAACAGAGAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 722

RESULT 10
AF378093 3107 bp mRNA linear ROD 11-SEP-2002
LOCUS AF378093
DEFINITION Rattus norvegicus sodium channel beta 3 subunit (SCN3B) mRNA,
complete cds.
ACCESSION AF378093
VERSION AF378093.1 GI:14165175
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 3107)
 AUTHORS Qu,Y., Curtis,R., Lawson,D., Gilbride,K., Ge,P., DiStefano P.S.,
 TITLE Siles-Santiago,I., Caterall W.A. and Scheuer,T.
 JOURNAL Differential modulation of sodium channel gating and persistent
 MEDLINE sodium currents by the beta1, beta2, and beta3 subunits
 PUBMED Mol. Cell. Neurosci. 18 (5), 570-580 (2001)
 REFERENCE 2 (bases 1 to 3107)
 AUTHORS Curtis,R.
 JOURNAL Direct Submission
 TITLE Submitted (05-MAY-2001) Neurobiology, Millennium Pharmaceuticals
 Inc., 75 Sidney Street, Cambridge, MA 02139, USA
 FEATURES
 SOURCE
 1. 3107
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 77. 724
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ORIGIN

Query Match 71.8%; Score 462.8; DB 10; Length 3107;
 Beac Local Similarity 58.4%; Pred. No. 1e-105;
 Matches 377; Conservative 145; Mismatches 123; Indels 0; Gaps 0;

Qy 1 ATGCCGNCNTTAAAYMGNYNTTTCYCNNTNGCNMSNTNGTNTATNTATYATGGTWSN 60
 Db 77 ATGCTGCTTCAACAAGATTCCTCCCTAGCTTCTAGTGCATCTACTGCTGCTAGA 136
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 Qy 121 ATGAARTTNGTGTATMTSNTGTATGAABNGNARGARGTNGARGCNAACNAGTGTN 180
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 Qy 361 AAYGTNMSNMGARTTYGARTTYGARGNCAYMNCNTTGTGTAARAACNMGNYTN 420
 Db 437 AATGTGTCCAGGAGGAGTGTGAATGAGGACACAGGCTTTTGTGAAGACACAGACTG 496
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RESULT 11
 AX047984 3108 bp DNA linear PAT 15-DEC-2000
 LOCUS Sequence 1 from Patent WO0069912.
 AX047984
 VERSION AX047984.1 GI:11876881
 KEYWORDS
 SOURCE Rattus sp.
 ORGANISM Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1
 AUTHORS Curtis,R.A.
 TITLE Gene encoding a sodium channel beta-3 subunit protein
 JOURNAL Patent: WO 0069912-A 1 23-NOV-2000;
 Millennium Pharmaceuticals, Inc. (US)
 FEATURES
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ORIGIN

Query Match 71.8%; Score 462.8; DB 6; Length 3108;
 Beac Local Similarity 58.4%; Pred. No. 1e-105;
 Matches 377; Conservative 145; Mismatches 123; Indels 0; Gaps 0;

Qy 1 ATGCCGNCNTTAAAYMGNYNTTTCYCNNTNGCNMSNTNGTNTATNTATYATGGTWSN 60
 Db 78 ATGCTGCTTCAACAAGATTCCTCCCTAGCTTCTAGTGCATCTACTGCTGCTAGA 137
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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullan, S.J., Boeck, S.A., McEwan, P.J., McKernan, K.U., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouckard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dieckson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E., Scherf, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 3910)

Director MGC Project.

Direct Submission

Submitted (17-MAY-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: gcgabs-remail.nih.gov

Tissue Procurement: Howard Jacobs

cDNA Library Preparation: Express Genomics

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@nigr.nih.gov

Ahter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Maduro, Q.L., Mastello, C., Maskett, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Staniford, S., Thomas, P.J., Touchman, J.W., Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILML at: <http://image.llnl.gov>

Series: IRAC Plate: 175 Row: 9 Column: 5

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4757878.

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ORIGIN

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Matches 377; Conservative 145; Mismatches 123; Indels 0; Gaps 0;

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71.8%; Score 462.8; DB 10; Length 3910;

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498 ATGAAGCTGAGTGTCTCATCTCTGATGAGAGGAGAGGAGGAGGAGGAGGAGG 557

181 GATGCTTGTATYMGNCNGARNGNGNAGATTTTNTATNTATYATYMGNAAYGN 240

558 GAGTGTCTTCAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 617

241 CAYCARGARNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNG 300

618 CACGAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 677

301 CARGAYTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNG 360

678 CAGAGCTATCCATCATCTGATCACTGATCACTGATCACTGATCACTGATCACT 737

361 AAYGTMSMNGNARTTYGARTTYGAGCNCAYGNCNTTYGTNARACACMNGTYN 420

738 AATGTGCCAGGAGGCTTGAATTCAGAGCACAGGCTTGTGAGAGCACACAGCTG 797

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RESULT 14

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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Okazaki, N., Kikuno, R.F., Ohara, R., Inamoto, S., Koseki, H., Hirakawa, S., Suga, Y., Seino, S., Nishimura, M., Kaisho, T., Hoshino, K., Kitamura, H., Nagase, T., Ohara, O. and Koga, H.

Prediction of the Coding Sequences of Mouse Homologues of KIAA

Gene: IV. The Complete Nucleotide Sequences of 500 Mouse

KIAA-Homologous cDNAs Identified by Screening of Terminal Sequences

of cDNA Clones Randomly Sampled from Size-Fractionated Libraries

DNA Res. 11, 205-218 (2004)

2 (bases 1 to 4025)

JOURNAL

REFERENCE

AUTHORS Okazaki, N., Kikuno, R.F., Nagase, T., Ohara, O. and Koga, H.
 TITLE Direct Submission
 JOURNAL Submitted (19-MAY-2004) Hirosaki Koga, Kazusa DNA Research Institute, Laboratory for Genome Informatics, 2-6-7 Kazusa-Kametari, Kisarazu, Chiba 292-0818, Japan (E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)
 COMMENT The CREATE program supported by Japan science and technology corporation; cDNA full insert sequencing; Kazusa DNA Research Institute; cDNA library construction, clone selection and 5'- & 3'-end one pass sequencing.
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 Best Local Similarity 58.3%; Pred. No. 2.8e-105;
 Matches 376; Conservative 145; Mismatches 124; Indels 0; Gaps 0;
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 Db 410 ATGAAGCTGAGATGATCTCTCTCATGAAGAGAGAGAGGTGAGGCCACCATGTAATG 469
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 BC053919
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 ACCESSION BC053919
 VERSION BC053919.1 GI:32172797
 KEYWORDS MGC.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 4169)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Caranci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Miliyah, S.J., Bosak, A.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hultk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E., Scherf, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16699-16903 (2002)
 12477932
 2 (bases 1 to 4169)
 Strausberg, R.
 Direct Submission
 Submitted (16-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Susan L. Sullivan, PhD.
 CDNA Library Preparation: ResGen, Invitrogen Corp.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbiology.org>
 contact: amadn@systemsbiology.org
 Anup Madan, Jessica Fahy, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
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ORIGIN

Query Match 71.5%; Score 461.2; DB 10; Length 4169;
Best Local Similarity 58.3%; Pred. No. 2.8e-105;
Matches 376; Conservative 145; Mismatches 124; Indels 0; Gaps 0;

QY 1 ATGCCGNTTYAAYMGVNTTYCCNTYNGCMNSNTYNTNATYATYGGTMSN 60
DB 308 ATGCGCTGCTCAACAGATGCTTCCCTAGCTCTCTAGTCTCATCTAGGTCAGA 367
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 19:47:17 ; Search time 434 Seconds
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 8780412

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	466	72.2	1261	10 ADB78651	Adb78651 Human ion
3	466	72.2	1261	10 ACFS7870	Acfs7870 Human SCN
4	466	72.2	1510	4 AAF84146	Aaf84146 Human nov
5	466	72.2	4052	6 ABA93727	Aba93727 Human sig
6	462.8	71.8	645	5 AAC90601	Aac90601 Rat sodiu
7	462.8	71.8	2220	3 AAC67836	Aac67836 Rat betas
8	462.8	71.8	2632	5 AAC90602	Aac90602 Rat sodiu
9	462.8	71.8	3108	5 AAC90600	Aac90600 Rat sodiu
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16	285.2	44.2	3531	5 AAS86763	Aas86763 DNA encod
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38	56.6	8.8	842	12 ADM66943	Adm66943 Murine ad
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40	52.6	8.2	6217	6 ABL32938	Ab32938 Human imm
41	51	7.9	5454	3 AAAT0236	Aat0236 Plasmodiu
42	49.6	7.7	2415	4 AAC84367	Aac84367 Human Zac
43	49.6	7.7	2415	10 ABX93334	Abx93334 Degenerat
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ALIGNMENTS

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5	cerebroprotective; vasotropic; cardiant; nootropic; cytostatic;				
6	dermatological; gene therapy; voltage-gated sodium channel; pain;				
7	epilepsy; stroke; ischaemia; heart disease; Jacobsen Syndrome;				
8	familial nonchromatin paraganglioma; phenylketonuria;				
9	Charcot Marie Tooth disease; ss.				
10	Homo sapiens.				
11	WO200063367-A1.				
12	26-OCT-2000.				
13	24-FEB-2000; 2000WO-BP001783.				
14	15-APR-1999; 99US-0129473P.				
15	(WARN) WARNER LAMBERT CO.				
16	(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.				
17	Cox P, Dixon A, Jackson A, Morgan K;				
18	WPI; 2000-665241/64.				
19	P-PSDB; AAB36002.				
20	Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium				
21	channel, and their corresponding polypeptides, useful for detecting and				
22	treating sodium channel-associated conditions, e.g. pain, epilepsy and				
23	stroke.				
24	Claim 10; Page 70-71; 88pp; English.				
25	The present sequence is given in the claims of a specification relating				


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Db      496 ATGAGCGCTGCTCATCTCTGATGAGAGAGAGGAGGAGCCACCGAGTGTG 555
Qy      181 GARTGTTTAAVMGNCNGARNGNGNAARGAYTTTATNTATNTATYGAARTAYMNAAYG 240
Db      556 GAATGTTCTACAGCCCGAGGGCGGTAAAGATTCTTATTTACAGATACGGAATGCG 615
Qy      241 CAYCARGARGTNGARWNSCNTTYTCARGNMGNTNCAFTGAAAYGGMNSNARGAAYTN 300
Db      616 CACGAGAGGTGAGAGCCCTTTCAGGGGCGCTGACGTGAATGCGACGAGACCTG 675
Qy      301 CARGAYGMMNSNATNACNGTNTTAAAYGTNACNTNAYGVMGNGYNTTAAVACNTGY 360
Db      676 CAGGACGTTCATCATCTGTGCTCAACGTCACTTGAAACGACTGTGCTTACACCTGC 735
Qy      361 AAYGTMNSMNGNARTTYGARTTYGARGCNCAYMNGCNTTYGTNAAACNACMNGYTN 420
Db      736 AATGTGTCGGGGAGTTTGAGTTGAGCGCGATCGGCCCTTTGTGAAGACACCGGCTG 795
Qy      421 ATNCCNTNMGNGTNAACNGARNGARNGCNGNGARAYTTTACNMSGNTNGTNSGADTN 480
Db      796 ATCCCCCTAAGAGTCACTGAGAGAGCTGAGAGAGACTTCACTGTGTCTCAGAAATC 855
Qy      481 ATGATGTAATNTNTNGTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNT 540
Db      856 ATGATGTACATCTCTGTGTCTTCTCACTGTGTGCTGCTCATGAGATGATATATTTGC 915
Qy      541 TAYMGNARGTNMSNARNGCNGARNGCNGCNGCNGARARAYGCMWSNGATAYTNGCN 600
Db      916 TACGAAAGGTCTCAAAAGCCGAAAGCCAGACCCCAAGAAAACGGGTCTGACTACCTTGCC 975
Qy      601 ATNCCMNSNGARAYAAARGARAAATWSNGCNGTNCNGTNGARAR 645
Db      976 ATCCATCTGAGAACAGAGAACTCTGCGGTACCACTGAGGAGAA 1020

```

RESULT 3

ACF57870
ID ACF57870 standard; cDNA; 1261 BP.

ACF57870;
15-JAN-2004 (first entry)

Human SCN3B protein encoding cDNA.
SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
neuroprotective; anesthetic; cytoprotective; cerebroprotective; cardiac;
hypotensive; gene therapy; SCN3B; human; gene; ss.

Homo sapiens.
Key CDS location/Qualifiers
376..1023
/*tag= a
/product= "SCN3B"

MO2003072751-A2.

04-SEP-2003.

25-FEB-2003; 2003WO-US006010.

25-FEB-2002; 2002US-0359382P.

(UYVA-) UNIV VANDERBILT.

George AL, Losein C;

WPI; 2003-712725/67.

P-PSDB; ABR83183.

Recombinantly expressed sodium channel type 1 alpha subunit, useful in

screening for modulators, for treating e.g. epilepsy.
Disclosure; Page 145-147; 176pp; English.
The invention relates to a recombinantly expressed and isolated human SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally incorporated into a cell, is used to screen for specific modulators, potentially useful as anticonvulsant, antiepileptic, neuroprotective, analgesic and/or anesthetic agents, e.g. for treating severe myoclonic epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis, motor endplate diseases, hypertension, congestive heart failure and muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic and metastatic cancer cell lines). These activities can also be provided by gene therapy vectors that express (I) or the modulators. The modulators, also antibodies directed against (I), are used to detect sodium channel polypeptides. The present sequence represents a human SCN3B protein encoding cDNA

Sequence 1261 BP; 263 A; 366 C; 372 G; 260 T; 0 U; 0 Other;

Query Match 72.2%; Score 466; DB 10; Length 1261;

Best Local Similarity 58.8%; Pred. No. 1.6e-117; Matches 379; Conservative 145; Mismatches 121; Indels 0; Gaps 0;

```

Qy      1 ATGCNCCNTTYAAYMGNNTTYCCNYTNGCMNSNTNGTNTATNTATYGGTWSN 60
Db      376 ATGCTCTCCCTTCAATATATATGTTTCCTCGCTTCTCTGCTATCTACTGGTCAGT 435
Qy      61 GTNTGTTTCNGNTNTYGTNGARNTCCNWSNARACNGARGCNGTNCARGNAAYCN 120
Db      436 GTCTGCTTCCCTGTGTGTGTGAGAGTCCCTCGAGACGAGGCGGTGACGAGGACCC 495
Qy      121 ATGAARYTNMGNTGYATNMSNTGYATGAAMNGARNGARGTNGARCNACNCTNGTN 180
Db      496 ATGAAGCTGCGCTCATCTCTCGATGAAGAAGAGAGGTGAGGACACCAACGCTGCTG 555
Qy      181 GARTGTTTAAVMGNCNGARNGNGNAARGAYTTTATNTATNTATYGAARTAYMNAAYG 240
Db      556 GAATGTTCTACAGCCCGAGGGCGGTAAAGATTCTTATTTACAGATACGGAATGCG 615
Qy      241 CAYCARGARGTNGARWNSCNTTYTCARGNMGNTNCAFTGAAAYGGMNSNARGAAYTN 300
Db      616 CACGAGAGGTGAGAGCCCTTTCAGGGGCGCTGAGAGAGACTTCACTGTGTCTCAGAAATC 675
Qy      301 CARGAYGTMNSNATNACNGTNTTAAAYGTNACNTNAYGVMGNGYNTTAAVACNTGY 360
Db      676 CAGGACGTTCATCATCTGTGCTCAACGTCACTTGAAACGACTGTGCTTACACCTGC 735
Qy      361 AAYGTMNSMNGNARTTYGARTTYGARGCNCAYMNGCNTTYGTNAAACNACMNGYTN 420
Db      736 AATGTGTCGGGGAGTTTGAGTTGAGCGCGATCGGCCCTTTGTGAAGACACCGGCTG 795
Qy      421 ATNCCNTNMGNGTNAACNGARNGARNGCNGNGARAYTTTACNMSGNTNGTNSGADTN 480
Db      796 ATCCCCCTAAGAGTCACTGAGAGAGCTGAGAGAGACTTCACTGTGTCTCAGAAATC 855
Qy      481 ATGATGTAATNTNTNGTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNT 540
Db      856 ATGATGTACATCTCTGTGTCTTCTCACTGTGTGCTGCTCATGAGATGATATATTTGC 915
Qy      541 TAYMGNARGTNMSNARNGCNGARNGCNGCNGCNGARARAYGCMWSNGATAYTNGCN 600
Db      916 TACGAAAGGTCTCAAAAGCCGAAAGCCAGACCCCAAGAAAACGGGTCTGACTACCTTGCC 975
Qy      601 ATNCCMNSNGARAYAAARGARAAATWSNGCNGTNCNGTNGARAR 645
Db      976 ATCCATCTGAGAACAGAGAACTCTGCGGTACCACTGAGGAGAA 1020

```

RESULT 4

AAF84146
ID AAF84146 standard; cDNA; 1510 BP.

XX

AC AAF84146;
 XX 07-SEP-2001 (first entry)
 XX Human novel sodium channel beta1-like subunit encoding cDNA.
 DE Sodium channel; sensory neurone specific channel, beta1-like subunit;
 KM SNS; therapeutic; pain; analgesic; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 213..860
 FT /tag= a
 FT /product= "sodium channel beta1-like subunit"
 XX
 XX WO200144293-A2.
 XX 21-JUN-2001.
 XX 14-DEC-2000; 2000MO-GB004802.
 XX 17-DEC-1999; 99GB-00029970.
 XX (GLAX) GLAXO GROUP LTD.
 XX Plumpston M, Powell AJ, Sansau P;
 XX WPI; 2001-398129/42.
 DR P-PSDB; AAB85206.
 XX Novel sub-unit for voltage-gated sodium channel proteins for producing
 PT agents useful for treating pain.
 XX Claim 4; Page 29-30; 31pp; English.
 XX The invention provides a novel beta1-like sub-unit for voltage-gated
 CC sodium ion channel polypeptide, specifically a sensory neurone specific
 CC channel (SNS) subunit. The novel beta1-like subunit is useful for
 CC producing a therapeutic agent which is useful treating pain in a patient.
 CC The subunit can be expressed by standard recombinant methodology. The
 CC present sequence represents a human novel sodium channel beta1-like
 CC subunit encoding cDNA
 CC
 SO Sequence 1510 BP; 350 A; 410 C; 414 G; 336 T; 0 U; 0 Other;
 Query Match 72.2%; Score 466; DB 4; Length 1510;
 Best Local Similarity 58.8%; Pred. No. 1.8e-117;
 Matches 379; Conservative 145; Mismatches 121; Indels 0; Gaps 0;
 QY 1 ATGCCGCGCTTAAAGNTNTTCCNYTNCNMSNTYNTNTAATNTATYGGGTMSN 60
 DB 213 ATCCCTGCGCTCAATGATGTTCCCTGCTTCTCTGCTATCTAAGGTCAGT 272
 QY 61 GTNTGTTCCGNTNTGTTNGARGTNCNMSNGARACNGARCGTNCARGNAAYCCN 120
 DB 273 GTCTGCTTCCCTGTGTGTGAAGTCCCTCGAGACGAGGCCCGTCAGGCAACCCC 332
 QY 121 ATCAATYTMNGTNTGATNTSNTGATGARMNGARGARGTNGARCNACNCGTNGTN 180
 DB 333 ATCAACCTGCGCTCAATCTCTCTCATGAAGAGAGAGAGCTGAGGCCACACGGTGTG 392
 QY 181 GATGTGTTTAAVNGNCNGARGGNGNAARGATTTTAAATNTAATNTAATYMGNAAYGVN 240
 DB 393 GAATGTGTTCAAGGCCCGAGGCGGGAAGATTTCTTAATTAACGATTCGGAATGGC 452
 QY 241 CAYCARGARGTNGARNSNCCNTTYTCARGGNGMYTNCARTGAAYGNSNAARGAYTN 300
 DB 453 CACCAAGAGGTGAGAGGCCCTTTCAAGGGGCGCTGAGTGAATGCAAGCAAGACCTG 512
 QY 301 CARGAYGTMSNAATNACNGTNTYTAAGTNAAGTNAAGTNAAGTNAAGTNAAGTNA 360
 DB 513 CAGGAGCTGTCACTCACTGTCTCAACGTCTGAACGACTGCGCTCTCAACCTGC 572

QY 361 AAATGTMNSMNGARGARTTYGARGCNCAVMGNCNTTYGTNARAONACNMGNNTN 420
 DB 573 AATGTGTCCCGGAGCTTGAAGTTCGCGCAATCGGCTTGTGAAGACGACGGCTG 632
 QY 421 ATNCCNYTMNGTNCNARGARCGNGNGARGATYTAACNWSNGTNGTNSNGARATN 480
 DB 633 ATCCCTTAAGATCCAGAGAGGCTGAGAGGATTCACCTCTGTGTCTCAGAAATC 692
 QY 481 ATGATGTAAATNTYNTNGTNTTYTNAACNYNTGTYTNTAATNGARATGATNTATG 540
 DB 693 ATGATGTACATCTCTTGTGTCTTCCACCTTGTGCTCTCATCAAGATGATATTTGC 752
 QY 541 TAYMGAARGTMSNARGNGARGNGGNCARAAVAGCNSNGATYATYNTGNCN 600
 DB 753 TACAGAAAGGTCTCAAAAGCGAAGAGGACCCCAAGAAAGCGCTGACTACTTGC 812
 QY 601 ATNCCNMSGARAAVARGARAAVWSNGNTNCCNGTNGARGAR 645
 DB 813 ATCCCATCTGAGAACAGAGAACTCTGCGTACCACTGAGAGAA 857
 RESULT 5
 ID ABA93727 standard; cDNA; 4052 BP.
 XX ABA93727;
 AC 30-APR-2002 (first entry)
 DT Human signal transduction cDNA clone amy2_2f18.
 XX Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
 KM gene therapy; ss.
 XX Homo sapiens.
 OS
 XX WO200198454-A2.
 XX 27-DEC-2001.
 XX 25-APR-2001; 2001WO-IB002050.
 XX 25-APR-2000; 2000US-0199380P.
 PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
 XX Wiemann S;
 PI WPI; 2002-055860/07.
 DR P-PSDB; ABB05689.
 XX Human cDNA sequences and clones derived from human fetal brain, fetal
 PT kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
 PT screening and therapy.
 XX Claim 1; Page 174-175; 611pp; English.
 XX The present invention describes assemblages and computer readable media
 CC comprising novel human cDNA sequences and clones derived from human
 CC foetal brain, foetal kidney, melanoma, testis and amygdala cDNA
 CC libraries. ABA93702 to ABA93766 represent human cDNA sequences from the
 CC present invention which encode the proteins given in ABB05662 to
 CC ABB05729. The human cDNA sequences and clones can be used in gene
 CC therapy. The clones may be used in a variety of applications, for example
 CC they may be used in profiling assays, for providing large arrays of human
 CC genetic material for implementing large-scale screening strategies and
 CC for treating diseases via gene therapy procedures
 SO Sequence 4052 BP; 994 A; 1033 C; 1036 G; 989 T; 0 U; 0 Other;
 Query Match 72.2%; Score 466; DB 6; Length 4052;
 Best Local Similarity 58.8%; Pred. No. 3.8e-117;

[illegible]

XX MPI: 2001-122743/13.

DR New rat sodium channel beta-3 subunit gene isolated from a rat dorsal

XX rat ganglion cDNA library for use in chromosome mapping, forensic

PT medicine, monitoring clinical trials and therapeutics.

XX

PS Claim 1; Page 40-41; 145pp; English.

XX

CC The present invention provides the protein and coding sequences of the

CC rat sodium channel beta protein, designated Alrxs945. This protein is

CC involved in the generation of pain and other sensory or perceptible nerve

CC impulses, in the establishment and endurance of mood, neurodegenerative

CC and sleep disorders, and in the control of muscle contraction, including

CC movements such as the heartbeat, digestion and vascular tone. The

CC sequences can be used in predictive medicine, screening and diagnostic

CC assays, and in pharmacogenomics

XX

SQ Sequence 645 BP; 155 A; 154 C; 181 G; 155 T; 0 U; 0 Other;

Query Match 71.8%; Score 462.8; DB 5; Length 645;

Best Local Similarity 58.4%; Pred. No. 7.4e-117;

Matches 377; Conservative 145; Mismatches 123; Indels 0; Gaps 0;

QY 1 ATGCCNGCNTYYAAMGMYTNTYCCNTYNCNMSNTYNGTNTYNTATNTAYTGGTSMNSN 60

DB 1 ATGCGTGCCTTCACAGATGTCTCCCTACCTTCTCTAGGCTCATCTACTGAGTCA 60

QY 61 GTMTGYTTCNCGNTGYGTNGARGTNCNMSNGARACNGARGCNGTCARGNAAYCN 120

DB 61 GTCTGCTTCCCTGTGTGTGTGTGAAAGTCCCTCGAGACAGAGCGGTGACAGGCAATCC 120

QY 121 ATGAARYTNMGNTGYATYNTMSNTGYATGAARWNGARGARGTNGARGCNACNCGTNGTN 180

DB 121 ATGAAGCTGAGATGTGATCTCTCGATGAAGAGGAGGAGGTGAGAGCCACCACTGTGTG 180

QY 181 GARGTGCTTYTAMGNCNGARGCNGNARARAYTTYNTATNTAYGARTATWGNAAAYGN 240

DB 181 GAGTGCTTCTACAGGCTGAGGGGGGTAAATATTCCTTATATATGATATCGGAATGGC 240

QY 241 CAYCARGARGTNGARMSNCCNTTYCARGGNGNTNCCARTGGAAYVGNWMSNARAGAYTN 300

DB 241 CACCAAGAAAGTGGAGAGCCCTTCCAGGCGCTGTGAGTGAATGGAGCAAGAAAGCTGTG 300

QY 301 CARGAYTNMSNATNACNGTNTYNAAYGTNACNTYNAAYGAYWSNGNTYNTAYACNTGY 360

DB 301 CAGAGCGATCATCATCTGTACTCAATGTACTCTTGAATGACTGTGGCTCTCAACATGTC 360

QY 361 AAYGTNMSNMGNGARTTYGARTTYGARGCNCAYMNCNTTYTGNAPACNACMNGNTN 420

DB 361 AATGTGTCACAGGAGTTCGAAATTCGAGGACACAGGCGCTTGTGTGAACACACAGGACTG 420

QY 421 ATNCCNNTNMNGNACNGARGCNGGNGNARGAYTTYACNMSNGTNGTMSNGARATN 480

DB 421 ATACCTTTCAGATCAGAAAGGCGGAGAGACCTTACCTCGTGCTCGGAAATTC 480

QY 481 ATGATGTATYATNTYNTNGTNTTYTNAACNTYNTGGYNTYNTATNGARATGATYATGY 540

DB 481 ATGATGTATCATCTCTGTGCTTCTCTCACTTGTGGCTGTTATGTAGATATCATATTGC 540

QY 541 TATWGNARAGTNSNARCGARGARGCNGCNCARARAYVGCNWSNGATYATYNTGN 600

DB 541 TACAGAAAGGTCTCTTAAGGCGGAAGAGCAGACAGGAAATGTGCTGACTACCTGTCT 600

QY 601 ATNCCNMSNGARAYAAARGAATWNSNGTNCNGTNGARGAR 645

DB 601 ATCCCTCAGAAACAGAGAACTCTGTGTACTGTGGAGAA 645

RESULT 7

ID AAC67836

XX AAC67836 standard; cDNA, 2220 BP.

XX

AC	AAC67836;	
DT	15-FEB-2001	(first entry)
DE	Rat beta3 subunit cDNA.	
XX		
XX	Rat; beta sub-unit; beta3; analgesic; anticonvulsant; cerebroprotective;	
KW	vasoregulatory; cardiac; nootropic; cytotactic; dermatological;	
KW	gene therapy; voltage-gated sodium channel; pain; epilepsy; stroke;	
KW	ischemia; heart disease; Jacobsen Syndrome;	
KW	familial nonchromaffin paraganglioma; phenylketonuria;	
XX	Charcot Marie Tooth disease; ss.	
OS	Rattus sp.	
XX		
PN	WO20006367-A1.	
PD		
XX	26-OCT-2000.	
PF		
XX	24-FEB-2000; 2000WO-EP001783.	
PR		
XX	15-APR-1999; 99US-0129473P.	
PA	(WARN) WARNER LAMBERT CO.	
XX	(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.	
PI		
XX	Cox P, Dixon A, Jackson A, Morgan K;	
DR	WPI; 2000-665241/64.	
XX	P-PSDB; AAB36001.	
PT		
XX	Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium	
PT	channel, and their corresponding polypeptides, useful for detecting and	
XX	treating sodium channel-associated conditions, e.g. pain, epilepsy and	
PT	stroke.	
PS		
XX	Claim 6, Page 69-70; 88pp; English.	
XX		
CC	The present sequence is given in the claims of a specification relating	
CC	to a novel family of beta sub-unit proteins from a voltage-gated sodium	
CC	channel. Human and rat beta sub-units, which have been collectively	
CC	identified as beta3, have been isolated. The polynucleotides and	
CC	polypeptides are useful for screening for agonists and antagonists of	
CC	sodium channels. The agonists, antagonists, proteins and nucleic acids	
CC	may be used diagnosing of treating diseases or conditions associated with	
CC	voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,	
CC	heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma,	
CC	Phenylketonuria and Charcot Marie Tooth disease	
XX		
XX	Sequence 2220 BP; 573 A; 557 C; 561 G; 529 T; 0 U; 0 Other;	

Query Match	71.8%;	Score 462.8;	DB 3;	length 2220;
Best Local Similarity	58.4%;	Pred. No. 1,8e-116;		
Matches	377;	Conservative 145;	Mismatches 123;	Indels 0; Gaps 0
Qy	1	ATGCCGNCNTTYAAWMENYNTTYCCNYTNGCNSMNYNTGNTYTNATYTAATYGGTWNMSN	60	
Db	363	ATGCTCGCTTCAACAGATGCTTCCCTAGCTTCTTAGTGTCTCATCTCACTGGCTCAGA	422	
Qy	61	GTNTGYTTCGNGTNTGYGTNGARBTNCCMSNGARACNGARGCNGTNCARBGAAYCCN	120	
Db	423	GTCGCTTCCCTGTGTGTGTGAATGCTCTCGAGACAGAAACCGTGCAGGGCAATCCC	482	
Qy	121	ATGAARYTMCNTGYATYNTMSNTGYTAAPRMNGARGARTNGARGACNACNCGTNGTN	180	
Db	483	ATGAAGCTGAGAGTGCATCTCTCGCATGAAGAGGAGAGGTGAGAGGCCACCACTGTGTG	542	
Qy	181	GARTGCTTYTYAMGNCNGARGGNGNARGAYTYYTYTNATYNTAYGARTAYMGNAYGN	240	
Db	543	GAGTGCTTCAACAGGCTGAGGGCGGTAAAGATTTCTTATATATGAGATGGAATGGC	602	
Qy	241	CATCARGARGTNGARGMSNCNTTYCARGNMGTNTNCARTGGAATGGMNSNARAYTNTN	300	

Db	603	CACACAGAAAGTGAGAGGCCCTTCCAAAGCCGTCGACAGTGAAATGGGAGCAAGAACCTG	662
Qy	301	CAGACAGTMSNAATNACNGTNTYTNAAYGTNACNTNAAVGAYSNGNGNYNTNAYACNTG	366
Db	663	CAGGACGATTCACATCACTGTACTCAATATCACTTGAATGACTGTGCCTCTTCACACATGC	722
Qy	361	AAVGTMSMWNGARTTYTGATTTYGARGCNCAYMNCNTTYGTNAARACNACMNGYTN	420
Db	723	AATGTGTCCAGGAGATTGCMAATTCCAGGACACACAGCCTTTTGTGMAAGACCAAGACCTG	782
Qy	421	ATNCNYYTMWNGTNAACNGARGCNGNGARGAYTTTACNWSNGTNGTMSNGARATN	480
Db	783	ATACCTTTGGAGTCACTGAAGGCGGGAAGACCTTCACTCGTGGTCTCGGAATC	842
Qy	481	ATGATGTAYATNTYNTNGTNTTYYTNAACNTYNTGGTYNTNATNAGARATGATATATGY	540
Db	843	ATGATGTACATCCTCCTGGTCTTCTTCACTTGTGTGCTGTTATTTGAGATGATCTATTTGC	902
Qy	541	TATMGNAAGTMSNABRNCNGARABRNCNCGARBARAYGCMWSNGAYTAYTNGN	600
Db	903	TACAGAAAGTCTCTAAGGCCGAGAGGACAGCAAGAAAATGCGTCTGACTACCTTGCT	962
Qy	601	ATNCNWSNGARAAYARAGARAAVYNSNCNGTNCNGTNGARGAR	645
Db	963	ATCCCTTCCAGAGACAGAGNAATCTGTGTGTAACCTGTGTGAGGAA	1007

XX	RESULT 8
XX	AAC90602
ID	AAC90602 standard; DNA; 2632 BP.
XX	
AC	AAC90602;
XX	
DT	13-MAR-2001 (first entry)
XX	
DE	Rat sodium channel beta3 protein Alrx94h5 related sequence.
XX	
KM	Rat; sodium channel beta3 protein; Alrx94h5; pain, sleep disorder;
KM	neurodegenerative disorder; mood disorder; muscle contraction; ds.
XX	
OS	Rattus sp.
XX	
PN	WO20069912-A1.
XX	
PD	23-NOV-2000.
XX	
PF	12-MAY-2000; 2000WO-US013144.
XX	
PR	14-MAY-1999; 99US-0134198P.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
XX	
P1	Curtis RAJ;
XX	
DR	WPI; 2001-122743/13.
XX	
PT	New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
PT	root ganglion cDNA library for use in chromosome mapping, forensic
PT	medicine, monitoring clinical trials and therapeutics.
XX	
PS	Claim 1; Page 41-42; 145pp; English.
XX	
CC	The present invention provides the protein and coding sequences of the
CC	rat sodium channel beta3 protein, designated Alrx94h5. This protein is
CC	involved in the generation of pain and other sensory or perceptive nerve
CC	impulses, in the establishment and endurance of mood, neurodegenerative
CC	and sleep disorders, and in the control of muscle contraction, including
CC	movements such as the heartbeat, digestion and vascular tone. The
CC	sequences can be used in predictive medicine, screening and diagnostic
CC	assays, and in pharmacogenomics
XX	
XX	Sequence 2632 BP; 693 A; 636 C; 611 G; 692 T; 0 U; 0 Other;

Query Match 71.8%; Score 462.8; DB 5; Length 2632;
Best Local Similarity 58.4%; Pred. No. 2.1e-116;
Matches 377; Conservative 145; Mismatches 123; Indels 0; Gaps 0;

QY 1 ATGCNCNTTAAVMGNVNTTTCNTYNGCNMSNYNTGNTYNTATNTATYATGGGTMSN 60
DB 78 ATGCTGCTTCAACAGATTCTCTCCCTAGCTTCTAGTGTCTATCTAGGTGCGA 137
QY 61 GTNTGTTTCGNTGT 120
DB 138 GTCTGCTTCCCTGT 197
QY 121 ATGAATYNTMNTGATYNTMNTGATYNTMNTGATYNTMNTGATYNTMNTGATYNT 180
DB 198 ATGAAGCTGAGGTGATCTCTGTGATGAAGAGGAGGAGGAGGAGGAGGAGGAGG 257
QY 181 GARTGTTTAAVMGNCCNGARNGNGNAAAGATTTTNTATNTATNTATNTATNTATNT 240
DB 258 GAGTGTCTTACAGGCTGAGGCGGTAAAGATTTCTTATATATAGTATCGGAATGC 317
QY 241 CAYCARGARGTNGARWNSCNTTYCARGANNNTNCTARTGAAVYGNMSNAARGAYTN 300
DB 318 CACGAGGAGAGTGAGAGCCCTTCCAGGCCGTCTGAGTGAATGGAGCAAGACCTG 377
QY 301 CARGAYGTMSNATNACNGTNTTAAVGTNACNTTAAVYGNMSNGNTTATYACNTGY 360
DB 378 CAGGACGTATCTCATCTGATCTCATATGTCACTTGAATGACTGTGGCTCTACCATGC 437
QY 361 AAYGTMSNMNGARTTYGARTTYGARGCNCAYMNCNTTYGTNTAARACNACMNGYTN 420
DB 438 AATGTGTTCAGGAGGAGTGTGATTTGAGGACACAGGCTTTTGTGAAGACACAGACTG 497
QY 421 ATNCCNTYNTMNGTNAACNGARNGCNGNGNGARAYTTTACNMSNGTNGMSGARATN 480
DB 498 ATACCTTTCGAGTCACTGAGAGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 557
QY 481 ATGATGTAAVNTYNTYNTGNTTYYTNAANTYNTGTYNTNTATNTGAAATGATYATGY 540
DB 558 ATGATGTAACTCTCTGCTGTCTCTCACTTGTGGCTGTTATATGATATCTATATTC 617
QY 541 TAYMGNARGTMSNARNGCNGARNGCNGCNGARBARAYGCMWSNGATYATYNGCN 600
DB 618 TACGAAAGGTCTTAAGCGCGAAGAGGACAGACAGGAAATGCGTCTGACTACTGCT 677
QY 601 ATNCCMSNGARAAVYARBARAYWSNGCNGTNGCNGTNGARBAR 645
DB 678 ATCCCTTCAGAGAACAGAGAACTCTGTGTACTGTGTGAGAGAA 722

RESULT 9
AAC90600 standard; cDNA; 3108 BP.
AAC90600;
AAC90600;
13-MAR-2001 (first entry)
Rat sodium channel beta3 protein A19x94h5 coding sequence.
Rat sodium channel beta3 protein; A19x94h5; pain; sleep disorder;
neurodegenerative disorder; mood disorder; muscle contraction; ss.
Rattus sp.
W0200069912-A1.
23-NOV-2000.
12-MAY-2000; 2000MO-US013144.
14-MAY-1999; 99US-0134198P.
(MILL-) MILLENNIUM PHARM INC.

XX XX
PI Curtie RAI;
XX WPI; 2001-122743/13.
DR P-PSDB; AAB50243, AAB50245.
PT New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
PT root ganglion cDNA library for use in chromosome mapping, forensic
PT medicine, monitoring clinical trials and therapeutics.
XX PS
XX Claim 1; Fig 1; 145pp; English.
XX CC
XX The present invention provides the protein and coding sequences of the
XX rat sodium channel beta3 protein, designated A19x94h5. This protein is
XX involved in the generation of pain and other sensory or perceptive nerve
XX impulses, in the establishment and endurance of mood, neurodegenerative
XX CC and sleep disorders, and in the control of muscle contraction, including
XX movements such as the heartbeat, digestion and vascular tone. The
XX sequences can be used in predictive medicine, screening and diagnostic
XX assays, and in pharmacogenomics
XX SQ
Sequence 3108 BP; 830 A; 748 C; 727 G; 803 T; 0 U; 0 Other;

Query Match 71.8%; Score 462.8; DB 5; Length 3108;
Best Local Similarity 58.4%; Pred. No. 2.4e-116;
Matches 377; Conservative 145; Mismatches 123; Indels 0; Gaps 0;

QY 1 ATGCNCNTTAAVMGNVNTTTCNTYNGCNMSNYNTGNTYNTATNTATYATGGGTMSN 60
DB 78 ATGCTGCTTCAACAGATTCTCTCCCTAGCTTCTAGTGTCTATCTAGGTGCGA 137
QY 61 GTNTGTTTCGNTGT 120
DB 138 GTCTGCTTCCCTGT 197
QY 121 ATGAATYNTMNTGATYNTMNTGATYNTMNTGATYNTMNTGATYNTMNTGATYNT 180
DB 198 ATGAAGCTGAGGTGATCTCTGTGATGAAGAGGAGGAGGAGGAGGAGGAGGAGG 257
QY 198 ATGATGTAAVNTYNTYNTGNTTYYTNAANTYNTGTYNTNTATNTGAAATGATYATGY 240
DB 258 ATGATGTAACTCTCTGCTGTCTCTCACTTGTGGCTGTTATATGATATCTATATTC 317
QY 241 TAYMGNARGTMSNARNGCNGARNGCNGCNGARBARAYGCMWSNGATYATYNGCN 300
DB 318 TACGAAAGGTCTTAAGCGCGAAGAGGACAGACAGGAAATGCGTCTGACTACTGCT 377
QY 301 CAYCARGARGTNGARWNSCNTTYCARGANNNTNCTARTGAAVYGNMSNAARGAYTN 360
DB 378 CACGAGGAGAGTGAGAGCCCTTCCAGGCCGTCTGAGTGAATGGAGCAAGACCTG 437
QY 378 CARGAYGTMSNATNACNGTNTTAAVGTNACNTTAAVYGNMSNGNTTATYACNTGY 420
DB 438 CAGGACGTATCTCATCTGATCTCATATGTCACTTGAATGACTGTGGCTCTACCATGC 497
QY 421 AAYGTMSNMNGARTTYGARTTYGARGCNCAYMNCNTTYGTNTAARACNACMNGYTN 480
DB 498 AATGTGTTCAGGAGGAGTGTGATTTGAGGACACAGGCTTTTGTGAAGACACAGACTG 557
QY 481 ATNCCNTYNTMNGTNAACNGARNGCNGNGNGARAYTTTACNMSNGTNGMSGARATN 540
DB 498 ATACCTTTCGAGTCACTGAGAGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 557
QY 481 ATGATGTAAVNTYNTYNTGNTTYYTNAANTYNTGTYNTNTATNTGAAATGATYATGY 540
DB 558 ATGATGTAACTCTCTGCTGTCTCTCACTTGTGGCTGTTATATGATATCTATATTC 617
QY 541 TAYMGNARGTMSNARNGCNGARNGCNGCNGARBARAYGCMWSNGATYATYNGCN 600
DB 618 TACGAAAGGTCTTAAGCGCGAAGAGGACAGACAGGAAATGCGTCTGACTACTGCT 677
QY 601 ATNCCMSNGARAAVYARBARAYWSNGCNGTNGCNGTNGARBAR 645
DB 678 ATCCCTTCAGAGAACAGAGAACTCTGTGTACTGTGTGAGAGAA 722

RESULT 10

AAK52345
ID AAK52345 standard; cDNA; 1045 BP.
XX
AC AAK52345;
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 890.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
XX (HYSE-) HYSEQ INC.
PI Tang YT, Liu C, Dmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
XX
XX MPI; 2001-476283/51.
XX P-PSDB; AAM79212.
DR
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
XX Claim 1; Page 2934-2935; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 1045 BP; 222 A; 289 C; 314 G; 220 T; 0 U; 0 Other;

Query Match 65.9%; Score 424.8; DB 4; Length 1045;
Best Local Similarity 58.7%; Pred. No. 3,2e-106;
Matches 348; Conservative 133; Mismatches 114; Indels 0; Gaps 0;

QY 1 ATGCCGNCNTTAAVGNNTNTTCCNYINGCNMSVNTGNTNTATNTATYTGCGTNMSN 60
DB 302 ATGCCGTCCTCAATGATGATGTTCCCTGCTCTCTCTGCTTACTCTGCTCAAGT 361
QY 61 GTTGTGTTTCGATGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNTGNT 120
DB 362 GTCTGCTTCCCTGTGTGTGTGGAAGTGCCTCGAAGAGGCGGTGCAAGCAACCCC 421

QY 121 ATGAARYTNMGNTGYATNMSNTGYATGAARMGNGARGGTNGARGCNAACNGTNGTN 180
DB 422 ATGAAGCTGCGCTGCATCTCTGTCATGAAGAGAGAGAGGTGAGGCCACACGGTGTG 481
QY 181 GARTGTTTAAVGNCCNGARGGNGNNAARGAYTTTNTATNTAVGARTAVGNNAVGN 240
DB 482 GAATGTTCTACAGGCCCGAGGCGGTAAAGATTCTTAATTTACGATATCGAATGCG 541
QY 241 CAYCARGARTGARGNSCNTTTCARGGMMGNTNCAATGGAAYGNSNARGAYTN 300
DB 542 CACGAGAGGTGAGAGGCCCTTTCAGGGGCCCTGCACTGGAATGCGCAAGGACCTG 601
QY 301 CARGAYTNMSNATNACNGTNTNTNAAVGTNACNTTAAVGAWSNGNTNTAYACNTGY 360
DB 602 CAGGAGCTGCATCCTGCTGCTCAACGTCACTGTAAGCACTGCGCTCTACACTGCG 661
QY 361 AAVGTNMSMNGARTTGYARTTGYARGNCAYMGNCCNTTGTNTAARACNMGNTYN 420
DB 662 AATGTGTCCTGGGAGTGTGAGTGTGAGCGCATCGCCCTTGTGMAAGCAGCGCGCTG 721
QY 421 ATNCCNYTMNGTNAACNARGARGCGNGNGARGAYTTTACNMSNGTNGTNGARATN 480
DB 722 ATCCCTTAAGAGTACCGAGAGGCTGAGAGACTTCACTGTGTGTTCAAGAAATC 781
QY 481 ATGATGATATNT 540
DB 782 ATGATGTACATCTTCTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 841
QY 541 TAYMGNANGTNMSNARGCNGARGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGC 593
DB 842 TACAGAAAGTCTCAAAAGCCGAAAGAGGAGCGCCCAAGAAACCGCTAAGTCCA 894

RESULT 11

AAH98320
ID AAH98320 standard; cDNA; 978 BP.
XX
XX AAH98320;
AC
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST-derived coding sequence SEQ ID NO: 177.
XX
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostic; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition; ss.
XX
XX Homo sapiens.
XX
XX WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002687.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
XX
XX (HYSE-) HYSEQ INC.
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Dmanac RA, Zhang J, Wehrman T;
XX
XX MPI; 2001-476164/51.
XX P-PSDB; AAM23661.
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
XX Claim 1; Page 299-300; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA
 CC of the invention

XX Sequence 978 BP, 193 A; 283 C; 293 G; 209 T; 0 U; 0 Other;

Query Match 63.9%; Score 412.4; DB 4; Length 978;

Best Local Similarity 56.3%; Pred. No. 8.1e-103;

Matches 363; Conservative 139; Mismatches 141; Indels 2; Gaps 2;

QY 1 ATGCNCNCTTAAAYMGNNTTCCNTYNGCMNSNTYNTNATNTATYATGGTMSN 60
 DB 295 ATGCTGCTTCAATAGATTGTTCCCTGCTCTCTCGTCTTACTGAGTCACTG 354
 QY 61 GTNTGTTTCNGNTGTGTGATGATGATGATGATGATGATGATGATGATGATG 120
 DB 355 GTCTGCTTCCCTGTGTGTGTGATGATGATGATGATGATGATGATGATGATG 414
 QY 121 ATGAARYTNNMNTGATNTMTGATGAABMGNGARGGTNGARGCNAACNGTNTN 180
 DB 415 ATGAAGCTGGCGCTCATCTCTGATGATGAAGAGAGAGAGAGAGAGAGAGAG 474
 QY 181 GARTGTTTAAVMGNCNGARGNGNAAAGATTTTATNTATNTATNTATNTATNTA 240
 DB 475 GAATGTTTCAAGCGCCGAGGGGGGTAAAGATTTCTTATTTACGATATCGAAT 534
 QY 241 CAYCARGARGTNGARMSNCTTTCARNGMNGNTNARTGAAAYGMSNAARAYTN 300
 DB 535 CACGAGAGGTGAG 594
 QY 301 CARGAYGTMNSNATNACNGTNTTAAVGTNAANTNAYGMSNGNTTATYACNTG 360
 DB 595 CAGAGAGGTGATCATCTGCTCAACGCTCACTGGAACGACTGCGCTCTACACCT 654
 QY 361 AAYGTNNSMNGARTTGTGATGARGCNCAMGNCNTTGTGTAACACMNGNTN 420
 DB 655 AATGTGTCCTCGGAGATTGATGAGCGCATCGGCCCTTGTGAGAACACCGGCT 714
 QY 421 ATNCCNTYNNMNGTNAACNGARGAGCGNGARGAGATTTTACMNSNGTNGM 480
 DB 715 ATCCCCCTAAGAGTCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 774
 QY 481 ATGATGTAAATNTNTNTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNT 539
 DB 775 ATGATGTAAATNTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNT 834
 QY 540 YTAGNNAARGTNNNAARGNGARGAGCGNGCNCARGARAAAYGCMNSNGATY 598
 DB 835 CTACAGAAAGGTGATTCACAGACGAAACGAGGCCCAACAGAAACGAGTGC 894
 QY 599 CNAATCCMNSGADAAAYAAAGARAAAYMSNGNTNCCNGTNGARG 643
 DB 895 CGATTCCATTGTGAGAAACGAGAAATCTTCGTACCTGCGGGG 939

RESULT 12

ADSI1487 ID ADSI1487 standard; DNA; 978 BP.

XX AC ADSI1487;

XX DT 16-DEC-2004 (first entry)

XX DE Human therapeutic contig DNA - SEQ ID 1724.

XX KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
 inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;

KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.

XX Homo_sapiens.

XX MO2004080148-A2.

XX 23-SEP-2004.

XX 30-SEP-2003; 2003WO-US030720.

XX 02-OCT-2002; 2002US-0416186P.

XX (NUVE-) NUVELO INC.

XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y,
 PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;

XX WPI: 2004-668857/65.

XX P-PSDB; ADSI2085.

PT New polynucleotide, useful in preparing a composition for diagnosing or
 PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
 PT aplastic anemia or cancer for promoting wound healing.

XX Example 2: SEQ ID NO 1724; 718bp; English.

CC The invention relates to a novel isolated polynucleotide and the encoded
 CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
 CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
 CC be useful in preparing a composition for diagnosing or treating
 CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
 CC disorders, such as aplastic anaemia or cancer, as well as for promoting
 CC wound healing. The molecules may also be utilised during gene therapy
 CC procedures. The current sequence is that of a human therapeutic contig
 CC DNA of the invention. The current sequence is not shown explicitly within
 CC the specification but can be accessed from the WIPO web-site.

XX Sequence 978 BP, 193 A; 283 C; 293 G; 209 T; 0 U; 0 Other;

Query Match 63.9%; Score 412.4; DB 13; Length 978;

Best Local Similarity 56.3%; Pred. No. 8.1e-103;

Matches 363; Conservative 139; Mismatches 141; Indels 2; Gaps 2;

QY 1 ATGCNCNCTTAAAYMGNNTTCCNTYNGCMNSNTYNTNATNTATYATGGTMSN 60
 DB 295 ATGCTGCTTCAATAGATTGTTCCCTGCTCTCTCGTCTTACTGAGTCACTG 354
 QY 61 GTNTGTTTCNGNTGTGTGATGATGATGATGATGATGATGATGATGATGATG 120
 DB 355 GTCTGCTTCCCTGTGTGTGTGATGATGATGATGATGATGATGATGATGATG 414
 QY 121 ATGAARYTNNMNTGATNTMTGATGAABMGNGARGGTNGARGCNAACNGTNTN 180
 DB 415 ATGAAGCTGGCGCTCATCTCTGATGATGAAGAGAGAGAGAGAGAGAGAGAG 474
 QY 181 GARTGTTTAAVMGNCNGARGNGNAAAGATTTTATNTATNTATNTATNTATNTA 240
 DB 475 GAATGTTTCAAGCGCCGAGGGGGGTAAAGATTTCTTATTTACGATATCGAAT 534
 QY 241 CAYCARGARGTNGARMSNCTTTCARNGMNGNTNARTGAAAYGMSNAARAYTN 300
 DB 535 CACGAGAGGTGAG 594
 QY 301 CARGAYGTMNSNATNACNGTNTTAAVGTNAANTNAYGMSNGNTTATYACNTG 360
 DB 595 CAGAGAGGTGAG 654
 QY 361 AAYGTNNSMNGARTTGTGATGARGCNCAMGNCNTTGTGTAACACMNGNTN 420
 DB 655 AATGTGTCCTCGGAGATTGATGAGCGCATCGGCCCTTGTGAGAACACCGGCT 714
 QY 421 ATNCCNTYNNMNGTNAACNGARGAGCGNGARGAGATTTTACMNSNGTNGM 480

QY 301 CARGAYGTMNSNATNACNGTNTNAAYGTNACNYTNAAYGAYMSNGNNTNTAYACNTGY 360
 Db 328 CAGGACGTGTCCATCACTGTGCTCAAGTCACTGTGAGACTGTGGCCTCTACACTGC 387
 QY 361 AAYGTNMSNMNGARTTYGARITTYGARGCNCAYMGNCNTTYGTNAARACNACMGNTYN 420
 Db 388 AATGTGTCCCGGAGTTTGAGITTYGAGGCGCATCGGCCCTTGTGAAGACGACGCGGCTG 447
 QY 421 ATNCCNYTNNNGT 434
 Db 448 ATCCCCCTAAGAGT 461

Search completed: April 7, 2005, 21:46:50
 Job time : 438 secs

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OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 21:25:38 ; Search time 164 Seconds

(without alignments)
6435.357 Million cell updates/sec

Title: US-09-977-579-2-REV

Perfect score: 645

Sequence: 1 ATGCCNCCNTTAAATMGNT.....SNGCNGTNCNCTGANGAR 645

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813859 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	155.6	24.1	617	US-09-949-016-2369	Sequence 2369, Ap
2	60	9.3	1141	US-09-806-708B-22	Sequence 22, Appl
3	57.8	9.0	11174	US-09-949-016-14111	Sequence 14111, A
4	57.8	9.0	30337	US-09-949-016-13053	Sequence 13053, A
5	56.4	8.7	1141	US-09-806-708B-22	Sequence 22, Appl
6	53.8	8.3	7218	US-08-233-463-14	Sequence 22, Appl
7	53.4	8.3	832	US-09-621-976-2813	Sequence 2813, Ap
8	51.6	8.0	505	US-09-621-976-15639	Sequence 15639, A
9	50.4	7.8	474	US-09-621-976-18033	Sequence 18033, A
10	50	7.8	832	US-09-621-976-2813	Sequence 2813, Ap
11	48.6	7.5	505	US-09-621-976-15639	Sequence 15639, A
12	46.2	7.2	399	US-09-621-976-8976	Sequence 8976, Ap
13	46	7.1	1342	US-09-949-016-787	Sequence 787, Ap
14	46	7.1	1708	US-09-949-016-4948	Sequence 4948, Ap
15	46	6.9	399	US-09-621-976-8976	Sequence 8976, Ap
16	44.8	6.9	474	US-09-621-976-18033	Sequence 18033, A
17	44.2	6.9	1055	US-09-806-708B-23	Sequence 23, Appl
18	44.2	6.6	430	US-09-621-976-16565	Sequence 16565, A
19	42.2	6.5	1055	US-09-806-708B-23	Sequence 23, Appl
20	41.6	6.4	7568	US-08-694-869-2	Sequence 2, Appl
21	41.6	6.4	7568	US-09-349-546-2	Sequence 2, Appl
22	41.6	6.4	7568	US-09-502-831-2	Sequence 2, Appl
23	41.2	6.4	1176	US-09-072-384-16	Sequence 16, Appl
24	40.8	6.3	101011	US-09-949-016-16933	Sequence 16933, A
25	40.4	6.2	423	US-09-621-976-16656	Sequence 16656, A
26	40.2	6.2	423	US-09-431-480-15	Sequence 15, Appl
27	40.2	6.2	423	US-09-617-302-15	Sequence 15, Appl

C	28	40	6.2	819	3	US-09-288-143-18	Sequence 18, Appl
	29	40	6.2	2681	1	US-08-070-165F-9	Sequence 9, Appl1
	30	40	6.2	2681	2	US-08-885-418-9	Sequence 9, Appl1
	31	39.6	6.1	601	4	US-09-949-016-124797	Sequence 124797, A
	32	39.6	6.1	1497	4	US-09-220-132-94	Sequence 94, Appl
	33	39.6	6.1	2135	4	US-08-933-711B-17	Sequence 17, Appl
	34	39.6	6.1	192302	4	US-09-949-016-15270	Sequence 15270, A
	35	39	6.0	70088	4	US-09-949-016-16845	Sequence 16845, A
	36	39	6.0	129778	4	US-09-949-016-16845	Sequence 16845, A
	37	39	6.0	129778	4	US-09-949-016-12191	Sequence 12191, A
	38	39	6.0	580073	4	US-08-545-528D-1	Sequence 1, Appl1
	39	38.8	6.0	106418	4	US-09-949-016-13974	Sequence 13974, A
	40	38.8	6.0	228851	4	US-09-949-016-13781	Sequence 13781, A
	41	38.4	6.0	364	4	US-09-621-976-17202	Sequence 17202, A
	42	38.4	6.0	601	4	US-09-949-016-69577	Sequence 69577, A
	43	38.2	5.9	546	4	US-09-134-000C-861	Sequence 861, App
	44	38.2	5.9	601	4	US-09-949-016-161346	Sequence 161346, A
	45	38.2	5.9	907	3	US-09-209-525-1	Sequence 1, Appl1

ALIGNMENTS

```
RESULT 1
US-09-949-016-2369
Sequence 2369, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASCSEQ for Windows Version 4.0
SEQ ID NO 2369
LENGTH: 617
TYPE: DNA
ORGANISM: Human
US-09-949-016-2369

Query Match 24.1%, Score 155.6, DB 4, Length 617;
Best Local Similarity 39.2%, Pred. No. 1.3e-36;
Matches 230; Conservative 97; Mismatches 239; Indels 21; Gaps 3;

66 YTTCCNGTGTGTCNGARCTCCNMGNGARCGNCGTNCARGNAAVCNATGAA 125
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
11 CTGCGGGGGGCTGCTGAGGTGAGCTCGAGACCGAGCCGTGATGCGATCTTCAA 70

126 RYTNMGTYATYTNMSTGYATGAARMNGARGARGTNGARCNACNCGTNGARTG 185
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
71 AATCTTGATCTCTCCGCAAGCGCCGACGAGACCAACGCTGAGACCTTCAACGAGTG 130

186 GTTATATMGCCNGARCGNNGNARGAATYTTTNA-----TNTATGARTATMNA 236
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
131 GACCTTCGCGCAAGGCGACCTGAGGAGTTTGCAAGATCTCGCGCTATAGATGAGGT 190

237 YGNCACACGARGTNGARNMNCNTTYCARGMNGYTCARTGAAV-----CG 287
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
191 GTTGACACTGAGAGAGATGAGCGCTTCGAGGCGCGGTGTGATGAGACGCGGG 250

288 NMSNARGATYTNCAARGAYTNTSMNATNACNGTNTNAAYTNACNTNAYGAYMSNG 347
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
251 CACCAAGACCTGAGAGATCTGTCTATCTTCATCAACCAAGTCACTTCAACGCGG 310

348 NNTNTATACNTGYAAVGTNMNNGNARTTYGARTTYGARGCNCAVYNGNCNTTYGTNA 407
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Db 311 CGACTACGAGTGCACAGTCTACACCGCCCTCTCTTCTGAAAACTAGACAGACAACACG 370
Qy 408 RACNACMNGYNTATNCCNTYNTNGNTNACNGARGCNGGARGAYTTVA CNMSNGT 467
Db 371 CGTCGTCAAGAAATCCACATGAGTAGTGACAAAGCAACAGACATGCGATCCAT 430
Qy 468 NGTNMNGARATNATGATGTAATNTYNTNTYNTNTYNTNACNTYNTGTNTNTATNGA 527
Db 431 CGGTCTGAGATCATGATGATGTGCTCATTTGTGTGTGACATATGCTGCTGCACGA 490
Qy 528 RATGATNTATYGTATYAGNAGRTNMSNARGCNGARGAR---GCNGCNGARGARAAYGC 584
Db 491 GAGGATTTACTGCTACAGAAAGATCGCTGCCGCCACGAGACTGCTGCACAGAGAATGC 550
Qy 585 NMSNGAYTATYNTGNCNATNCCNMSNGARAAAYARBARAYWSNGCNG 631
Db 551 CTGGAATACCTGCGCATCCTCTGAAAGCAAGAACTGCACGG 597
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RESULT 2

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US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.T., L.a., and B.n. PAB1 promoters
US-09-806-708B-22
```

Query Match 9.3%; Score 60; DB 4; Length 1141;

Best Local Similarity 10.5%; Pred. No. 2.5e-07; Matches 64; Conservative 217; Mismatches 311; Indels 0; Gaps 0;

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Qy 15 YMGNTNTTTCYTCNTYNGCMNSNTYNTNTATNTATYTGCGTWSNGTNTGYTTCNGT 74
Db 764 THTDWCYKTMNTMYMDMTTMTTTRNTTSTNTNNNNNNMMACTNNNNNNMMKAYY 705
Qy 75 NTGYGTNGARGTNCNWSNGARGCNGGNTNCARGNAAYCNAATGAATYTNMGNTG 134
Db 704 AATNTNMGCMWNTTDRNTNTTVMRRRMTNTKTWYSTTRRHATYGTATNNNNNNNN 645
Qy 135 YATNMGNTGATGAAHMGNGARGARGTNGACNACGNTGNTGARTGTTATYAG 194
Db 644 NNNNNNSCTCTMTMTTRMTKDGMTVRKKVRRDTTCTTYVDVMDSVWMTYANMRRC 565
Qy 195 MCCNGARGGNGNAGAYTTTNTATNTATYAGARTAYMGNAAYGNCAYCARGARTNGA 254
Db 584 DVTYTNNTYCKSYASWYWSNNAWYRYARSANSSMARWTTTRNNMMMSGVRMRWAG 525
Qy 255 RMSNCCNTTYCARGNGNTNCARTGGAAYGNGNAAAGAYTTNCARGAYGTMSNAT 314
Db 524 TMMWRHNNNNNTTTRYYMMWRBARBTTYTYSMCNAKSWRGNRRAMMMMAANNDA 465
Qy 315 NACNGNTNTAAAGTACNTNATNAYGAYMSNGNTNTATYACNTGYAAAYGTNSMNGNA 374
Db 464 AMDHWTYMGNGNTTMMRRARWMMMAWCRPACNNNNNNRACVHHGKRMWTKWTMCA 405
Qy 375 RTTYGARTTYGARGCAYWNCNTTYGTNABACNACMNGYNTAATNCNTYTNMGNT 434
```

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Db 404 ACNNNNBKAMMYRVMAMMTSRDTNTDMMWMTSDHMMHYTYDTYMRAMNNNNNNMB 345
Qy 435 NACNGARGCNGGNGARGAYTTVA CNMSNGTNTNMSNGARATNATGATGATATNTY 494
Db 344 CTTSSMMWMDHNTHTCTYGNNTWGSAYBMAAMSMWAAASBVTYNMCRRMTYMGKMT 285
Qy 495 NTYNTGNTTYNTNACNTYNTGTYNTNTATNTNGARATGATNTATYGTATYMGNAARGTNS 554
Db 284 NNNNNKAYTYRTKYAVMCNNRYDTAVTBKRNKYCYAYBWTYBMTMGKHMBMR 225
Qy 555 NARGCNGARGCNGCNGCARGARAAYGNCNNGAYTATYNTGNCNATNCCNMSNGARAA 614
Db 224 ABHRSMNMWVACRNKYMTSMYHARVEKMAVAGCANNWDBMHMHKCATNNNNMMW 165
Qy 615 YARGARAAWWS 626
Db 164 WYAYMHMHKKG 153
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RESULT 3

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US-09-949-016-14111
; Sequence 14111, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PaedSeq for Windows Version 4.0
; SEQ ID NO 14111
; LENGTH: 11174
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(11174)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14111
```

Query Match 9.0%; Score 57.8; DB 4; Length 11174;

Best Local Similarity 44.3%; Pred. No. 9.4e-06; Matches 62; Conservative 23; Mismatches 55; Indels 0; Gaps 0;

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Qy 442 GARGCNGARGAYTTVA CNMSNGTNTNMSNGARATNATGATGATYATNTYNTNGTN 501
Db 8586 GCAGCAACAGACATGATCATCATCGTCTGAGATCATGATGATGCTCATTTG 8645
Qy 502 TTYTNTACNTYNTGTYNTNTATNGARATGATNTATYGTATYMGNAARGTNSNARGCN 561
Db 8646 GTGTGACCATYATGCTGTCGACAGATGATTTACTGCTACAGAAAGATCGCTGCC 8705
Qy 562 GARGARGCNGCARGARAA 581
Db 8706 ACGGAGACTGCTGCACAGGA 8725
```

RESULT 4

```
US-09-949-016-13053
; Sequence 13053, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13053
LENGTH: 30337
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(30337)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13053

Query Match 9.0%; Score 57.8; DB 4; Length 30337;
Best Local Similarity 44.3%; Pred. No. 2,3e-05;
Matches 62; Conservative 23; Mismatches 55; Indels 0; Gaps 0;

QY 442 GARGCNGNGARGAYTTACNWSNGTNGTNSNGARATNATGATGATAYATNTYNTGNTN 501
DB 608 GCAGCCCAAGAGACATGCATCGTCTGTGAGATCATGATGATGATGATGATGATGATG 667
QY 502 TTYTNAACNTYNTGNTYNTATGATGATGATGATGATGATGATGATGATGATGATGATG 561
DB 668 GTGTGACCAATATGCTGTGCGAGATGATGATGATGATGATGATGATGATGATGATG 727
QY 562 GARGCNGCNGCARGAAA 581
DB 728 ACGGAGCTGCTGCACAGGA 747

RESULT 5
US-09-806-708B-22
Sequence 22, Application US/09806708B
Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 1141
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: promoter
LOCATION: (1)-(1141)
OTHER INFORMATION: consensus sequence of A.T., L.A., and B.N. PAB1 promoters
US-09-806-708B-22

Query Match 8.7%; Score 56.4; DB 4; Length 1141;
Best Local Similarity 11.2%; Pred. No. 3,1e-06;
Matches 70; Conservative 232; Mismatches 323; Indels 2; Gaps 1;

QY 8 CNTTYAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 67
DB 134 BDYDHHVYVTAANNAATTCMDXDDKTRTWMMKKNNATGMDDTTKHMMNNNGCBVT 193
QY 68 TYCNGTNTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 127

DB 194 WMAVXTDRDMSBKRMVYGMWKMWSYDTYYWVWDMDCKRKYRBRWVTRGMRMTV 253
QY 128 TNNMGNTGATNTNSNTGYATGAARMNGARGAGTNGARGCNAACNGTNGTNGTNGTNGT 187
DB 254 AMBTAFHRRRYNNGTBTBMAVYRMTNNNNNNNAKMKCRAYKMGWRABVNSTCTTMSKT 313
QY 188 TTYTAMGNCNGARGNGGNAARAGATTTTNTATNTATYGAATYMGAAAGCAYCARG 247
DB 314 TYKRTSCWANNCRDANKDKHMKWSAAMGVNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 373
QY 248 ARGNGARMSNCNTTYCARGNNNGTNGCARTGAAYGGWSAARGAAYTNGCARGAYG 307
DB 374 WKKHAAAHYSRQKTBKRYKTYVNNNNNTTMMKRMATYTKMDMBGTYYNNNNNGR 433
QY 308 TNSNATNACNGTNTYNAAYGTNACNTYNAAYGAYWSNGGNTYNTAAYCUTGAYAGTNN 367
DB 434 TYGWTYKMKMTYTKKWKANNCKRAWMDHKTCTHNTTMMKTYNNNNNNNNNNNNNNNN 493
QY 368 SNNMGARTTYGATTTYGAGCNCAYVGNCCNTTYGTTNABACNACMGATNTATNCNTY 427
DB 494 RBAAAYTYWMMWRRYAHANN 553
QY 428 TNNMGNTNACGARGCNGCNGARGAGATTTACNWSNGTNGTNSNGARATNATGATGAT 487
DB 554 RYRYMKTNNMSRMSDTRSMGRANNYARABHYGKNTTRWBSHBTBHBAGAAHYMMB 613
QY 614 MMYBAKCHCMKAWYKAKYAGAGSNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 673
QY 548 ARGTNMNA--RCNCRARGCNGCNGCARGAAAAGCMWSNCAATYATYNTGNCATNCC 605
DB 674 AKWTYTBAAANNAATYTAANWGGCWNATDTTRTMMNNNNNNNNNNNNNNNNNNNN 733
QY 606 NWSNGARAAYARGAAYWSNGCNGT 632
DB 734 AKVYAAAAYKAKKMMWMAKMMARGW 760

RESULT 6
US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768

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?
?
? REFERENCE/DOCKET NUMBER: 30472/114 IMMUT
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703)836-9300
? TELEFAX: (703)683-4109
?
? TELEX: 899149
?
? INFORMATION FOR SEQ ID NO: 14:
?
? SEQUENCE CHARACTERISTICS:
? LENGTH: 7218 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? CLONE: pTZgpc-F18
?
? US-08-232-463-14

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Query Match 8.3%; Score 53.8; DB 1; Length 7218;
Best Local Similarity 9.7%; Pred. No. 0.0001;
Matches 41; Conservative 171; Mismatches 212; Indels 0; Gaps 0;

Qy	56	TNNNGNTGTTTCGNGTNTGYGTNGARGTNCNWSGARGACNGARCNCTNCARGNA	115
Db	1488	TCACCTGAATACTACTATCTATGCAAGTAGTTAAAGAGATGAGAALTTTGGTACRRRRR	1423
Qy	116	AYCCNATGAARYTMGNTGYATMNSNTGYATGAABMGARGARGTCARGCNAACNG	175
Db	1428	RR	1363
Qy	176	TNGTNGARTGTGTTVAYMNCNGARGGNGNAARGAVTYYTNATNTAAGARTVYMNA	235
Db	1368	RR	1309
Qy	236	AYGNCAYCARGAGTNGARWNSNCNTTYCARGMNGYTNCAITGGAAYGNNMAARG	295
Db	1308	RR	1244
Qy	296	AYTNCARGAVGTWMSNATNACNGTNTYNAAYGTNACYYTAAAYGAYNSNGNTNTTAYA	355
Db	1248	RR	1189
Qy	356	CNTGYAAYGNTWSMNGARTTYGARTTYGARGCAYMGNCCNTTYGTNARACNACNM	415
Db	1188	RR	1122
Qy	416	GNYTNAATCCNYTMNGTNAACNGARGCNGGNGARGAVTTCNWSNGTNGTWSNG	475
Db	1128	RR	1063
Qy	476	ARAT 479	
Db	1068	RRAT 1065	

```

RESULT 7
US-09-621,976-2813
, Sequence 2813, Application US/09621976
, Patent No. 6639063
, GENERAL INFORMATION:
, APPLICANT: Dumas Milne Edwards, J.B.
, APPLICANT: Jobert, S.
, APPLICANT: Giordano, J.Y.
, TITLE OF INVENTION: ESTs and Encoded Human Proteins
, FILE REFERENCE: GENSET 054PR2
, CURRENT APPLICATION NUMBER: US/09/621,976
, CURRENT FILING DATE: 2000-07-21
, NUMBER OF SEQ ID NOS: 19335
, SOFTWARE: Patent.pm
, SEQ ID NO 2813
, ,
, LENGTH: 832
, ,
, TYPE: DNA
, ,
, ORGANISM: Homo sapiens
, ,
, FEATURE:
, NAME/KEY: CDS
, ,
, LOCATION: 235..399

```

US-09-621-976-2813

Query Match	8.3%;	Score 53.4;	DB 4;	Length 832;
Best Local Similarity	9.8%;	Pred. No. 1.9e-05;		
Matches 35; Conservative	155;	Mismatches 166;	Indels 1;	Gaps 1,

[illegible]

```

RESULT 8
US-09-621-976-15639
; Sequence 15639 Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15639
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-15639

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[illegible]

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Db      241 TCTYKSKSYTCKRSYTYTTRTSTSKGKMGCTKSRMSYTMMSKSYTTCGSKKKRMYMSAGA 300
Qy      397 CCNTTGTNARACNACNMGNTYNTATNCNTNMGNGTNAACGARGCGNGGARGAY 456
Db      301 WYAMWSMWCAMCMAMGMRGAMKSRBAKRYTMAKSCMYCAMKSCSARABAGRSCT 360
Qy      457 TTYACMSNGTNGTNGTNGTNGATATATATATATATATATATATATATATATATATAT 516
Db      361 TTKYKMTTTCYCMYKRCMWSMCAVCTGYCTGYCTGYCTGYCTGYCTGYCTGYCTGY 420
Qy      517 YTYNTAT 524
Db      421 TKMYTMT 428

RESULT 9
US-09-621-976-18033
; Sequence 18033, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent .pm
; SEQ ID NO 18033
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 16
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-18033

Query Match      7.8%; Score 50.4; DB 4; Length 474;
Best Local Similarity 8.7%; Pred. No. 9.4e-05;
Matches 29; Conservative 142; Mismatches 164; Indels 0; Gaps 0;

Qy      210 RGATTTTATNTATYAGRTYMGNAAGNCAYCARGATNGARSNCCNTTYCARGG 269
Db      14  SGCYCCMAKMSYKGRMYKSMRGSSCYKSCMCMKSCYSKSGYKKTITTTTAAWW 73
Qy      270 NMGNVTCARTGAAYGSMGNAARAGAYTNCARGAVGTMSNATNACNGTNTNAAAGT 329
Db      74  WTTTGGKMAARRRSGGKTYTMMCSKKTKSCMAGRWKGKTYTSMYTYCYKACATYMW 133
Qy      330 NACNTTAAAGYVNSNGNTNTATYACNTGYAAYGTNMSNMGARTTYGARTYGARGC 389
Db      134 KRWYSSCCMYTGGGSMWTTTMMRRBKSKYKRWTKGKKKTTMMAMCTTWRSY 193
Qy      390 NCAYMGCCNTTGTNARACNACNMGNTYNTATNCNTNMGNGTNAACGARGCGNGG 449
Db      194 WMMMRRAAAAKTYTTCMSKTMCMACCCMCMCRRARSOCMSKMSYTMCCYYM 253
Qy      450 NGARATTTTACMSNGTNGTNGTNGATATATATATATATATATATATATATATAT 509
Db      254 MYKGRMYTMMRGMMKMYTMMYKKSMMKSSCMKMRMMAKTYTMMYTYTMMYK 313
Qy      510 NYTNTGTYNTATNGARATGATNTATYGTAYM 544
Db      314 CCYMRKTYTMMYMRGSMWTARAGAMWMCY 348

RESULT 10
US-09-621-976-2813/C
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
```

```

; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent .pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

Query Match      7.8%; Score 50; DB 4; Length 832;
Best Local Similarity 9.4%; Pred. No. 0.00021;
Matches 34; Conservative 157; Mismatches 169; Indels 2; Gaps 1;

Qy      2  TGCCNGCNTTYAAYMGNTYNTTTCNTNGCNSNGTNTNTATNTATYTGCGTMSNG 61
Db      365 TGTYYTWTWKTYTWTYTTTTRMMMKKARRYTMMKSYTACASRYKTYTGMWYTMK 306
Qy      62 TNGYTYCCNGTNTGYTGARGTNCNMSNGARACNGCNGTNCARGAAYCCNA 121
Db      305 RMSTRWYCYMCKCMYRGRRCAMYTMRGRMSYAMGKWSRMSMCTRYKKS 246
Qy      122 TGARNTMNGTGYATWMSNTGYATGAABMGNGARGRTNGARGCAACNACNGTNG 181
Db      245 TYWTMKTCTATWCYWKYKRMMSKTCWSGSRGTYTSTSTSYMYMA--SMYTM 188
Qy      182 ARTGTTTYAYMGNCNGARGGNGNARAGAYTNTATNTATYAGTAYGNAAYGNC 241
Db      187 WMRGRWSTYTYMAGKKWRRYATWRRAMMMMAATMMYMMMAACMSRGAAYRT 128
Qy      242 AYCARGARTNGARMSNCNTTYCARGGNGNTTNCARTGGAAYGWSNARAGAYTNC 301
Db      127 MMMGTYWRKSKSYRTTRCAMAAYAMTKRSYWCWKKWRCMMMAAYGKTMMR 68
Qy      302 ARGAYGTMSNATNACNGTNTNAAAGTNAACNTNAAAGYVNSGNTYNTATYACNTGYA 361
Db      67 ACWTRTYRWMAWMMWMTMMYTYWPAKGRMMKMSWSMMMAWGMTWAAR 8
Qy      362 AY 363
Db      7  MW 6

RESULT 11
US-09-621-976-15639/C
; Sequence 15639, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent .pm
; SEQ ID NO 15639
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-15639

Query Match      7.5%; Score 48.6; DB 4; Length 505;
Best Local Similarity 11.1%; Pred. No. 0.00035;
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	Matches	41;	Conservative	140;	Mismatches	187;	Indels	0;	Gaps	0;
Qy	244	CARGARGNGARMSNCNTTTCARGGNGNTNCARTGGAAYGGMWSAARAYTTNCAR	303							
Db	371	MAAAKMRMAAAGSGYCGMTSTSTSGSKTGRGSGWTKKRPMWTYSGMMWTSKYCKTKGK	312							
Qy	304	GAYGTNMSNATNACNGTNYTNAAYGTNACNYTNAAYGAYWSNGSYTNTAAYACNTGYAA	363							
Db	311	YTGWKSXTTRWTCISWRKYTMMMSGCMARSMKSMASISYTSMAACGMMSSASAYRABRSMY	252							
Qy	364	GTNMSNMGNGARPTTYGARPTTYGARGCNCAYMGNCCNTTYGTNAPACNAACNMGNTNATN	423							
Db	251	GARSMRPAAGAWPAPRRGKTKRABGKSSMMSKSSMMSGAKAMCRRMMSCRMSSYS	192							
Qy	424	CCNTNMNGTNAACNGARGCNGCNGNARAYTTTAACNWSGNTGTNWSNABATNATG	483							
Db	191	CMGSCMSCRGTCAKMMRYARAKRYASMSGTYMGCRCYAKCAKRYGYRBSRSTGS	132							
Qy	484	ATGTAYATNTNYNTGNTTYYTNAACNTNTGTYNTYNTAATGARGATGATNTAYTGYTAY	543							
Db	131	RGMYKRRRKMYTMMKYMMWSMWCRYMGAAATGMSABAYRMTYASMAACMGCSMMMGMS	72							
Qy	544	MGNAPARGTNSNAARCGNGARGCNGCNCARGARAAVGCNWSNGAYTAYTTCNATN	603							
Db	71	MMMCMBRSRYCOWSGKWCSCCGYCSACBMCYCTMRMKSWSYSSRKSRCMCCRYSMS	12							
Qy	604	CCNWSNGA	611							
Db	11	AYRYSKR	4							

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RESULT 12
US-09-621-976-8976
: Sequence 8976, Application US/09621976
: Patent No. 6639063
: GENERAL INFORMATION:
: APPLICANT: Dumas Milne Edwards, J.B.
: APPLICANT: Jobert, S.
: APPLICANT: Giordano, J.Y.
: TITLE OF INVENTION: ESTs and Encoded Human Proteins.
: FILE REFERENCE: GENSET.054PR2
: CURRENT APPLICATION NUMBER: US/09/621,976
: CURRENT FILING DATE: 2000-07-21
: NUMBER OF SEQ ID NOS: 19335
: SOFTWARE: Patent.pm
: SEQ ID NO 8976
: LENGTH: 399
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-621-976-8976

```

	Query Match	7.2%	Score 46.2;	DB 4,	Length 399;
	Best Local Similarity	10.2%;	Pred. No. 0.0015;		
	Matches	32;	Conservative 129;	Mismatches 153;	Indels 0; Gaps 0
Qy	135	YATWMSNTGYATGARMNGARGARGTNGARCNA	CNACNGTNGTGARTGTTAYWG	194	
	:	:	:	:	:
	:	:	:	:	:
Db	5	YMCWAKGWBARMTBRAYMGMYTRSGKSKSWP	AKWSMMKKRRRRRBRAPMWMWSMCWKSKS	64	
Qy	195	NCCGARGCNGGNARGA YTTYTYTATTAATAA	TATPATYAGMAAYGCNCAYCARGARGTGA	254	
	:	:	:	:	:
	:	:	:	:	:
Db	65	SMWSBWCMMTFRMKRGASAWGYSWMTYTMR	RRYRYRKRCACTTKPRAAGMWKAWA	124	
Qy	255	RWSNCNTTYCARGGNNNTNYTCARGTAAAG	GNNSSNARGAYYTNCARGATWSNAT	314	
	:	:	:	:	:
	:	:	:	:	:
Db	125	WMAVAXXWYMAWRRAFKYWMAMMSKSBR	MBRRRRRAYAMYIYMBAARTTMGWPASCY	184	
Qy	315	NACNGTNTTAAYGTNA	CNYTNAAYGAYWSNGCNTTATYACNTGYAA	YGTWSSMWNGA	374
	:	:	:	:	:
	:	:	:	:	:
Db	185	MASAGMYTWMYIYMMGRCKMYISAGSNMR	KWTJRRCASYSWSCSSYCMGAKMMYIKTSRW	244	
Qy	375	RTTYGARFTYGARGCNCA YMGNCNTTEYGT	NAABACNA CNMNGNYTNATNCNYTIMGNGT	434	
	:	:	:	:	:
	:	:	:	:	:

Db 245 SYRYSSYRCKTKYRRSCCSMSCYMKYTRSMYCASCYYSYKTRRASCMCMCCMKRRKM 304

QY 435 NACNGARGARGCNG 448
| : : : : | :
Db 305 MAMMYMMKMYCYCK 318

```

RESULT 13
US-09-949-016-787
; Sequence 787, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 787
; LENGTH: 1342
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-787

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Query Match	7.1%: Score 46; DB 4; Length 1342;
Best Local Similarity	28.4%: Pred. No. 0.0053;
Matches 137; Conservative	62; Mismatches 280; Indels 3; Gaps 1;
QY	89 C N M S N G A R C A N G A R C N G T N C A R G A N A A C C N A T G A A R Y T M G N T G Y A T M S N T G A T G A 148
Db	214 C C C G G G T C T G G A G C T G T T A A T G G G A C A G A T G C T C G G T T A A A T G C A C T T C T C C A G C T 273
QY	149 A R M N G A R G A R G T M G A R G C N A C N A C N G T N G T N G A R T G T T Y T A Y M G N C N G A R G N G S -- 206
Db	274 T T G C C C T G T G G G T G A T G C T C T A C A G T G A C T T G A A T T T T C G T C T C T T A G A C G G G G A C 333
QY	207 - N A A R G A Y T T Y T N A T N T A Y A G A R T A Y M G N A A Y G N C A Y C A R G A R G T N G A R M S N C N T T Y C 265
Db	334 C T G A G C A G T T T G T A T T C T A C A C A C A T A G A T C C C T C C A A C C A T G A G T G G G C G G T T A 393
QY	266 A R G N M G N Y T N C A R T G G A A Y G G M S N A R G A Y Y T N C A R G A Y G T M S N A T N A C N G T N Y T N A 325
Db	394 A G A C A C G G G T G T C T T G G A T G G A A T C C T G A C G G T A C G A T G C C T C A T C C T T C T C T G A 453
QY	326 A Y G T N A C N Y T N A A Y G A Y M S N G A T T N T A Y A C N T G T A A Y G T M S M M G A R P T T Y G A R T T Y G 385
Db	454 A A C T G C A G T T C G A C G A C A A T G G G A C A T A C A C C T C C A G G T G A A A A C C C A C C T G A Y G T T G 513
QY	386 A R G C N A Y M E N C N T T Y G T N A B A C N A C M N G Y T N A T C N Y T M G N G T N A C N G A R B A R G 445
Db	514 A T G G G G T G A T A G G G A G A T C C G G C T C A G C G T C G C A C A C T G T A C G C T T C T T G A G A T C C 573
QY	446 C N G N G A R G A Y T T A C N M S N G T N G T N M S N G A R A T N A T G A T G A T A Y A T N Y T N T N T T Y Y 505
Db	574 A C T T C C T G G C C T G G C A T T G G C T C T G C T G C A C T G A T G A T C A T A A T A G T A A T T G A G 633
QY	506 T N A C N Y T N T G Y T N Y T N A T N G A R A T G A T N T A Y T G T A Y M G A A A G T M S N A A R G C N A R G 565
Db	634 T G T C T C T T C C A C A T T A C C G A A A A A G C A T G G C G A A A G A G C T C A T A A A G T G T G 693
QY	566 A R 567
Db	694 A G 695


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RESULT 14
US-09-949-016-4948
; Sequence 4948; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4948
; LENGTH: 1708
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4948

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Query Match 7.1%; Score 46; DB 4; Length 1708;
Best Local Similarity 28.4%; Pred. No. 0.0066;
Matches 137; Conservative 62; Mismatches 280; Indels 3; Gaps 1;

QY	89	CNWSGGAACNARGCNGTNCARGGAAACNCAATGARYYTNMNTGTYATMSWTGATGA	148
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QY	149	ARMNGARGARGTNGARGCNACNACNGTNGTNGARTGTGTTTAYMGNCCNARGNGG--	206
Db	319	TTGCCCTGTGTGGGTGTGCTCTTAACAGTACCTGGAATTTTGGTCTCTTAGACGGGGGAC	378
QY	207	-NARGAYTTTNTATNTATYAGARTAYMGNAAAYGNCAYCARGARGTNGARWSNCCNTTTC	265
Db	379	CTGACGACGTTGTATTTCTATCTACACATAGATCCCTTCCACCACTGAGTGGCGGGTTTA	438
QY	266	ARGMNGMYNTNCARTGGAAYGGNWSNAARGAAYTTCARGAAYGTMSNATNACNGTYTNA	325
Db	439	AGGACCGGGGTGTCTTGGGATGGGAATCCGAGCGGTACGATGCTCCATCTCTTCGTGA	498
QY	326	AYGTNACNYTNAAYGAYWSNGNYNTNTAAYCNTGYAAYGNMNMNGARTTCGARTTGY	385
Db	499	AACTCAGATTGCACGACGATGGGACATTAACCTGCGAGGGAAGAACCCACTGAATGTTG	558
QY	386	ARGCNAYMGNCCNTTGTGTNAARACNACNMGNTYTNAATNCNTYTMNGNTNACNGARG	445
Db	559	ATGGGGGTATAGGGGAGATCCGGCTCAGCGTGGTGACACTGPAACGCTTCTGAGATCC	618
QY	446	CNNGNGARGAYTTTACNMSNGTNGTMSNGARATNTATGATGYAATNYTNYTNGTNTTYY	505
Db	619	ACTTCCTGCTCTGGCCATTGGCTCTGCTGTCGACCTGATGATCATTAATGTAATGTAG	678
QY	506	TNACNYTNTGTYTNTATNAGARTATNTAATGYTAYMGNAAAGTMSNAARGNCARG	565
Db	679	TGATCTCTTTCACAGCTTACCGGAAAAAAGCAGATGGGCCGAAAGAGCTCATMAAGTGGTG	748
QY	566	AR 567	
Db	739	AG 740	

RESULTS
US-09-621-976-8976/c
; Sequence 8976, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.

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? APPLICANT:  Giordano, J.Y.
? TITLE OF INVENTION:  ESTs and Encoded Human Proteins
? FILE REFERENCE:  GENSERT_054PR2
? CURRENT APPLICATION NUMBER:  US/09/621,976
? CURRENT FILING DATE:  2000-07-21
? NUMBER OF SEQ ID NOS:  19335
? SOFTWARE:  Patent.pm
? SEQ ID NO 8976
? LENGTH:  399
? TYPE:  DNA
? ORGANISM:  Homo sapiens
? US-09-621-976--8976

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Query Match 6.9%; Score 44.8; DB 4; Length 399;
Best Local Similarity 7.7%; Pred. No. 0.004;
Matches 28; Conservative 161; Mismatches 172; Indels 2; Gaps 1.

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Search completed: April 7, 2005, 23:32:04
Job time : 167 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 21:39:28 ; Search time 502 Seconds
(without alignments)
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Title: US-09-977-579-2-REV
Sequence: 1 ATGCCGNCNTTYAAYMGNNT.....SNGCNGTNCNGTNGARGAR 645

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues
Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- Published Applications NA:*
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 - 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
 - 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
 - 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
 - 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
 - 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
 - 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
 - 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
 - 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
 - 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 - 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
 - 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 - 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	462.8	71.8	11	US-10-029-191-21	Sequence 4, Appl1
3	462.8	71.8	2220	11	US-09-977-579-3
4	462.8	71.8	2632	13	US-10-029-191-22
5	462.8	71.8	3108	13	US-10-029-191-1
6	158.4	24.6	1335	18	US-10-723-860-2247
7	158	24.5	6357	13	US-10-029-191-23
8	156.8	24.3	1414	18	US-10-477-872-1
9	152.2	23.6	1490	9	US-09-917-800A-1654
10	105	16.3	407	17	US-10-276-774-718
11	81.2	12.6	807	17	US-10-401-916-12

12	81.2	12.6	974	17	US-10-401-916-13	Sequence 13, Appl1
13	57.8	9.0	3583	18	US-10-723-860-6471	Sequence 6471, Ap
14	52.6	8.2	6217	15	US-10-311-455-911	Sequence 911, App
15	50	7.8	671	14	US-10-184-644-346	Sequence 346, App
16	50	7.8	671	14	US-10-184-634-346	Sequence 346, App
17	49.6	7.7	2415	9	US-09-978-385-3	Sequence 3, Appl1
18	49.4	7.7	633	17	US-10-338-110-121	Sequence 121, App
19	49.4	7.7	691	14	US-10-123-155-16	Sequence 16, Appl1
20	49.4	7.7	691	15	US-10-146-731-16	Sequence 16, Appl1
21	49.4	7.7	691	15	US-10-140-472-16	Sequence 16, Appl1
22	49.4	7.7	691	15	US-10-141-761-16	Sequence 16, Appl1
23	49.4	7.7	691	16	US-10-142-885-16	Sequence 16, Appl1
24	49.4	7.7	691	16	US-10-158-790-16	Sequence 16, Appl1
25	49.4	7.7	691	17	US-10-137-871-16	Sequence 16, Appl1
26	49.4	7.7	691	17	US-10-140-923-16	Sequence 16, Appl1
27	49.4	7.7	691	17	US-10-141-756-16	Sequence 16, Appl1
28	49.4	7.7	691	17	US-10-141-759-16	Sequence 16, Appl1
29	49.4	7.7	691	17	US-10-140-805-16	Sequence 16, Appl1
30	49.4	7.7	691	17	US-10-140-864-16	Sequence 16, Appl1
31	49.4	7.7	691	17	US-10-142-426-16	Sequence 16, Appl1
32	48.4	7.5	1089	10	US-09-813-153-57	Sequence 57, Appl1
33	47.8	7.4	765	14	US-10-123-155-28	Sequence 28, Appl1
34	47.8	7.4	765	15	US-10-146-731-28	Sequence 28, Appl1
35	47.8	7.4	765	15	US-10-140-472-28	Sequence 28, Appl1
36	47.8	7.4	765	15	US-10-141-761-28	Sequence 28, Appl1
37	47.8	7.4	765	16	US-10-142-885-28	Sequence 28, Appl1
38	47.8	7.4	765	16	US-10-158-790-28	Sequence 28, Appl1
39	47.8	7.4	765	17	US-10-137-871-28	Sequence 28, Appl1
40	47.8	7.4	765	17	US-10-140-923-28	Sequence 28, Appl1
41	47.8	7.4	765	17	US-10-141-756-28	Sequence 28, Appl1
42	47.8	7.4	765	17	US-10-141-759-28	Sequence 28, Appl1
43	47.8	7.4	765	17	US-10-140-805-28	Sequence 28, Appl1
44	47.8	7.4	765	17	US-10-140-864-28	Sequence 28, Appl1
45	47.8	7.4	765	17	US-10-142-426-28	Sequence 28, Appl1

ALIGNMENTS

RESULT 1
US-09-977-579-4
Sequence 4, Application US/09977579
Publication No. US20040248240A1
GENERAL INFORMATION:
APPLICANT: Cambridge University Technical Services
TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodi
TITLE OF INVENTION: channel
FILE REFERENCE: 674558-2001
CURRENT APPLICATION NUMBER: US/09/977, 579
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: PCT/EP00/01783
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 1261
TYPE: DNA
ORGANISM: Homo sapiens
US-09-977-579-4
Query Match 72.2%, Score 466, DB 11, Length 1261;
Best Local Similarity 58.8%; Pred. No. 1.1e-120;
Matches 379; Conservative 145; Mismatches 121; Indels 0; Gaps 0;
Oy 1 ATGCCGNCNTTYAAYMGNNTTYCCYTCGMSNTNTNTNTAATYTGCGTMSN 60
Db 376 ATGCCGNCNTTYAAYMGNNTTYCCYTCGMSNTNTNTNTAATYTGCGTMSN 60
Oy 61 GTTGTGTTTCGNCNTTYGNGARGTNCNMSNGARGCNGTNGARGGAAVCCN 120

Db	436	CTCTGCTTCCCTGTGTGTGTGAAGTGGCCCTGGAGACGGAAGCCGTGACGGGCACACCC	495
Qy	121	ATGAARYTNMGTYATNWSNTGTATGAARPMNGARGGNTGARGCNACMACNNTNGTN	180
Db	496	ATGAAGCTGCGCTGCATCTCCCTGCATGAAGAGAGAGAGAGTGGAGGCCACACGCTGTG	555
Qy	181	GARTGGTYYTATMGNCCNARGGNGNARGVATYYTNTATNTATYARATPYMGNAAVGN	240
Db	556	GAATGGTCTTACAGGCGCCAGAGGCGGTAAAGATTTCTTATYTTTACAGATTCGGAATGGC	615
Qy	241	CAYCARGAGTGTGARSNCCNTFYCARGGNMGNYTNCARTGGAAVYGGNNSNAARGAYTN	300
Db	616	CACCAAGAGGTGGAGAGCCCTTTCAAGGGGCGCTGCATGGAAATGGCAGCAAGACCTG	675
Qy	301	CARGAYGTNWSNATNACNGTNYTNAAYGTNACNYTNAAYGAVYWSNGYNTNTAYACNTGY	360
Db	676	CAGACGAGTGTCAATCATCTGTCTGCAACGTCATCTGAAAGACTCTGGCCCTCTACACTGC	735
Qy	361	AAVGTNWSNMGARTTYTARTTYYGARGCNCAMGNCCNTTYGTNAAABACNACMGNAYTN	420
Db	736	AATGTGTCCCGGAGATTGTGAGTTTGAGGGGCATCTGGCCCTTTGTGTGAAGACGAGCGGCTG	795
Qy	421	ATNCCNNTMNGTNAACNGARGGCGNGNGARGATYYTACMNSNTNTGNMNSGARATN	480
Db	796	ATCCCCCTPAAGGATCCGAGAGGCTGGAAGAGACTTCACTCTGTGTGCTPAGAAATC	855
Qy	481	ATGATGTATVATYTYTNTGNTTNTTYTNAACNYTNTGVTYTYTNTATNAPATGATNTATVGY	540
Db	856	ATGATGTATCATCTTCTTGTGTCTTCTTCCACCCCTGTGCTCTCATCGAGATGATATATTTGC	915
Qy	541	TAYMGNAARGTNMSNAARGCNGARGGCGNCCARGAARAAGCWNNSNGAYTYAYTNGCN	600
Db	916	TACAGAAAGGTCTCAAAAACCGAAGGAGGAGCCCAAGAAAACGCGTGTGACTACCTTGGC	975
Qy	601	ATNCCNWSNGAAPAAAYARBARAAYMSNGCNMTNCCNGTNGARGAR	645
Db	976	ATCCCATCTGAGAACCAAGAGAACTGTGGCGTATCCAGTGGAGGAA	1020

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RESULT 2
US-10-029-191-21
; Sequence 21, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL, BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; TITLE OF INVENTION:
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: SeqIdNOS Ver. 2.1
; SEQ ID NO 21
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-21

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Query Match	71.8%	Score 462.8	DB 13	Length 645
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Matches 377	Conservative 145	Mismatches 123	Indels 0	Gaps 0

Qy 1 ATGCNGCNITTAAYWAGNNTNTTTCANYNCGMWSVYNTGINTVNTAINTPAVYSGGNTSMN 60
Db 1 ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTTAAGTGTCTATCTAGTGGTCAGA 60
Qy 61 GTNTGTTTCCNGINTGTGTNGARGTNGCNMSNGAPACNGARGCNGTNCARGMAAYCCN 120
Db 61 GCTCTCTTCCCTGTGTGTGTGTGAAAGGCCCTCGGACACGAAACGGGTGACGGGCAATCCC 120

OY	121	TGGAATNMNNTGTATMTWSTNGVATGAABMGNRGARGTMGAGCNACNA CNNGTNGT	180
Dd	121	ATGAAGCTGAGGTGCATCTCTCCGTCAITAAAGGGAGSGAGGTGGAGGCCA CACTGTGGTG	180
OY	181	GARTGGTTYYTA YMGNCNGARGGNGNARGA YTTYTYTNATNTAYGARTAYMGNAAYGN	240
Dd	181	GAGTGGTTCTCAGCGCTCAGGGCGGGTAAAGATTTCCTTA TATAGAATATCGAATGCG	240
OY	241	CAYCARGARGNNGARWMSNCNTTYYCARBGMNGMYNRCARTGAAAYGGMNSNARGA YYTN	300
Dd	241	CACCGAGNAAGTGGAGAGGCCCTTCCAGAGCCGTCTGCAGTGSAAITGGAGCAAAGACTTG	300
OY	301	CARGAYGTWMSNATNACNGINTYYNAA YGTNACNYTNAA YGAYWSNGNYTNTAYA CNTGY	360
Dd	301	CAGGACGTATCATCATCTACTCATCTCAATGTCTCA TTGAAATGACTCTGGCCTCTNACAATGC	360
OY	361	AAYGTNMSNMNGARTTYGARPTTYBARCONCA YMGNCNTTYYGTNAAARCNACNNGYTN	420
Dd	361	AATGTGTCCAGGAGMTTGGAAITCGAGGACACAGGCCCTTTTGTGAAGCACCGAGACTTG	420
OY	421	ATNCCNYTNMNGTNAACNGARGARCGCNGNGARGA YTTYNACMSNGTNGTWNMSNGARATN	480
Dd	421	ATACTTTGGCAGTCACTGAAGAGGCGGGAAAGACTTCA CTCCGTGGTCTCGGAAAATC	480
OY	481	ATGATGTAYATNYTNMTNGTNTTYYTNACNTNNGSYNTYNATNGARBATGATNTNAYTGY	540
Dd	481	ATGATGTACATCTCTCTGGTCTTCTCACTTGTGGCTGTTATATGAGATGATCTATYTGC	540
OY	541	TAYMNAARGTWNMSNABRGNGARGARCGCNGCNCARGA RAAAYGCNWSNNGAYTAYTYTNGCN	600
Dd	541	TACGAAAGGTCTCTPAAGCGCGAAGGACGACGACAGAAAAAGCGTCTGACTACACTTGCT	600
OY	601	ATNCCMSNGAPAAAYARGAAPYA WSNCCNGTNCNCGTNGANGAR	645
Dd	601	ATCCCTTCAGAGAACAGGAGAACTCTGTGTA ACTGTGGAGGAA	645

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RESULT 3
US-09-977-579-3
; Sequence 3, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodium channel
; TITLE OF INVENTION: channel
; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses thereof
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977,579
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: rat
US-09-977-579-3

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Query Match	71.8%	Score 463.8	DB 11	Length 2220
Best Local Similarity	58.4%	Pred. No. 1.4e-119		
Matches 377	Conservative 145	Mismatches 123	Indels 0	Gaps 0

QY	1	ATGCGCGNTTAAAMGAVINTTTCNCNTYNGGMSNYITGVYTAINTAATYAGGGTMMN	60
Db	363	ATGCGCGCTTCAACAGATGCTTCCCTAGCTTCTTAAGTCTCATCTACCTGGGTGACA	422
QY	61	GTMTGTYTTCNGTNTGYGTMGARGTGNCMSNGAPACNGARGCNGTNCARCGMAATCCN	120
Db	423	GTCTGCTTCCCTGTGTGTGTGGAAATGCTCTGAGACAGAAAGCGATGACGGGCAATATCC	482

Db 198 ATGAGAGCTGAGGTGATCTCTCTGACATGAAGAGGAGAGGTGAGGCCACACTGTGGTG 257
Qy 181 GARTGTTTATYMGNCNGARGNGNAAARGATTTTATNTAYGARTATMGNAAYGN 240
Db 258 GAGTGTCTTACAGGCGCTGAGGGCGGTAAAGATTTCTATATATATAGATCGAAATGCG 317
Qy 241 CAYCARGARTGABNSCNTTYCARGGMMGYTCARTGAAAYGNNMNAARGAYTN 300
Db 318 CACGAGAAAGTGAGAGGCCCTTCCAAAGCCGTCTGACGTGGAATGGAGCAAAAGCTCG 377
Qy 301 CARGAYTNMNAATNACNGTNTYNAAYGTNACNYTNAAYGAYVNSNGYNTNTAYACNTGY 360
Db 378 CAGGAGTATCATCACTGATCAATGTCATTGATATGACTCTGGCCCTCAACATGCG 437
Qy 361 AAYGTMSMNGARTTYGARTTYGARGNCAMGNCNTTYTNAARAACNMGNTYN 420
Db 438 AATGTGTCCAGGAGATTGAAATTCAGAGCACACAGGCCCTTTGTGTGAAGCAACGAGACTG 497
Qy 421 ATNCCNYTMNGTNCNGARGARGNGNGARGATTTTACNWSNGTNGTMSNGARATN 480
Db 498 ATACCTTTGGAGTCACTGAAGAGCGGAGAGAACTTCACTCCGTGTCTGGAAATC 557
Qy 481 ATGATGTAAATYNTYNTGNTTNTYTNACNYTNTGYTYNTATNGARATGATNTATGY 540
Db 558 ATGATGTATACCTCTCTGCTCTTCTCACTGTGCTGTTTATGATGATCTATTCG 617
Qy 541 TAYMGAATGTMSNAAARGCNGARGARGCNGCNCARGAARAYGCMNSNAYTYTNGCN 600
Db 618 TACAGAAAGTCTCTTAAAGCCGAAAGAGGACGACACAGAAAATGCGCTGATACCTTGCT 677
Qy 601 ATNCCMWSNARAAAYARGAARAYWSNGCNGTNCNGTNGARGAR 645
Db 678 ATCCCTTCAGAGAACAGAGAACTCTGTGTGTACTGTGAGAGAA 722

RESULT 6

US-10-723-860-2247
; Sequence 2247, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2247
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2247

Query Match 24.6%; Score 158.4; DB 18; Length 1335;
Best Local Similarity 38.2%; Pred. No. 1.5e-33;
Matches 240; Conservative 101; Mismatches 266; Indels 21; Gaps 3;

Qy 25 CCNYTNGCMWSNYTNGTNTATNTATYATGGTMSNGTNTGYTTCNGTNGTNGARG 84
Db 34 CTGCTGGCCTTATGTTTCGCGCGGCACTGTGTCTCTCAGCTCGCGGGGCGTGGAG 93
Qy 85 GTNCCMWSNABARCNARGCNGTNCARGNAAYCCNATGAARYYTNMNGTYATMNSNTGY 144
Db 94 GTGGAATCGAGACCGAGGCCGTGTATGGATGACCTTCAAAATCTTTGGCATCTCTCG 153
Qy 145 ATGAARMGANGARGTNGARGCNCACNGTNGTNGARTGTTTAYMGNCNGARGN 204

Db 154 AAGCGCCGAGGAGACCAACCTGAGACCTTCAACGATGAGACTTCCGCCAGAGGGC 213
Qy 205 GGNAAAGATTTTATYNA-----TNTAYGARTATMGNAAYGNACARGARGTNGAR 255
Db 214 ACTGAGGAACTTTGTCAAGATCTCGGCTATYAGAAATGAGTGTGTGAGCTGGAGAGGAT 273
Qy 256 WSNCCNTTYCARGMMNGYNTNCARTGAAV-----GCMWSNABARAYTNCARGAY 306
Db 274 GAGCGCTTGAAGGGCGCGGTGTGTGAATGCGACGCGGGGACCAAAACCTCGACGAGAT 333
Qy 307 GTNMSNATNACNGTNTYNAAYGTNACNYTNAAYGAYWSNGYNTNTAYACNTGYATN 366
Db 334 CTGTCTATCTTATCATCACCATGTCTCAACCACTCGGGGACATCAACAGTCCACGTC 393
Qy 367 WSNMNGARTTYGARTTYGARGONCAVMNCCNTTYGTNABARACNMGNTNTATNCCN 426
Db 394 TACCGCTCTCTTCTTTCGAAAACCTACGAGCACACACACAGCGTCTCAAGAAATCCAC 453
Qy 427 YTNMNGTNCNGARGARGCNGNGARGATTTTACNWSNGTNGTMSNABARATNATGATG 486
Db 454 ATTGAGTGTGAGCAAAACCAACAGAGCATGCGATCATGTGTCTGAGATCATGATG 513
Qy 487 TAYATNTYNTYNTYNTYTNACNYTNTGYTYNTATNGARATGATNTATYTYTAYMGN 546
Db 514 TATGTGCTCATTTGTGTGTGACATATGCTGTGCGAGATGATTTTACTGTCTAACAG 573
Qy 547 AARGTMSNABARGCNGARGAR---GCGNCARGAARAYGCMNSNAYTYTNGCNATN 603
Db 574 AAGATGCTGTCCGCCACGAGAGCTGTGACAGAGAAATGCTCGGATATCTGCGGCATC 633
Qy 604 CCNWSNABARAAAYARGAARAYWSNGCNG 631
Db 634 ACCTGTGAAGCAAGAGAACTGCAACGG 661

RESULT 7

US-10-029-191-23
; Sequence 23, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/501
; CURRENT APPLICATION NUMBER: US/10/029,191
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Lepus Sp.
US-10-029-191-23

Query Match 24.5%; Score 158; DB 13; Length 657;
Best Local Similarity 38.1%; Pred. No. 1.1e-33;
Matches 239; Conservative 102; Mismatches 266; Indels 21; Gaps 3;

Qy 25 CCNYTNGCMWSNYTNGTNTATNTATYATGGTMSNGTNTGYTTCNGTNGTNGARG 84
Db 10 CTGCTGGCCTTGTGTGTCGCGCGCGCGCTGTGTCTCTCGGCTCGGGGGGCTGTGGAG 69
Qy 85 GTNCCMWSNABARCNARGCNGTNCARGNAAYCCNATGAARYYTNMNGTYATMNSNTGY 144
Db 70 GTGGAATCGAGACCGAAGCCGTGTATGGATGACCTTCAAAATCTGTGCACTCTCTCG 129
Qy 145 ATGAARMGANGARGTNGARGCNCACNGTNGTNGARTGTTTAYMGNCNGARGN 204
Db 130 AAGCGCCGAGGAGACACGCGCGAGACCTTCAAGAGTGAACCTTCCGCCAGAGAGGC 189

Db 350 GAGTCTTCAAGGCCCGCTGGTGTGGAATTGGCAGCCCGGGCGACCAAGACTCGACGAT 409
 Oy 307 GTTMSNATNACNGTNTYTAAYGTNACNTTMAAYGAYWSNNGYNTTAYACNTGYAAYGTN 366
 Db 410 CTGTCTATCTTCATCAACCAATGTCCACTCAACCACTCGGGGGACTCAACAGTGCACGTC 469
 Oy 367 WSNMNGARITYGATTTYGARCGNCAYMGNCGNTTYGTNABACNACNMNGNTNATNCGN 426
 Db 470 TACCGCTGCTCTTCTTGGAAATACTACGAGCAACAACACAGCGTGGTCAAGAAGATCCAC 529
 Oy 427 YTNMNGNTNACNAGARCGNCGNNGARAYTTCMSNGTNGTMSNABATNATNAGAT 486
 Db 530 ATTGAGGTAGTGGACAAAGCCACAAGACATGGCATCATGTGTCTGAGATCATGATG 589
 Oy 487 TAYATNTYNTNGTNTTYTNAcNTNTGGYNTYNTATNGARATGATNTAYTGYTAYMGN 546
 Db 590 TATGTGCTCATGTGTGTGTGACCATATGTGCTCGTGGCAGAGATGATTTAACTCTCTCAAG 649
 Oy 547 AARGTMSNMAARGCMGARGAR---GCGNCGNCGARGAAPAAVCGMWSNAGAYAYTNTGNCATN 603
 Db 650 AAGATCGCTGCCGCCACGAGGACTGCTCACAGGAGAAATGCTCGGAATTAACCTGGCCATC 709
 Oy 604 CCNMSNGARAAVYAARGAPAAVWSNCGNG 631
 Db 710 AACTCTGAAGCAAGAGAACTGCACGG 737

RESULT 9
 US-09-917-800A--1654
 ; Sequence 1654, Application US/09917800A
 ; Patent No. US20020119462A1

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US-09-917-800A-1654
Sequence 1654, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Blashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-503-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIORITY APPLICATION NUMBER: US 60/222,040
PRIORITY FILING DATE: 2000-07-31
PRIORITY APPLICATION NUMBER: US 60/222,880
PRIORITY FILING DATE: 2000-11-02
PRIORITY APPLICATION NUMBER: US 60/290,029
PRIORITY FILING DATE: 2001-05-11
PRIORITY APPLICATION NUMBER: US 60/290,645
PRIORITY FILING DATE: 2001-05-15
PRIORITY APPLICATION NUMBER: US 60/292,336
PRIORITY FILING DATE: 2001-05-22
PRIORITY APPLICATION NUMBER: US 60/295,798
PRIORITY FILING DATE: 2001-06-06
PRIORITY APPLICATION NUMBER: US 60/297,457
PRIORITY FILING DATE: 2001-06-13
PRIORITY APPLICATION NUMBER: US 60/298,884
PRIORITY FILING DATE: 2001-06-19
PRIORITY APPLICATION NUMBER: US 60/303,459
PRIORITY FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1654
LENGTH: 1490
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_017288
US-09-917-800A-1654
Query Match 23.6%; Score 152.2; DB 9; Length 1490;
Best Local Similarity 38.7%; Pred. No. 9; Se-32;

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Matches 232; Conservative 96; Mismatches 250; Indels 21; Gaps 3;

QY 54 GGTMSNGNTNTGTYTTCNGTNTGTGTNGARNTCCMSNGARAACGAGCNGTNCARBG 113
DB 258 GGATATCTCAGCCTGGGGGGGCGTGTGAGGATTCCTGAGACGAGGCACTGTATG 317
QY 114 NAAVCNATGAARYTMTGTYATMTSNTGYATGARBMGNGARGGTNGARCNACNAC 173
DB 318 GATGACCTTCAAAATCTGTGTATCTCTGTAGACCTGTGAGTACACACCGCCAGAC 377
QY 174 NGTNGTNGARTGTGTYTAYMNCNGARGNGNNAARAVTYTNA-----TNTA 224
DB 378 CTTCACGAGGTGACCTTCGCGCAGAGGCAACAGAGATTTGTCAAGTCTTACGTA 437
QY 225 YGARTAYMNAAYGNCAYCARBGTNGARMSNCCNTTYCARGMNGVYTNARGAA 284
DB 438 TGAAGATGAGTGCTGCAAGTGAAGATGAGCCCTTGGAGGCGGTGTGTGAA 497
QY 285 Y-----GGMNSNARGAYTTCNARGAYGTMSNATNACNGTYTNAAYGTNACNT 335
DB 498 CGGTACTCGGGGACCAAGGACCTGACAGACCTGTCTCATCTTATCACCAGTGTCACTA 557
QY 336 NAAVGAYSNGNYTNTAYACNTGYAAYGTMSNMNGARTTYGARTTGARGCNCAYNG 395
DB 558 CAACCACTCTGGCGACTAGCAAGTGTACCGTCTCTCTCTTGATTAATTAACA 617
QY 396 NCNTTYGTNAARACNACMNGVNTNATNCNTNMNGTNGACGARGCNGNARGA 455
DB 618 GCACAAACACGAGCGTGTCAAGAAATCCACCTGGAGGTGTGACACAGGCAACAGAG 677
QY 456 YTTVACNMSNGTNGTMSNGARATNATGATGATVATNTYNTGTYTNAACNTNTG 515
DB 678 TATGATCATCATGTGTACAGATCATGATGATGATGATGATGATGATGATGATGATG 737
QY 516 GTTNTATNATGAT 572
DB 738 GCTCGGCGGAGATGTGTATGCTGACAGAAAGATGCTGCTGCCACGAGAGCTGTGC 797
QY 573 NCARGAARAYGCMWSNGAYATAYTNGCNATNCNMSNGARAARAYARGAAYVSNCG 631
DB 798 ACAAGAAATGCTCGAAATACCTGGCCTTACTTCGAGAGCAAGAGAACTGTACAG 856

RESULT 10
US-10-276-774-718/c
; Sequence 718, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 718
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-718

Query Match 16.3%; Score 105; DB 17; Length 407;
Best Local Similarity 58.0%; Pred. No. 7.4e-19;
Matches 87; Conservative 33; Mismatches 30; Indels 0; Gaps 0;

QY 444 RCGNGNGARGATYTTACMSNNGTNGTMSNGARATNATGATATATNTYNTGNTT 503
DB 231 AGCTGAGAGGACTTACCTGTGTGTCTCAGAAATCATGATGTATCTCTCTGTGCTT 172

QY 504 YTTNACNTNTGTYTNTATNATGARTGATNTATYTGATYMGNAARGTMSNARGCNGA 563
DB 171 CCTACCTTGAGCTGCTCATGAGATGATATATATCTACAGAAAGTCTCAAAAGCCCA 112
QY 564 RGARGCNGCARGAARAYGCMWSNGAYTA 593
DB 111 AGAGGAGCCCAAGAAACGCGTAAGTCCA 82

RESULT 11
US-10-401-916-12
; Sequence 12, Application US/10401916
; Publication No. US20040002439A1
; GENERAL INFORMATION:
; APPLICANT: Qln, Ning
; APPLICANT: Codd, Ellen
; APPLICANT: D'Andrea, Michael
; TITLE OF INVENTION: DNAs encoding human beta1a sodium channel subunit
; FILE REFERENCE: ORT-1221
; CURRENT APPLICATION NUMBER: US/10/401,916
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/875,456A
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-401-916-12

Query Match 12.6%; Score 81.2; DB 17; Length 807;
Best Local Similarity 33.5%; Pred. No. 7.3e-12;
Matches 157; Conservative 72; Mismatches 222; Indels 18; Gaps 2;

QY 25 CCNTYNGCMWSNYTNGTNTATNTATYTGAGTMSNGTGYTTCNGTNGTGTNGAR 84
DB 10 CTGTGCGCTTATGTGTGCGCGGCGGCACTGGTCTCAGCTGCGGGGCGTGTGAG 69
QY 85 GTNCCMSNGAARACNARGCNGTNCARGMAAYCCNATGAARTYNTGNTGYATMTSNTGY 144
DB 70 GTGACTCGAGACGAGGCGGTGTATGAGATGACCTTCAAAATCTTTGCACTCTCTGC 129
QY 145 ATGAARMNGARGARTNGARCNACNACNGTNGTNGARTGTGTYTAYMNCNARGTNGAR 204
DB 130 AAGCGCCGACGAGACCAACGCTGAGACCTTACCGAGTGTGACCTTCCGCCAGAAAGGC 189
QY 205 GGNARGATYTYTNA-----TNTAYGARTAYMNAAYGNCAYCARGARTNGAR 255
DB 190 ACTGAGAGTGTGTCAAGATCTGTGCGCTATGAGAAATGAGGTGTGACGCTGAGAGGAT 249
QY 256 WSNCCCTTYCARGMNGVNTNARGGAAY-----GGMNSNARGAYTNCARGAY 306
DB 250 GAGCGCTTGAGGGCGCGGTGTGTGAATGCGAGCGGGGCAACAAAGCCTGCAAGAT 309
QY 307 GTMSNATNACNGTNTNAAAYGTNACNTNAAAYGAYMSNGNYTNTAYACNTGYAAYGTN 366
DB 310 CTGTCTATCTTATCATCAACATGTCACTTCAACACACTCGGGGCACTACAGAGTCCACGTC 369
QY 367 WSNMNGARTTYGARTTYARGCNCAYMNCNTTYGTNAARACNACMNGVNTNATNCCN 426
DB 370 TACCGCTGCTCTTCTTGGAAACTGAGACCAACACAGCGGTCTCAAGAAATCCAC 429
QY 427 YTMNGTNAACNARGARGCNGNARGAYTTYACMWSNGTNGTMSNG 475
DB 430 ATTGAGTGTGACAAAGATGTCGGGTGTCTGCTGCCCTTTAACG 478

RESULT 12
US-10-401-916-13
; Sequence 13, Application US/10401916
; Publication No. US20040002439A1


```

; GENERAL INFORMATION:
; APPLICANT: Qin, Ning
; APPLICANT: Codd, Ellen
; APPLICANT: D'Andrea, Michael
; TITLE OF INVENTION: DNAs encoding human beta2a sodium channel subunit
; FILE REFERENCE: ONT-1221
; CURRENT APPLICATION NUMBER: US/10/401,916
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/875,456A
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-401-916-13

Query Match      12.6%; Score 81.2; DB 17; Length 974;
Best Local Similarity 33.5%; Pred. No. 8.5e-12;
Matches 157; Conservative 72; Mismatches 222; Indels 18; Gaps 2;

QY 25 CCATYTCGMSNTYNTGNTATNTATYTGCTGMSNGTNTGYTTCNGTNTGYTGAR 84
DB 13 CTGCTGCTTGTAGTGTGCGCGCGCACTGTGTCTCAGCCTCGGGGCTGCTGAG 72
QY 85 GTNCMSNGARACNGARCGNTGNCARGNAAVCNATGARYTNGTGYATMSNTGY 144
DB 73 GTGGACTCGAGACCGAGCGCGGTGTATGGATGACCTTCAAAATCTTGTGATCTCTGC 132
QY 145 ATGAARNGARNGARNGTNGARCNACNCTGNTGNTGRTGTTATYMGNCNGARNGN 204
DB 133 AAGGCGCGACGAGCAACGCTGAGACCTTCAACCGAGTGAACCTTCCGCAAGGCGC 192
QY 205 GGNARAGATTTTATNA-----TNTAYGARTAYMGNAVGCNCAVCARAGRTNGAR 255
DB 193 ACGGAGAGTGTTCAGATCTCGCTGATGAGATGAGGTGTGCGAGCTGAGAGAGAT 252
QY 256 WSNCCNTTTCARCGMNGNTNCACTGGAAY-----GGMSNAARAGATTTTCARAY 306
DB 253 GAGGCGCTTCAGAGCGCGCGTGTGTGATGAGACCGCGGACCAAAAGACCTGAGAT 312
QY 307 GTTMSATNACNGTNTNATYATGATNATYATGATYATGATYATGATYATGATYATG 366
DB 313 CTGCTATCTTCAACCAATGCTACCTACCAACCTGCGGCGAGCTGAGAGTGCACGTC 372
QY 367 MSNMGNGARTTGTGATTTGAGAGCNCAYMNCNTTGTNABACNACMNGTNTATNCCN 426
DB 373 TACGCGCTGCTCTTCTTGAAATACTACGAGCACAACACCGCTGCTGCAAGAAATCCAC 432
QY 427 YTNMGNTNACNGARCGNGNGARAGATTTTACNMSNGTNTGMSNG 475
DB 433 ATTGAGGTAGTGACAAAGGTGAGTGGGTGCTGCTGCTTACCG 481

RESULT 13
US-10-723-860-6471
; Sequence 6471, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6471
```

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; LENGTH: 3583
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (294)..(315)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1696)..(1712)
; OTHER INFORMATION: n is a, c, g, or t
; US-10-723-860-6471

Query Match      9.0%; Score 57.8; DB 18; Length 3583;
Best Local Similarity 44.3%; Pred. No. 0.00011;
Matches 62; Conservative 23; Mismatches 55; Indels 0; Gaps 0;

QY 442 GARGCNGNGARAGATTTTACNMSNGTNTGMSNGARTNATGATGATATNTYNTGNTN 501
DB 2217 GCAGCCACAGAGACATGCAATCCATGCTGTCTGAGATCAATGATGATGCTCATTTG 2276
QY 502 TTYTNACTNTGTYTNTYNTATNATGATATATATYATGATYATGATYATGATYATG 561
DB 2277 GTGTGACATATGCTGCTGCGAGAGATGATTTACTGCTACAAAGAGATGCTGCCGCC 2336
QY 562 GARGCNGCNCARARAA 581
DB 2337 ACGGAGACTGCTGCACAGGA 2356

RESULT 14
US-10-311-455-911
; Sequence 911, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: Olex, Alexander
; APPLICANT: PIRENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 911
; LENGTH: 6217
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-311-455-911

Query Match      8.2%; Score 52.6; DB 15; Length 6217;
Best Local Similarity 27.9%; Pred. No. 0.0051;
Matches 127; Conservative 61; Mismatches 268; Indels 0; Gaps 0;

QY 96 RACNGRCNGTNCARGNAAVCNATGARYTNGTNTGYATNMSNTGYATGAARMNGA 155
DB 3262 AATTGAAGAATAGAGGTTTGAAGATATGAGTATTTGGTAAAGTATATATGTTGTT 3321
QY 156 RGARGTNGARCGNACNACNCTGNTGNGARTGTTTATATMGNCNARGNGNARGAYTT 215
DB 3322 AGTGTAGAGTTAGTTTGAATTTGATTTTGGTTTGTGATGAGTTACGGTTTACGTA 3381
QY 216 YTNATNTATGARTAYMGNAAYGNCAYCARGAGTNGARMSNCCNTTTCARCGMNGNT 275
DB 3382 TCGTGTGAGGGTTTATGAATGATATAGATGTCGTTTCAGAGTATATAGGAGTAGT 3441
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QY 276 NCARTGCAAYGGMWSNABGAYVYTNCGARCAIGTMSNATNACNGTNTYNAAGTNCANT 335
DB 3442 TGGGGGTGATTTTATTAGGTTATTAGGTTGGGATTTAATTAATTAATGATATAT 3501
QY 336 NAYGAYWSNGNGYNTTAYACNTGAYAGTMSNMNGARTTYGARTTYGARGCNCAYMG 395
DB 3502 TAGGTTAGGAGGTTGAGTTATTATTATTAAGTTTATATAGTTAGTTATATATTTA 3561
QY 396 NCCNTTYGNABACNACMNGNTNATNCCNTYTMNGTNCNCGARGANGCNGARGA 455
DB 3562 GGTGTTAGTGTAGTTGGGTTATTTTATTTGTTGGTTTGTGTGTTAATAGAA 3621
QY 456 YTTTACMWSNGTNGTMSNGARATNATGATATNTYNTNGTNTYTNACNTNTG 515
DB 3622 TATGATATTATTCGTTGTTGAGATTTATGATGATGTTATTTGTTGTTGTTATATG 3681
QY 516 GYTNNTNATNGARATGATNTATYGTAYTMGNNAARGT 551
DB 3682 GTTCGTGTAGAGATGATTTATTTATTAAGAAGAT 3717

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RESULT 15
US-10-184-644-346
; Sequence 346, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; PRIOR APPLICATION DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 346
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-644-346

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Query Match 7.8%; Score 50; DB 14; Length 671;

Best Local Similarity 5.0%; Pred. No. 0.0043;

Matches 31; Conservative 193; Mismatches 394; Indels 0; Gaps 0;

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QY 28 YTNCGMWSNTYNTNGTNTNATNTATYTGCGTMSNGTNTGYTTCNGTNGTNGARGTN 87
DB 11 VPAKMGYHPHWPARIDIDAGAVKPPNKYPIFFPGTHETAPLGPDKLPYDCKDXGK 70
QY 88 CCNWSNGARACNGARGCNGTNCARGGNAAYCNAATGAAATYTMNGTNGTATMSNTGYATG 147
DB 71 PNRKGFNEGLMEIQNNPHASYSAPPPVSSDSEAPANPADSDADEDEDEGVAVTA 130
QY 148 AARMGNGARGARGTNGARGCNAACNCGTNGTNGARTGTTTAYTMGNCCNGARGGNGN 207
DB 131 VTATAASDRHESDSDSDSGNLKRTPALMSVSKRRKASDDDOASVSPSEENS 190
QY 208 AARGATYYTNTATNTAYGARTAYMGAAAYGNCAYCARGARGTNGARWSNCCNTTYCAR 267
DB 191 ESSSESEKTSDDQFTPEKKAAYAPRGPGRKKKKAPASDSDDAKSDAKPEPVAM 250
QY 268 GGMNGYNTNARTGCAAYGGMWSNABGAYVYTNCGARCAIGTMSNATNACNGTNTYNAAY 327

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DB 251 ARSASSSSSSSDSDSVKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDV 310
QY 328 GTCNACNTTAAAGAYWSNGANTNTAYACNTGYAAVGTWMSNMNGARTTYGARTTYGAR 387
DB 311 DRISEWKRRDEARRRLEARRRREDEELRLRLEOEKEKEKRRERREADHGEARSGSS 370
QY 388 GCNCAYMNCNTTYGTNABACNACMNGNTNATNCCNTYTMNGTNCNCGARGARGCN 447
DB 371 GDELRDEDPVVKRGRKGRGPSSSDSEPEALEREAKSKAKQSSSTBPARKPGOK 430
QY 448 GNGARGAYTYACMWSNGTNGTMSNGARATNATGATATAYATNTYNTNGTNTTYTN 507
DB 431 EKRVPRERKQAKPVYERTRRSEBFSMDRVEKKEKPSVEBKQKHSBKFKALKVDS 490
QY 508 ACNTYNTGYTYNTATNBARATGATNTATYGTAYTMGNABGTMWSNABGCGNGARGAR 567
DB 491 PDVKRCLNLEELGTLQVTSQILQKNTDVVATLKIRRYKANDVWEKAAEYTRLSKV 550
QY 568 GCNCGNCARGARAAAYGCMWSNGAYTYATYTMGNATNCCMWSNGARAAAYARGARAAWSN 627
DB 551 LBPXLEAVQKVKAKGMEKEKAEKLEAGBELAGBEAPQEKAEKPSYDLAPVNGEATSQK 610
QY 628 GCNCGTNCNGTNGARGAR 645
DB 611 GSAEDKHEHBGRDSHEG 628

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Search completed: April 7, 2005, 23:40:37
Job time : 504 secs

QY 61 GNTTGYTTCNGTNTGTTGNGARGTNCNWSNGARACNGRGCNGTNGARAGNAAYCCN 120
 DB 61 GTCGTCTTCCCTGTGTGTGTGAAGTCCCTCGAAGACGAGGCGGTGACGGGCAACCCC 120
 QY 121 ATGAARVTMGNTGATYTNMSNTGYATGAARMNGARAGTNGARACNAACNCGTNGTN 180
 DB 121 ATGAAGCTGGCGCTGATCTCTGATGAAGAGAGAGAGTGAAGCCACACCGTGTG 180
 QY 181 GARTGTTTAYWNCNCGNARNGNNAARGAATTTTNTATNTAYARTAYMGNAAYGN 240
 DB 181 GAATGTCTTACAGGCGCCGAGGCGGTAAAGATTTCTTATTTACAGATATCGAATGCG 240
 QY 241 CAYCARGARTNGARMSNCCNTTYCARGGNGMYTNCARTGAAAYGNNMSNARAGAYTN 300
 DB 241 CACGAGAGGTGAGAGGCCCTTTCAGGGGCGCTGAGAGATGACAGACGAGACCTG 300
 QY 301 CARGAYTMSNATNACNGTNTTAAATGTAACNTYTAAGVMSNGANTNTATYACNTGY 360
 DB 301 CAGGAGGTGTCCATCACTGTGCTCAAGTCACTGAAGCATCTGGCCCTACACCTG 360
 QY 361 AAYGTMSMNGARTTYGARTTYGARGCNCAYMNCNTTYTNTAARACNACNMGNTN 420
 DB 361 AATGTGTCCCGGAGTTTGAGTTGAGGCGCATCGGCCCTTGTGAAAGACGACGCGCTG 420
 QY 421 ATNCCNYTMNGNTNACNGARCGNCGNGARAYTAYACNMSNGTNGTNGARATN 480
 DB 421 ATCCCTTAAGATCAACGAGAGGCTGAGAGAGACTTCACTCTGTGTCTCAGAAATC 480
 QY 481 ATGATGTAAATYNTYNTGNTTNTYTNACNTYNTGTYNTYNTATNGARATGATNTATGY 540
 DB 481 ATGATGTATACATCTTCTGTGTCTTCTCACTGTGTGTCTCATCAGATGATATATTCG 540
 QY 541 TAYMNAAGTMSNARCGNCGNARCGNCGNCAAGARAAAYCNCMSNATYTYTNGCN 600
 DB 541 TACAGAAAGGTCTCAAAAGCCGAGAGGACGACCAAGAAACCGCTCTGACTACCTTGC 600
 QY 601 ATNCCMSNGARAAAYARGAAYMSNGTNGTNCNGTNGARAGAR 645
 DB 601 ATCCCATCTGAGAACAGAGAACTCTGCGGTACAGTGGAGGAA 645

RESULT 2
 CRE09664 2555 bp mRNA linear HTC 21-JUL-2004
 LOCUS Full-length cDNA clone CS0DF023YA09 of Fetal brain of Homo sapiens (human).
 DEFINITION
 CRE09664 GI:50490471
 VERSION CR609664
 KEYWORDS HTC; cNSLT cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2555)
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/InvitrogenCorporation1600
 Faraday Avenue
 Genoscope.
 2 (bases 1 to 2555)
 Direct Submission
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
 FEATURES Location/Qualifiers

source 1..2555
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DF023YA09"
 /issue_type="Fetal brain"
 /plasmid="pCMVSPORT_6"

Query Match 72.2%; Score 466; DB 3; Length 2555;
 Best Local Similarity 58.8%; Pred. No. 4,8e-105;
 Matches 379; Conservative 145; Mismatches 121; Indels 0; Gaps 0;

QY 1 ATGCCNCGNTTAAAYMGNTNTTCCNYTNGCWSNYTNGTYNTATNTAYTGGTNGN 60
 DB 235 ATGCTGCTTCAATAGATGTTTCCCTGGCTTCTCTGTGTTATCTACTGGGCACT 294
 QY 61 GNTTGYTTCNGTNTGTTGNGARGTNCNWSNGARACNGRGCNGTNGARAGNAAYCCN 120
 DB 295 GTCGTCTTCCCTGTGTGTGTGAAGTCCCTCGAAGACGAGGCGGTGACGGCAACCCC 354
 QY 121 ATGAARVTMGNTGATYTNMSNTGYATGAARMNGARAGTNGARACNAACNCGTNGTN 180
 DB 355 ATGAAGCTGGCGCTGATCTCTGATGAAGAGAGAGAGTGAAGGACCAACGCTGTG 414
 QY 181 GARTGTTTAYWNCNCGNARNGNNAARGAATTTTNTATNTAYARTAYMGNAAYGN 240
 DB 415 GAATGTCTTACAGGCGCCGAGGCGGTGAAGATTTCTTATTTACAGATATCGAATGCG 474
 QY 241 CAYCARGARTNGARMSNCCNTTYCARGGNGMYTNCARTGAAAYGNNMSNARAGAYTN 300
 DB 475 CACGAGAGGTGAGAGGCCCTTTCAGGGGCGCTGAGAGATGACGAGCAAGACCTG 534
 QY 301 CARGAYTMSNATNACNGTNTTAAATGTAACNTYTAAGVMSNGANTNTATYACNTGY 360
 DB 535 CAGGAGGTGTCCATCACTGTGCTCAACGTCATGAAAGACTCTGGCCCTTACACCTGC 594
 QY 361 AAYGTMSMNGARTTYGARTTYGARGCNCAYMNCNTTYTNTAARACNACNMGNTN 420
 DB 595 AATGTGTCCCGGAGTTTGAGTTGAGGCGCATCGGCCCTTGTGAAAGACGACGCGCTG 654
 QY 421 ATNCCNYTMNGNTNACNGARCGNCGNNGARAYTAYACNMSNGTNGTNGARATN 480
 DB 655 ATCCCTTAAGATCAACGAGAGGCTGAGAGAGACTTCACTCTGTGTCTCAGAAATC 714
 QY 481 ATGATGTAAATYNTYNTGNTTNTYTNACNTYNTGTYNTYNTATNGARATGATNTATGY 540
 DB 715 ATGATGTATACATCTTCTGTGTCTTCTCACTGTGTGCTCTCATGAGATGATATTCG 774
 QY 541 TAYMNAAGTMSNARCGNCGNARCGNCGNCAAGARAAAYCNCMSNATYTYTNGCN 600
 DB 775 TACAGAAAGGTCTCAAAAGCCGAGAGGACGACCAAGAAACCGCTCTGACTACCTTGC 854
 QY 601 ATNCCMSNGARAAAYARGAAYMSNGTNGTNCNGTNGARAGAR 645
 DB 835 ATCCCATCTGAGAACAGAGAACTCTGCGGTACAGTGGAGGAA 879

RESULT 3
 HSM801563 4052 bp mRNA linear HTC 22-SEP-2004
 LOCUS Homo sapiens mRNA, cDNA DKFZp761F182 (from clone DKFZp761F182).
 DEFINITION
 ACCESSION AL136589
 VERSION AL136589.1 GI:13276680
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 4052)
 AUTHORS Oetzelweider, B., Obermaier, B., Deutschenbaur, S., Schaipe, A., Mewes, H.W., Weill, B., Amid, C., Oesinger, A., Fobbo, G., Han, M. and Wiemann, S.

CONSRM The German cDNA Consortium

TITLE	Direct Submission
JOURNAL	Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
COMMENT	clone from S. Wiemann, Molecular Genome Analysis, German Cancer

sequencing consortium of the German Genome Project. This clone (DKFZp761f182) is available at the RPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RPD for ordering:
<http://www.rpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp761f182>
Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.

FEATURES

Source

gene	1. .4052
	/gene="DKFZp761F182"
CDS	804. .1451

CDS

ORIGIN

Query Match	72.2%;	Score 466;	DB 3;	Length 4052;
Best Local Similarity	58.8%;	Pred. No. 6.1e-105;		
Matches 379;	Conservative 145;	Mismatches 121;	Indels 0;	Gaps 0;

Qy	1	ATGCNCNGNTVAAVVMGYNTVTVCCNCTNCCNMGNVNTGNVTAUATAVGGGTTNSN	60
Db	804	ATGCTCGCTTCAATAAGATTGTTTCCCTGGCTCTCTCGTGCTTAATCTACTGGGTCAGT	863
Qy	61	GTNTGYTTYCCNGTNTGYTGNGARGTNCNMNSNGARACNGACNGTNCARGNAAYCCN	120
Db	864	GTCTGCTTCCCTGTGTGTGTGGAAGTGCCCTCGAGAGACGAGGCCGTGCAGGGCAACCCC	923
Qy	121	ATGAARVTMNGNTGYATVWSTGYATGAARMGNGARGARGTNGARGCNAACNACNGTNGT	180
Db	924	ATGAAGCTGCCTCATCTCTCGATGAAGAAGAGAGAGGTGAGGCCACACACGCTGTGTG	983
Qy	181	GARNGSTTYTAYMNCNCNGARGNGNBARAGVTTYVNTAINTVYARATVWGNAAVGN	240
Db	984	GAATGTGTTCTACGAGCCCGAGGGCGGTAAAGATTTCTTATTTACGAGTATCGGAATGCG	1043
Qy	241	CAYCARGARGTNGARWNSNCNTTYCARGGNGNTNCTARTGGAAYGAWMSNAARGAVYT	300
Db	1044	CACACAGAGGTGAGAGAGGCCCTTTTCAGGGGGCGCTCGACGTGGAATGGACAGACGACTG	1100
Qy	301	CARGAGTMSNATNACNGTNTVNAAYGTNACNTYNAAYGAYWSNGVNTVTAACNTGY	360
Db	1104	CAGACGCTGCATCACTGCTGCTCAACGTCACTGAAACGACTCTGGGCTCTCAACCTGC	1163
Qy	361	AAVYTMNSMNGNARTTYGARTTYGARBCNCAVMNCCNTTYGTNAAACNAACMNGNTN	420
Db	1164	AAATGTGTCCTCGGAGTGTGAATTTGGAGGCGATCGGCTTTGTGTGAACAGACGGGCGTG	1223

OY		421	ATTCNCTNNNGGTTACNCAGRGARCGCNGGNGARCAVTTYACMSNGTNTGTWTSNGARTN	480
Db		1224	ATCCCCCTTAAGAGTCACCGAGGAGGGCTGGAGAGSACTTCACCTCTGTGTGTCTAGAATC	1283
OY		481	ATGATGTAAVATNYTYNTGTNTTTYTNACNYTNTGYTYNTATNATGARATGAINTAATGY	540
Db		1284	ATGATGTACATCTCTTGCTGCTTCTCCTCACCTGTGGCTGCATCATCGAGATGATATATTGC	1343
OY		541	TATYGNAABRTGTTWSNARGCNGRGARCGCNGCNCARBAPAAAYGCMWSNGATYAITYTNGCN	600
Db		1344	TACGAAAAGGTCTCAAAGGCCGGAAGAGCAGCCCAAMAAAAACGGGTCTGACTACTTGGCC	1403
OY		601	ATTNCCNSNBARAAAYARGARAAAYWSNGCNGTNCNGTNGANRARGAR	645
Db		1404	ATCCCATCTTAGAACCAAGAGAACTCTGCGGTACCACTGGAGGANA	1448

RESULT 4	1062 bp	EST 01-MAY-2004
LOCUS BX420015		
DEFINITION	BX420015 Homo sapiens PBTAL BRAIN Homo sapiens cDNA clone	
ACCESSION	CSDDF023YA09 5'-PRIME, mRNA sequence.	
VERSION	BX420015	
KEYWORDS	BX420015.2 GI:46929710	
SOURCE	EST.	
ORGANISM	Homo sapiens (human)	
	Homo sapiens	

FEATURES

Source

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/clone="CS0DF023YA09"
/issue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain Vector: PCWVSORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the PCWVSORT 6
vector. Library was not normalized."

```

ORIGIN

Query Match	72.2%;	Score 465.6;	DB 5;	Length 1062;
Best Local Similarity	58.6%;	Pred. No. 3.9e-105;		
Matches 378;	Conservative 146;	Mismatches 121;	Indels 0;	Gaps 0;

QY 1 ATGCGCGCTTAAAGMAGNNTTTCACATYNGCMWSNNTGNTATNATNTATYTGCGTWSN 60
Db 234 ATGCGCGCTTCAATATGATTGTTCCCTCGCTTCTTCTCGTGTATCTATCTGGTACGT 293
QY 61 GTTGTGTTTCCGNTNGTNGARGTNCMWSNAGACNARGCGCTNCCARGGAAATCCN 120

Db 294 GTCCTGCTCCCTGTGTGTGTGGAAGTGCCCTCGAGACGGAGCCGCTGACGGGCAACCC 353
 QY 121 ATGAAATYTMNGNTGYATMNSNTGYATGAARMGNGARGKTNGARCNACNACNGNTN 180
 Db 354 ATGAACTCGCGCTCATCTCTGCATGAAGAGAGAGAGTGAAGCCACACGGGTGG 413
 QY 181 GARTGTTTAAVWNCNGARGNGNAAARGATTTTNTATNTAYGARTAYMNAAYGN 240
 Db 414 GATGTTTCTACAGCGCCCGAGGGCGGTAAAGATTTCTTATTTTACAGATGCGAATGGC 473
 QY 241 CAYCARGATNGARNMNCNTTYCARGMNGYNTCARTGAAYGANSNAARGAYTN 300
 Db 474 CACCAAGAGTGAAGAGCCCTTTCAAGGGCGCCTCAGATGAATGACAGCAAGACCTG 533
 QY 301 CARGATYTMNSNATNACNGNTNTAAVGTNACNTYNTAAVAYMNSNGNTNTAYACNTG 360
 Db 534 CAGGAGGTGCTCACTGCTCAACGTCATCTGAACGACTGCTGCTTACACCTGC 593
 QY 361 AAVGTMSMNGNARTTYGARTTYGARGCNCAVMNCNTTYTNTAARACNACNMNGTN 420
 Db 594 AATGTCTCCCGAGTGTGATGTTGAGGGCATGGCCCTTTGTGAAGACAGCGGCTG 653
 QY 421 ATNCCNTYTMNGNTNACNGARGCGNGNGARGATYTYAACMNSNGTNGTMSNGARATN 480
 Db 654 ATCCCTTAAGAGTCAACCGAGGAGCTGAGAGAGACTTCACTGTGTGCTCAGAAATC 713
 QY 481 ATGATGTAATNTYNTNGTNTTYTNTACNTYNTGYTNTATNTGARAATNTATYTG 540
 Db 714 ATGATGTACATCTTCTGTCTTCTCTCACTGTGTGCTCTCAACGATGATATATGTC 773
 QY 541 TAYMNGNARTYTMNSNARGNGARGCGNGNGARGARAYTYAACMNSNGATYTYNTGNC 600
 Db 774 TACAGAAAGTCTCAAAAGCCGAAGAGGAGCCCAAGAAACGCTGCTGCTATGTC 833
 QY 601 ATNCCMWSNGARAAYARAGARAAYMNGCNGTNCNGTNGARGAR 645
 Db 834 ATCCATCTGAGAACAGAGAACTCTGCGGTACCGAGTGAGAGAA 878
 RESULT 5
 AY419147 648 bp DNA linear GSS 12-DEC-2003
 LOCUS Mus musculus HCM6793 gene, VIRUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AY419147
 VERSION AY419147.1 GI:39775107
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 648)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B.,
 Ferrieri,S., Wang,G., Zheng,X.H., White,T.J., Slinkin,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT These sequences were made by sequencing genomic exons and ordering
 them based on alignment
 FEATURES
 source Location/Qualifiers
 1..648 /organism="Mus musculus"

ORIGIN
 Query Match 71.5%; Score 461.2; DB 9; Length 648;
 Best local similarity 58.3%; Pred. No. 3,8e-104;
 Matches 376; Conservative 145; Mismatches 124; Indels 0; Gaps 0;
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 Db 61 GRTYGTTCCTGCTGTGTGTGTGTAAGTACCTCGAGACGAAAGCCGTGACGGGCAATTC 120
 QY 121 ATGAAATYTMNGNTGYATMNSNTGYATGAARMGNGARGKTNGARCNACNACNGNTN 180
 Db 121 ATGAACTCGCGCTCATCTCTGCATGAAGAGAGAGTGAAGCCACACGGGTGG 180
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 QY 301 CARGATYTMNSNATNACNGNTNTAAVGTNACNTYNTAAVAYMNSNGNTNTAYACNTG 360
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 QY 361 AAVGTMSMNGNARTTYGARTTYGARGCNCAVMNCNTTYTNTAARACNACNMNGTN 420
 Db 361 AATGTCTCCAGGAGTGTGATGTTGAGGGCATGGCCCTTTGTGAAGACCAACAACTA 420
 QY 421 ATNCCNTYTMNGNTNACNGARGCGNGNGARGATYTYAACMNSNGTNGTMSNGARATN 480
 Db 421 ATACCCCTCGAGTCACTGAAGGGCGGAGAAAGACTTCACTGTGTCTGCGAAATC 480
 QY 481 ATGATGTAATNTYNTNGTNTTYTNTACNTYNTGYTNTATNTGARAATNTATYTG 540
 Db 481 ATGATGTACATCTTCTGTCTTCTCTCACTGTGTGCTCTTATGATGATATATGTC 540
 QY 541 TAYMNGNARTYTMNSNARGNGARGCGNGNGARGARAYTYAACMNSNGATYTYNTGNC 600
 Db 541 TACAGAAAGTCTCAAAAGCCGAAGAGGAGCCCAAGAAACGCTGCTGCTATGTC 600
 QY 601 ATNCCMWSNGARAAYARAGARAAYMNGCNGTNCNGTNGARGAR 645
 Db 601 ATCCCTTCAAGAACAGAGAACTCTGTGTGATCCCTGTGAGAGAA 645
 RESULT 6
 AK076466 1359 bp mRNA linear HTC 03-APR-2004
 LOCUS Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
 DEFINITION library, clone:483414B02 product:VOLTAGE-GATED SODIUM CHANNEL
 BETA-3 SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog [Rattus
 norvegicus], full insert sequence.
 ACCESSION AK076466
 VERSION AK076466.1 GI:26345409
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carminci,P. and Hayashizaki,Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)

JOURNAL MEDLINE
PUBMED 99279253
REFERENCE 10349636

AUTHORS
TITLE Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komoto, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL MEDLINE
PUBMED 20499374
REFERENCE 11042159

AUTHORS
TITLE Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Komoto, H., Akiyama, J., Nishi, K., Kitasuna, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawaji, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kiru, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL MEDLINE
PUBMED 20530913
REFERENCE 11076861

AUTHORS
TITLE THE RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
JOURNAL MEDLINE
PUBMED Nature 409, 685-690 (2001)
REFERENCE 5

AUTHORS
TITLE The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL MEDLINE
PUBMED Nature 420, 563-573. (2002)
REFERENCE 6 (bases 1 to 1359)

AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,
Arkawa, T., Bono, H., Carninci, P., Fukuda, S., Fukuishi, Y.,
Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
Hiraoka, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,
Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Komoto, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishii, K.,
Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
Suetsugu, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
Tejima, Y., Toyota, T., Yamamura, T., Yamana, I., Yasuniishi, A.,
Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission
COMMENT Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suhei-ro-cho, Tsukuba-shi, Yokohama,
Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp]
URL: http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
Location/Qualifiers
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FEATURES
SOURCE

CDS

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ORIGIN

Query Match 71.5%; Score 461.2; DB 3; Length 1359;
Best Local Similarity 58.3%; Pred. No. 5.6e-104;
Matches 376; Conservative 145; Mismatches 124; Indels 0; Gaps 0;

Oy 1 ATGCCGNCNTTAAVWGNVTNTTTCNYTGCMNSNTYGTNATNTAYTGGCTMWSN 60
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 57 ATGCCTGCCTCAACAATGCTTCCCTCGAGCTTCTTAGTGCTCATCTACTGGGTAGA 116
|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Oy 61 GTTNVTYTTCCNGTNTGVTNGARGTNCMMWSNBARCONARCGNMGNCARGNAACVN 120
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Db 117 GTCTGCTTCCCCTGTGTGTGAAGATACCTCCGGAGACAGAGCCGTGCAGGGCAAATCC 176
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Oy 121 ATGAARYTNMGNTSYANTMSNTGYATAABMGNBARAGTNGARGCNAACNGTGTN 180
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 177 ATGAAGCTGAGATCATCTCCTGTGATBAAGGAGAGAGGTGCAGGCCAACACTGTAGTG 236
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Oy 181 GARTGTTTTAYWMGNCNGARGGNGSNAARGATYYTTYTNATNTAYGARPTAMGNAAYGN 240
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 237 GAGTGGTTCTPACAGGCCCTGAGGGCGGTAAAGATTCTTATATATGATATCGAAAATGCC 296
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Oy 241 CAYCARBARGTNGARMNSCNTTTCAGGNNMGNTNCRPTGGAAVYGMSNAARAGAYTN 300
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 297 CACCAGAGGTGGAGAACCCCTTCCAAGGTGCTGTGAGTGGAAVYGGAGCAAAAGACCTG 356
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Oy 301 CARGAYGTMSNATNACNGTNYTNAAYGTNACNTYAAGVWMSGNTYTAYAICNTGY 360
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 357 CAGAGCTATTCATCATCTGTTCTCAATGTCACTGTGAATGACTGTGGCTCTTAACATGT 416
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Oy 361 AAYGTNSNMNGARTTYGARITYGARCNCAVWGNCNTTYGTNAARCAACNMGYTN 420
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Db 417 AATGTGTCCAGGGAGTTTGAAGTGAAGACACCGGCCCTTTGGAAGACCAAGAAGTA 476
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
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Db 597 TAGAGAAAGGTCTCTAAGGCCGAAAGAGGAGCCTCAGGAAATATGCTGTGACTACTTGC 656
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Oy 601 ATTCCMWSNGARAAYARBARAAYWSGNCNGTNCNGTNGARGAR 645
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 657 ATTCCTTCAGAGAACAGAGAACTCTGTGTGTAACCTGTGAGAGAA 701
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

RESULT 7
AKO49747
LOCUS AKO49747 3549 bp mRNA linear HTC 03-Apr-2004
DEFINITION Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530046B12 product:VOLTAGE-GATED SODIUM CHANNEL BETA 3 SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog [Rattus norvegicus], full insert sequence.
ACCESSION AKO49747

VERSION AK049747.1 GI:26340475
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS 1. Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE
AUTHORS 2. Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komoto, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE
AUTHORS 3. Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komoto, H., Akiyama, J., Nishi, K., Katsunai, T., Taahito, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE
AUTHORS 4. The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
MEDLINE
PUBMED
REFERENCE
AUTHORS 5. The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE
PUBMED
REFERENCE
AUTHORS 6 (bases 1 to 3549)
ADACHI, J., AIZAWA, K., AKIMURA, T., ARAKAWA, T., BONO, H., CARNINCI, P., FUKUDA, S., FURUKO, M., HANAGAKI, T., HARA, A., HASHIZUME, W., HAYASHIDA, K., HAYATSU, N., HIRAMOTO, K., HIRAOKA, T., HIROZANE, T., HORI, F., IMOTANI, K., ISHII, Y., ITOH, M., KAGAWA, I., KASUKAWA, T., KATOH, H., KAWAI, J., KOJIMA, Y., KONDO, S., KONNO, H., KODA, M., KOYA, S., KURIHARA, C., MATSUYAMA, T., MIYAZAKI, A., MURATA, M., NAKAMURA, M., NISHI, K., NOMURA, K., NUMAZAKI, R., OHNO, M., OHSAO, N., OKAZAKI, Y., SAITO, R., SAITOH, H., SAKAI, C., SAKAI, K., SAKAZUME, N., SANO, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yaeunishi, A., Muramatsu, M., and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.

FEATURES
source Location/Qualifiers
1..3549
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="PANTOM DB:C530046B12"
/db_xref="taxon:10090"
/clone="C530046B12"
/issue_type="spinal cord"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"
232..879
/note="unnamed protein product; VOLTAGE-GATED SODIUM CHANNEL, BETA-3 SUBUNIT (SODIUM CHANNEL, BETA 3 SUBUNIT) homolog [Rattus norvegicus] (SPR|Q9JK00, evidence: PASTY, 99.5%id, 100%length, match=646)
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/codon_start=1
/protein_id="BAC33901.1"
/db_xref="GI:26340476"
/translation="MPAPRLPLASLVIYWRVCPVCVPSFEAEVQNSMELR CISKRESEVNTVEMFYRPEGGDFLITERNHGVSEPFQRLQNSKLDQ VSIYVNLVNSGLYTCNVSEFEFEAEFAPVKTTRLPLRVTEAGDFTSVSEI MMVILVFLTLWLFLEMICYRKVSKAEBAQENASDYLAIPESENKENVPEE"
ORIGIN
Query Match 71.5%; Score 461.2; DB 3; Length 3549;
Best Local Similarity 58.3%; Pred. No. 9.1e-104; Indels 0; Gaps 0;
Matches 376; Conservative 145; Mismatches 124;
1 ATGCCGCTTAAAYAGNATNTTCCNTYNGCNSNYTGTNTAATNTAATYGGGTGWSN 60
232 ATGCCGCTTCAACGAGATTTGCTTCCCTAGCTTCTAGTGCTATCTAGTGGTCAAG 231
61 GTNTGTTTCGNTGTGTGNGARGTGCCNSNGAPACNGARGCINTCARGNAAYCCN 120
292 GTCTGCTTCCGTGTGTGTAGAGTACCTCGGAGACGAAAGCCGTGACGGCAATTC 351
121 ATGAATYTMGNTGTATNWSNTGTATGARMGARGAGTNGARGCNAACNAGTNGTN 180
352 ATGAACCTGAGTGCATCTCCGATGAGAGGAGAGAGGTGAGGACACACTGATG 411
181 GARTGTTTAAVWNCNGARGGNGNARGATYTTTAAATNTAATYARTAYMNAAYGN 240
412 GAGTGTTTCAACGAGCTAGGCGGTAAAGATTCTTATATATAGATATGAAATGCG 471
241 CAVCARGANGTARGNSCNCNTTTCARGGNMGYNTCAATGCAAYGNSMAARGAYTN 300
472 CACCAAGAGGTGAGAGAGCCCTTCCAAAGTGTGCTGAGTGAATGGAGCAAAAGCT 531
301 CARGAGTMSNATNACGNTNTYNAAGTNAAGYNAAGVWSNGANTNTAYACNTGY 360
532 CAGGAGGTATCCATCACTGTTCAATGTCACCTGAATGACTCTGACCTCTACATGT 591
592 AATGTCTCAGGAGGATTAGTTGCAAGACACCGGCTTTGTGAAGACCAAGACTA 651
361 AAYGTMSNMNGARTTGTGARTTGTGARGNCAYMNCNTTGTNTAARACNACMANTTN 420
592 AATGTCTCAGGAGGATTAGTTGCAAGACACCGGCTTTGTGAAGACCAAGACTA 651
421 ATNCCNTYTMNGTNAACNGARGGNGNARGAGATTTTACNWSNGTNGTMSNGARATN 480
652 ATACCCCTCGAGTCACTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 711
481 ATGATGTAAATYNTYNTGNTTYYTNAACNTYNTGTYTNTAATNGARATGATNTAYTG 540
712 ATGATGTAAATCTCTGCTGCTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 771
541 TAYMNGAATGTMNGTNAACNGARGGNGNARGAGGNGCNCARBAAYGNSNGATYNTGNC 600
772 TACAGAAAGGTCTCTAAGGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 831
601 ATNCCNWSNGAARAAAYARBARAAAYMSNGCNGTNCNGTNGARGAR 645
832 ATCCCTTACAGAGAAACAGAGAACTCTGTGTATACCGTGTGAGGAA 876

RESULT 8	AK049286	4119 bp	mRNA	linear	HTC 03-APR-2004
LOCUS	AK049286				
DEFINITION	Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:c330019103 product:VOLTAGE-GATED SODIUM CHANNEL BETA-3 SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog [Rattus norvegicus], full insert sequence.				
ACCESSION	AK049286				
VERSION	AK049286.1	GI:26093400			
KEYWORDS	HTC, CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komoto, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20459374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komoto, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				
MEDLINE	5				
PUBMED	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.				
REFERENCE	Analyses of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs				
AUTHORS	Nature 420, 563-573 (2002)				
TITLE	6 (bases 1 to 4149)				
JOURNAL	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hizomoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imocani, K., Iehli, Y., Itoh, M., Kagawa, T., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Komoto, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohashi, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takanashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.				
REFERENCE	Direct Submission				
AUTHORS	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail:genome-res@gsc.riken.jp].				

[illegible]

```

Db      950 CTRACGAGAAAGCTCTCTAAGCCCAAGAGCAGCTCAGGAAATGCTGTGACTTCTGCTTGC 1009
Qy      600 NATNCCNSNGARAAAYAAAGARAAAYWSNGCNGTNGCNGTNGAR 645
      1010 TATCCCTTCAGAGAACAGAGAACTGTGTGATCCCGTGAGAGAA 1055

RESULT 9
BM933157      636 bp      mRNA      linear      EST 13-MAR-2002
LOCUS      BM933157
DEFINITION      UI-M-BH3-beg-d-04-0-UI.r1 NIH BMAP M S4 Mus musculus cDNA clone
ACCESSION      BM933157
KEYWORDS      UI-M-BH3-beg-d-04-0-UI 5', mRNA sequence.
SOURCE      EST.
ORGANISM      Mus musculus (house mouse)
MUSCULUS      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 636)
Normalisation and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL      97044477
MEDLINE      8689548
PUBMED
COMMENT      Contact: Chin, H
      National Institute of Mental Health
      6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
      20892-9643, USA
      Tel: 301 443 1706
      Fax: 301 443 9890
      Email: mestr@mail.nih.gov
      cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
      cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
      DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
      Clone Distribution: Researchers may obtain clones from Research
      Genetics (www.resgen.com).
      Seq primer: M13 REVERSE
      Location/Qualifiers
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      /dev_stage="27-32 days"
      /lab_host="DH10B (Life Technologies)"
      /note="Vector: PT73D-Pac (Pharmacia) with a modified
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      NIH_BMAP_M_S4 library is a subtracted library of a series,
      ultimately derived from a mixture of individually tagged
      normalized libraries from ten regions of the mouse brain
      (cerebellum, brain stems, olfactory bulbs, hypothalamus,
      cortex, amygdala, basal ganglia, pineal gland, striatum,
      hippocampus) after a series of subtractions to reduce the
      representation of cDNAs from which ESTs had already been
      generated. The following serially subtracted libraries
      were generated in this process: NIH_BMAP_M_S3.1,
      NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
      NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library
      (NIH_BMAP_M_S4) was constructed as follows: PCR-amplified
      cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and
      NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived
      was used as a driver in a hybridization with a pool of
      the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
      libraries in the form of single-stranded circles. The
      remaining single-stranded circles (subtracted library)
      was purified by hydroxyapatite column chromatography,
      converted to double-stranded circles and electroporated
      into DH10B bacteria (Life Technologies) to generate the
  
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ORIGIN

Query Match 69.4%; Score 447.8; DB 5; Length 636;
 Best Local Similarity 58.1%; Pred. No. 8.5e-101;
 Matches 365; Conservative 142; Mismatches 121; Indels 0; Gaps 0;

NIH BMAP M S4 library. This procedure has been previously
 described [Bonaldo, Lennon and Soares, Genome Research
 6:791-806, 1996]"

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Qy      1 ATGCCGNCNTTAAATGATTTTCCNTYNGCNSMYTNGTNTAATNTATYGGTNSN 60
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Qy      121 ATGAATYTMNGTATGATNTGATGAARMNGARAGTNGARCNACNACNGTNGTN 180
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Db      421 ATNCCNYTMNGTNCNGARCGNNGNGARAGATTTACNWSNNTNGTNGSNGARATN 480
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Qy      481 ATGATGATATATYNTYNTGNTTNTYTNACNTNTGTYNTYNTAATGATATATYTG 540
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Db      541 TATMGTAARCTWMSNARCGNARGCGNCGNCAAGAAAGCNSNAGATYATYNNCGN 600
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RESULT 10
BX445002      975 bp      mRNA      linear      EST 04-MAY-2004
LOCUS      BX445002
DEFINITION      CS0DF023YA09 5-PRIME, mRNA sequence.
ACCESSION      BX445002
VERSION      BX445002.2 GI:47009181
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 975)
REFERENCE      Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
      Full-length cDNA libraries and normalization
      Unpublished (2001)
      On May 15, 2003 this sequence version replaced gi:30782286.
      Contact: Genoscope
      Genoscope - Centre National de Sequencage
  
```

2 rue Gaston Cremieux, CP 5706 91057 Evry cedex - FRANCE
Email: segrif@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primer
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 6147.r
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdnats-CS1AF005ZED05QPlAc-6147.r>

FEATURES

SOURCE

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/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-1150 (dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

```

ORIGIN

Query Match	69.4%;	Score 447.8;	DB 5;	Length 975;
Best Local Similarity	57.9%;	Pred. No. 1.1e-100;		
Matches 373;	Conservative 146;	Mismatches 124;	Indels 1;	Gaps 1;

QY	1	ATGCNGCNITTYAAVMGVYNTTTCYCNNTGCGNMBNNTNGTNYTAATYAYGGGTNSN	60
Db	235	ATCGCTGCGCTTCAATAGATTGTTCCCTGCGCTCTCTCGTCTTATCTACGTGGTCACT	294
QY	61	GTNTGYTTYCCNGTNTGYGTNGARGTNCNMSNGARCNAGARGCNTGCARGNAAYCCN	120
Db	295	GTCTGCTCCCTGTGTGTGTGGAAATGCCCCGTGAGAGCGAGGCGCTGACAGGGCAACCCC	354
QY	121	ATGAARYNNMENTGYATMSNTGYATGAARMGNNGARGRGTNNGARGCNAACNCTNTGNT	180
Db	355	ATGAAGCTGCGCGCTGATCTCTCGCATYGAAGAGAGAGAGGTGAGAGCCACCACGTGTGTG	414
QY	181	GARTGTTYATVMGNCNGARGGNGNARGAITYTYNTATNTATYAGARTAYMNAAYGN	240
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QY	241	CAYCARGARGTNGARWNSNCNTTYCARGGNMNTNCAPIEGAAYGSMNSNAARGAYYTN	300
Db	475	CACCGAGAGGTGAGAGGCCCTTTTCAGGGGCGCTGCAGTGAATGGACGACGAAGACTCG	534
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Db	655	ATCCCCCTPAAGATCACCGAGAGGCGCTGAGAGGACTTCACCTCTGTGTCTTCAGAAATC	714
QY	481	ATGATGTATVATNTYNTYNTGNTTYTNAACNTYNNCGYNTYNTATNGARATGATNTAYGY	540
Db	715	ATGATGTATCATCTTCTGTGTCTTCTTCTCACCTTGTGGCTGCTCATCGAAGTGAITATATTCG	774
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Db	775	TACGAAAGGTCTCAAAAGCGAAGAGGAGGCCAAGAAAGCGCTGTGACTACTCTGCC	834
QY	601	ATNCCMSNGARAYAARGARAYYNSGNCNTNCCNTNGARGA	644
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RESULT 11	BB614118	LOCUS	DEFINITION	13CCEGCTON
	BB614118	672 bp	mRNA	linear
	BB614118	RIKEN full-length enriched, 0 day neonate head Mus musculus cDNA clone 4833414B02 5', mRNA sequence.		EST 26-OCT-2001

VERSION BB614118.1 GI:16454578
KEYWORDS EST.

ORGANISM

REFERENCES

ADDITIONAL INFORMATION

JOURNAL	Unpublished (2001)
TITLE	RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
COMMENT	Contact: Yoshihide Hayashizaki

Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: <http://genome.shiba.riken.jp/Cernici/>. P. Shibata, Y. Hayatsu, N. Sugahara, Y. Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

wagci, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubara, Y., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaka, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

Komuro, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Suganata, Y. and Hayashizaki, Y.,
Riken integrated sequence analysis (Risa) system--384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771. (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. *Genome Res.* 11(2), 281-289 (2001)

Kondo, S., Shimagawa, A., Saito, T., Kiyosawa, H., Yamashita, I., Mizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashibara, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

mouse tissues.

FEATURES

Source

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/organism="Mus musculus"
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head"
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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken

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Matches 375; Conservative 142; Mismatches 123; Indels 5; Gaps 2;

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DEFINITION 602391245F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4503250 5',
ACCESSION BG294174
VERSION BG294174.1 GI:13054543
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMU at:
http://image.llnl.gov

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Location/Qualifiers

FEATURES

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Note: this is a NIH_MGC library."

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DEFINITION BP200910 Sugano cDNA library, amygdala Homo sapiens cDNA clone
ACCESSION BP200910
VERSION BP200910.1 GI:52050356
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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 1 (bases 1 to 582)
 Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 Genome Res. 14 (9), 1711-1718 (2004)
 CONTACT: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.
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 DEFINITION IMAGE:6831594 5', mRNA sequence.

ACCESSION CAT49311
 VERSION CAT49311.1 GI:25570984
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 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 723)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bhs-remail.nih.gov
 Tissue Procurement: Dr. Jim Loh, University of Iowa
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA library arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
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 /note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is ACCGAGACG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."
 ORIGIN
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

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- 8: gb_pl:*
- 9: gb_dr:*
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- 14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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5	1116	99.3	3296	9 AB097521	AB097521 Macaca fa
6	1105	98.3	645	6 AX048004	AX048004 Sequence
7	1105	98.3	2220	6 AR359849	AR359849 Sequence
8	1105	98.3	2220	6 AX039099	AX039099 Sequence
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10	1105	98.3	2632	6 AX048005	AX048005 Sequence
11	1105	98.3	3107	10 AF378093	AF378093 Rattus no
12	1105	98.3	3108	6 AX047984	AX047984 Sequence
13	1105	98.3	3910	6 BC070899	BC070899 Rattus no
14	1097	97.6	4025	10 AK173115	AK173115 Mus muscu
15	1097	97.6	4169	10 BC053919	BC053919 Mus muscu
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22	714	63.5	1654	5 BC077295	BC077295 Xenopus 1
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26	473	42.1	1404	9 HUMSCN1B	L10338 Human sodi
27	473	42.1	1525	9 BC067122	BC067122 Homo sapi
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32	468	41.6	1125	10 MMU46681	U46681 Mus musculu
33	468	41.6	1340	10 MMU5786	U5786 Mus musculu
34	468	41.6	1568	10 BC009652	BC009652 Mus muscu
35	423	37.6	1239	9 BC021266	BC021266 Homo sapi
36	400.5	35.6	140307	2 AC135353	AC135353 Mus muscu
37	400.5	35.6	174285	2 AC145484	AC145484 Lemur cat
38	400.5	35.6	238861	2 AC148331	AC148331 Mus muscu
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40	396.5	35.3	127347	2 AP000682	AP000682 Homo sapi
41	396.5	35.3	144833	2 AC063921	AC063921 Homo sapi
42	396.5	35.3	149800	2 AC021981	AC021981 Homo sapi
43	396.5	35.3	172546	2 AC024604	AC024604 Homo sapi
44	396.5	35.3	178169	2 AP002765	AP002765 Homo sapi
45	396.5	35.3	178431	2 AP002749	AP002749 Homo sapi

ALIGNMENTS

RESULT 1	AR359850	Sequence 4 from patent US 6593565.	1261 bp	DNA	Linear	PAT 17-AUG-2003
LOCUS	AR359850					
DEFINITION	Sequence 4 from patent US 6593565.					
ACCESSION	AR359850					
VERSION	AR359850.1	GI:33766660				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1261)					
AUTHORS	Heslin,P. and Lynam,N.R.					
TITLE	Vehicle interior rearview mirror assembly including an					
JOURNAL	Patent: US 6593565-A 4 15-JUL-2003;					
FEATURES	Location/Qualifiers					
source	1..1261					
ORIGIN	/mol_type="genomic DNA"					
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Score:	1124.00	Matches:	215			
Percent Similarity:	100.00%	Conservative:	0			
Best Local Similarity:	100.00%	Mismatches:	0			
Query Match:	100.00%	Indels:	0			
DB:	6	Gaps:	0			


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MEDLINE      20160948
PUBMED      10688874
REFERENCE
AUTHORS      Morgan, K.
JOURNAL      Direct Submission
              Submitted (28-JUN-1999) Morgan K., Biochemistry, University of
              Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
REMARK       Revised by [4]
              (bases 1 to 1261)
REFERENCE
AUTHORS      Morgan, K.
JOURNAL      Direct Submission
              Submitted (13-MAR-2000) Morgan K., Biochemistry, University of
              Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
COMMENT       On Mar 14, 2000 this sequence version replaced gi:7160974.
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ORIGIN
3'UTR
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Alignment Scores:
Pred. No.:      1.98e-122      Length:      1261
Score:          1124.00      Matches:      215
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
Gaps:           9              0

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Qy      21 ValCysPheProValCysValGluValProSerGluThrGluValValGlnGlyAsnPro 40
Db      436 GTCTGCTCCCTGCTGTGTGTGGAAGTCCCTCGAGACGAGGCGCGTGCAGGCAACCCC 495
Qy      41 MetLeuLeuArgCysIleSerCysMetLeuArgGluGluValGluValaThrThrValVal 60
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Qy      61 GluTrpPheTyrArgProGluGluGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
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Qy      201 IleProSerGluLeuLysGluAsnSerAlaValProValGluGlu 215
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DEFINITION      Homo sapiens mRNA for KIAA1158 protein, partial cds.
ACCESSION      AB032984
VERSION      AB032984.1 GI:6330135
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Hiroseawa, M., Nagase, T., Ishikawa, K., Kikuno, R., Nomura, N. and
Ohara, O.
Characterization of cDNA clones selected by the Genemark analysis
from size-fractionated cDNA libraries from human brain
DNA Res. 6 (5), 329-336 (1999)
20039618
10574461
REFERENCE
2 (bases 1 to 5306)
Ohara, O., Nagase, T. and Kikuno, R.
Direct Submission
Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology, 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail: cdnainfo@kazusa.or.jp,
URL: http://www.kazusa.or.jp/huge/, Tel: +81-438-52-3913,
Fax: +81-438-52-3914)
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 QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuThrCys 120
 DB 306 CAGAGCGTGCATCAGCTGCTCAACGCTCACTGAAAGCACTGGGCTCTACACCTGCG 365
 QY 121 AsnValSerArgGluPheGluPheGluValHisArgProPheValIleThrArgLeu 140
 DB 366 AATGTGTCCCGGAGTTTGAGTTGAGCGCGATCGCCCTTGTGAAACACACCGCGCTG 425
 QY 141 IleProLeuArgValThrGluGluValGlyGluAspPheThrSerValIleSerGlu 160
 DB 426 ATCCCACTAAGAGCACCGAGGAGCGGAGAGGACCTTCACCTGTGTGCTCAGAAATC 485
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 DB 546 TACAGAAAGCTCTCAAAAGCCGAAAGGACGACCCCAAGAAAGCGTCTGACTACTGCTG 605
 QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
 DB 606 ATCCATCTGAGAACAGAGAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 650
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 DEFINITION Sequence 21 from Patent WO0069912.
 ACCESSION AX048004
 VERSION AX048004.1 GI:11876882
 KEYWORDS
 SOURCE Lepus sp.
 ORGANISM Lepus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Lepus.
 REFERENCE 1
 AUTHORS Curtiss, R. A.
 TITLE Gene encoding a sodium channel beta-3 subunit protein
 JOURNAL Patent: WO 0069912-A 21 23-NOV-2000;
 Millennium Pharmaceuticals, Inc. (US)
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 Score: 1105.00 Matches: 211
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 Best Local Similarity: 98.14% Mismatches: 4
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 Gaps: 0
 DB: 6
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 QY 81 HisGlnGluValGluSerProPheGlnGlyValGluGlnIntPaspGlySerIysAspLeu 100
 DB 241 CACCAAGAGTAGAGAGCCCTTTCAGAGGGGCGCTGACGTGAAATGACGACAGGACCTG 300
 QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuThrCys 120
 DB 301 CAGAGCGTGCATCAGCTGCTCAACGCTCACTGAAAGCACTGGGCTCTACACCTGCG 360
 QY 121 AsnValSerArgGluPheGluPheGluValHisArgProPheValIleThrArgLeu 140
 DB 361 AATGTGTCCCGGAGTTTGAGTTGAGCGCGATCGCCCTTGTGAAACACACCGCGCTG 420
 QY 141 IleProLeuArgValThrGluGluValGlyGluAspPheThrSerValIleSerGlu 160
 DB 421 ATACCTTGGAGTCACTGAAAGAGCGGAGAGACATTCACCTCGTGTCTCGGAATC 480
 QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuThrLeuLeuIleGluMetIleTyrCys 180
 DB 481 ATGATGATCATCTTCTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
 QY 181 TyrArgLysValSerIysValGluGluValAlaGlnGluAsnAlaSerAspTyrLeuAla 200
 DB 541 TACAGAAAGCTCTCAAAAGCCGAAAGGACGACCCCAAGAAAGCGTCTGACTACTGCTG 600
 QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
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 DEFINITION Sequence 3 from patent US 6593565.
 ACCESSION AR359849
 VERSION AR359849.1 GI:33766559
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1
 AUTHORS Heel, J. P. and Lynam, N. R.
 TITLE Vehicle interior rearview mirror assembly including an
 JOURNAL Patent: US 6593565-A 3 15-JUL-2003;
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Db	603	CACCAAGAGGTGAGAGGCCCTTCCAGGCCGCTGCAGCTGGAATGGAGCAAAAGACTTG	662
Qy	101	GIaSPaYValSerIeThrValIeuAsnValThrIeuAsnAsPSeGIYleuTYrThrCys	120
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Db	783	ATACCTTTGGAGTACCTGAAGAGGCGGGAAGAAAGCTTCACTCCGTGCTCGGAATTC	842
Qy	161	MeIeMetTYrIleIeuIeuValPheIeuThrIeuTYrIleuIleGIuMeIleTYrCys	180
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Db	363	ATGGCTGCTTCAACAGATTGCTTCCCTCAGCTTCTCTAGTCACTCATCTAGCTGAGT	422
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Qy	61	GluTrpPheTyrArgProGlnGlyGlyValAspPheLeuIleTyrGluTyrArgAsnGly	80
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Db	603	CACGAGAAAGTGGAGAGACCCCTTCCAGGCGCTGACAGTGAATGGAGCAAAAGACTG	662
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Qy	141	IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValIleSerGluIle	160
Db	783	ATACCTTTGGAGTCACTGAAAGGCGGGAGAAACATTCACCTCCGGTGTCCGAATTC	842
Qy	161	MetMetTyrIleIleuLeuValPheLeuThrIleuTrpLeuLeuIleGluMetIleTyrCys	180
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LOCUS	AX039099		linear
DEFINITION	Sequence 3 from Patent WO0063367.		
ACCESSION	AX039099		
VERSION	AX039099.1	GI:11229275	
VERSIONS			

SOURCE ORGANISM
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Rattus sp.
Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE	AUTHORS	TITLE	JOURNAL
1	Cox, P., Dixon, A., Jackson, A. and Morgan, K.	A novel family of beta sub-unit proteins from a voltage-gated sodium channel, nucleic acids encoding them and therapeutic or diagnostic uses thereof	Patent: WO 0063367-A 3 26-OCT-2000;

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Length:	2220

Pred. No.:	7.14e-120	Length:	2220
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Best Local Similarity:	98.14%	Mismatches:	4
Query Match:	98.31%	Indels:	0
DB:	6	Gaps:	0

US-09-977-579-2 (1-215) x AX039099 (1-2220)

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LOCUS DEFINITION	2220 bp	mRNA	linear	ROD 29-JAN-2003
LOCUS	RNO243395			
DEFINITION	Rattus norvegicus mRNA for voltage-gated sodium channel beta-3 subunit.			
ACCESSION	AJ243395			
VERSION	AJ243395.2			
KEYWORDS	scn3b gene; voltage-gated sodium channel beta-3 subunit.			
SOURCE	Rattus norvegicus (Norway rat)			
ORGANISM	Rattus norvegicus			
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
REFERENCE	1			
AUTHORS	Morgan, K., Stevens, E.B., Shaw, B., Cox, P., Dixon, A.K., Lee, K., Plincock, R.D., Hughes, J., Richardson, P.J., Mizuguchi, K. and Jackson, A.P.			
TITLE	beta 3: an additional auxiliary subunit of the voltage-sensitive sodium channel that modulates channel gating with distinct kinetics			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (5), 2308-2313 (2000)			
MEDLINE	20160948			
PUBMED	10688874			
REFERENCE	2			
AUTHORS	Morgan, K.			
TITLE	Direct Submission			
JOURNAL	Submitted (28-JUN-1999) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM			
REMARK	Revised by [3]			
REFERENCE	3 (base 1 to 2220)			
AUTHORS	Morgan, K.			

TITLE Direct Submission
JOURNAL Submitted (09-MAR-2000) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
COMMENT On Mar 14, 2000 this sequence version replaced gi:7161888.
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Pred. No.: 7,14e-120 Length: 2220
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Percent Similarity: 98.14% Conservative: 0
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Query Match: 98.31% Indels: 0
Gaps: 0
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QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTTPValSer 20
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DB 423 GTCTGCTTCCCTGTGTGTGTGGAAGTCCCTCGAGACAGAGCGGTGCGAGGCAATCC 482
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DB 483 ATGAAGCTGAGGTGCATCTCTGCATGAAGAGGAGGAGGTGAGGCGCACCATGCTG 542
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DB 543 GAGTGGTTCTACAGGCTGAGGCGGTAAAGATTCTTATATATGATGATCCGGAATGCG 602
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QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
DB 963 ATCCCTTCAGAGAACAGAGAACTCTGTGTGACTGTGAGAGAA 1007
RESULT 10
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DEFINITION Sequence 22 from Patent WO0069912.
ACCESSION AX048005
VERSION AX048005.1 GI:11876883
KEYWORDS
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ORGANISM
Rattus sp.
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE
1
AUTHORS Cutler,R.A.
TITLE Gene encoding a sodium channel beta-3 subunit protein
JOURNAL Patent: WO 0069912-A 22 23-NOV-2000;
Milleium Pharmaceuticals, Inc. (US)
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Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservative: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
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QY 41 MetValLeuArgCySileSerCyMetLysArgGluGluValGluAlaThrThrValVal 60
DB 198 ATGAAGCTGAGGTGCATCTCTGCATGAAGAGGAGGAGGTGAGGCGCACCATGCTG 257
QY 61 GluThrPheTyrArgProGluGluGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
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QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
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Qy      161 MetMetTyrIleLeuLeuValPheLeuThLeuTyrLeuLeuIleGluMetIleTyrCys 180
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Qy      181 TyrArgLysValSerLysAlaGluGluAlaAlaGluGluAsnAlaSerAspTyrLeuAla 200
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Qy      201 TLeProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db      678 ATCCCTTCAGAGAACAGAGAACTGTGTGACTGTGTGAGGAA 722

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LOCUS        Rattus norvegicus sodium channel beta 3 subunit (SCN3B) mRNA,
DEFINITION   complete cds.
ACCESSION   AF378093
VERSION     AF378093.1 GI:14165175
KEYWORDS
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
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REFERENCE    1 (bases 1 to 3107)
AUTHORS     Qu, Y., Curtis, R., Lawson, D., Gilbride, K., Ge, P., Distefano P.S.,
            Sillor-Santlago, I., Catterall W.A. and Schener, T.
TITLE       Differential modulation of sodium channel gating and persistent
            sodium currents by the beta1, beta2, and beta3 subunits
JOURNAL     Mol. Cell. Neurosci. 18 (5), 570-580 (2001)
MEDLINE     21919106
PUBMED      11922146
REFERENCE    2 (bases 1 to 3107)
AUTHORS     Curtis, R.
TITLE       Direct Submission
JOURNAL     Submitted (05-MAY-2001) Neurobiology, Millennium Pharmaceuticals
            Inc., 75 Sidney Street, Cambridge, MA 02139, USA
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Pred. No.:      1..1e-119      Length:      3107
Score:          1105.00      Matches:      211
Percent Similarity: 98.14%      Conservative: 0
Best Local Similarity: 98.14%      Mismatches: 0
Query Match:    98.31%      Indels:      4

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Qy      21 ValCysPheProValCysValGluValProSerGluThGluAlaValGluGluAsnPro 40
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Qy      81 HisGluGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
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LOCUS        Sequence 1 from Patent WO0069912.
ACCESSION   AX047984
VERSION     AX047984.1 GI:11876881
KEYWORDS
SOURCE      Rattus sp.
ORGANISM    Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE    1
AUTHORS     Curtis, R.A.
TITLE       Gene encoding a sodium channel beta-3 subunit protein
JOURNAL     Patent: WO 0069912-A 1 23-NOV-2000;
            Millennium Pharmaceuticals, Inc. (US)
FEATURES
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Alignment Scores:

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Pred. No.: 1.1e-119 Length: 3108
 Score: 1105.00 Matches: 211
 Percent Similarity: 98.14% Conservative: 0
 Best Local Similarity: 98.14% Mismatches: 4
 Query Match: 98.31% Indels: 0
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 QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
 Db 138 GTCTGCTTCCCTGCTGTGTGTGGAAGTGCCTCGAGAGACAGACCGCTCAGGCGCATCC 197
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 Db 678 ATCCCTTCAGAGAACAGAGAACTCTGTGTGTAAGCTGTGAGAGAA 722

RESULT 13
 BC070899
 LOCUS
 DEFINITION
 Rattus norvegicus sodium channel, voltage-gated, type III, beta,
 mRNA (cDNA clone MGC:91409 IMAGE:7100476), complete cds.
 ACCESSION
 BC070899
 VERSION
 BC070899.1 GI:47477789
 KEYWORDS
 MGC.
 SOURCE
 Rattus norvegicus (Norway rat)
 ORGANISM
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE
 1 (bases 1 to 3910)
 AUTHORS
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

TITLE
 JOURNAL
 PUBMED
 JOURNAL
 REFERENCE
 TITLES
 JOURNAL
 REMARK
 COMMENT

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huljk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shenchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Gironwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,
 Scherch, A., Schein, J.E., Jones, S.J. and Merrin, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 3910)
 Director MGC Project.
 Direct Submission
 Submitted (17-MAY-2004) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Howard Jacobs
 cDNA Library Preparation: Express Genomics
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nih.gov
 Akhter, N., Ayle, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Binkley, C., Brooke, S.,
 Dietrich, N.L., Granite, S., Guan, K., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, F., Legaaspi, R.,
 Maduro, Q.L., Masello, C., Masker, B., Mastlian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stanki, P., Thomas, P.J., Touchman, J.W.,
 Tsurgon, C., Vogt, D.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAX Plate: 175 Row: 9 Column: 5
 This clone was selected for full length sequencing because it
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ORIGIN

Alignment Scores:
Pred. No.: 1,48e-119 Length: 3910
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservative: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 10 Gaps: 0

US-09-977-579-2 (1-215) x BC070899 (1-3910)

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RESULT 14

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LOCUS AK173115
DEFINITION Mus musculus mRNA for mKIAA1158 protein.
ACCESSION AK173115
VERSION AK173115.1 GI:50510814
KEYWORDS FLI_CDNA.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

1 Okazaki, N., Kikuno, R.F., Ohara, R., Inamoto, S., Koseki, H., Hiraoka, S., Saga, Y., Seino, S., Nishimura, M., Kashi, T., Hoshino, K., Kitamura, H., Nagase, T., Ohara, O. and Koga, H.

TITLE

Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene: IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous cDNAs Identified by Screening of Terminal Sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries

JOURNAL

2 (bases 1 to 4025)
Okazaki, N., Kikuno, R.F., Nagase, T., Ohara, O. and Koga, H.
Direct Submission
Submitted (19-MAY-2004) Hisashi Koga, Kazusa DNA Research Institute, Laboratory for Genome Informatics, 2-6-7
Kazusa-Kametani, Kisarazu, Chiba 292-0818, Japan
(E-mail: mouse@kazusa.or.jp, Tel: 81-438-52-3919, Fax: 81-438-52-3918)
The CREATR program supported by Japan science and technology corporation; cDNA full insert sequencing; Kazusa DNA Research Institute; cDNA full insert construction, clone selection and 5'- & 3'-end one pass sequencing.

COMMENT

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gene

CDS

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Best Local Similarity: 97.67% Mismatches: 5
Query Match: 97.60% Indels: 0
DB: 10 Gaps: 0

ORIGIN

US-09-977-579-2 (1-215) x AK173115 (1-4025)

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Qy 141 IleProLeuArgValThrGluGluAlaGluGluPhePheThrSerValIleSerGluIle 160

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Db 770 ATGATGTACATCTCTCTGCT 829

Qy 181 TyrArgLyValSerLyValGluGluAlaAlaGluGluAlaSerAspTyrLeuAla 200

Db 830 TACGAAAGCTCTTAAGCCGGAAGAGCAGCAGCTCAGGAAATGCGTCTGACTACTTCT 889

Qy 201 IleProSerGluLeuValGluLeuSerAlaValProValGluGlu 215

Db 890 ATCCCTTCAGAGAACAGAGAACTCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 934

RESULT 15

BC053919 4169 bp mRNA linear ROD 08-OCT-2003

LOCUS Mus musculus sodium channel, voltage-gated, type III, beta, mRNA

DEFINITION (CDNA clone MGC:56857 IMAGE:6308278), complete cds.

ACCESSION BC053919

VERSION BC053919.1 GI:32172797

KEYWORDS MGC.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus (house mouse)

REFERENCE 1 (bases 1 to 4169)

AUTHORS Strausberg, R.D., Collins, F.S., Wagner, L.H., Shenmen, C.M., Schuler, G.D., Kluener, R.D., Collins, F.S., Grouse, L.H., Derge, J.G., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heien, F., Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedl, T.B., Tothiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mulhany, S.J., Boeck, S.A., McKernan, P.J., McKernan, K.D., Malek, U.A., Gunaratne, P.H., Richards, S., Wille, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Merris, M.A.

TITLE human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 4169)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (16-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: gcgaps-remail.nih.gov

Tissue Procurement: Susan L. Sullivan, PhD.

cDNA Library Preparation: Resgen, Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: amadan@systemsbiology.org

Rup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 105 Row: d Column: 7

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23943798.

Location/Qualifiers

1. 4169

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/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="MGC:56857 IMAGE:6308278"

/issue_type="Olfactory epithelium, neonatal mouse, C57BL/6"

/clone_1lb="NIH MGC_129"

/lab_host="DH10B"

/note="Vector: PCMV-SPORT6"

1. 4169

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308. 955

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/codon_start=1

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443. 673

/gene="Scn3b"

/note="IGV; Region: Immunoglobulin V-Type"

/db_xref="CCD:smat00406"

ORIGIN

Alignment Scores:

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Score: 1097.00 Matches: 210

Percent Similarity: 97.67% Conservative: 0

Best Local Similarity: 97.67% Mismatches: 5

Query Match: 97.60% Indels: 0

DB: 10 Gaps: 0

US-09-977-579-2 (1-215) x BC053919 (1-4169)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValIleuIleTyrTyrValSer 20

Db 308 ATGCTTCTCTTCAACACATTTCTTCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 367

Qy 21 ValCysePheProValCyValGluValProSerGluThrGluAlaValGluGluValPro 40

Db 368 GTGCTTCTCTCTGTGTGTGAAGATCCTCCGAGACAGACAGCCGCGGCAATTCC 427

Qy 41 MetLyLeuArgCyValIleSerCyMetLyArgGluGluValGluAlaThrThrValVal 60

Db 428 ATGAACTGAGATGACATCTCTCATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487

Qy 61 GluThrPheTyrArgProGluGluGlyLyValAspPheLeuIleTyrGluTyrArgAsnGly 80

Db 488 GATGTCTTCAACAGCTTGAAGCGCGGCGGAAAGATTCTTTATATAGTATCCAAAGCC 547

Qy 81 HisGluGluValGluSerProPheGluGluGlyLyValGluGluThrPheGlySerLyAspLeu 100

Db 548 CACGAGAGGTGAGAGAGCCCTTCAAGAGGTGCTGTGAGAGATGAGAGAGAGAGAGAG 607

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 7, 2005, 11:09:50 ; Search time 430 Seconds
(without alignments)
2959.871 Million cell updates/sec

Title: US-09-977-579-2
Sequence: 1 MPANRILPLASLVLYTWVS.....SDYLAIPSEKNSAVPEE 215

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Fgapop 6.0 , Fgapext 7.0
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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: geneseg.1980s:*
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- 4: geneseg.2000s:*
- 5: geneseg.2001bs:*
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- 7: geneseg.2003bs:*
- 8: geneseg.2004bs:*
- 9: geneseg.2005bs:*
- 10: geneseg.2006bs:*
- 11: geneseg.2007bs:*
- 12: geneseg.2008bs:*
- 13: geneseg.2009bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1124	100.0	1261	3 AAC67837	AAC67837 Human bet
2	1124	100.0	1261	10 ADB78651	ADB78651 Human ion
3	1124	100.0	1261	10 ACF57870	ACF57870 Human SCN
4	1124	100.0	1510	4 AAF84146	AAF84146 Human nov
5	1124	100.0	4052	6 ABA93727	ABA93727 Human sig

6	1105	98.3	645	5 AAC90601	AAC90601 Rat sodiu
7	1105	98.3	2220	3 AAC67836	AAC67836 Rat betac3
8	1105	98.3	2632	5 AAC90602	AAC90602 Rat sodiu
9	1105	98.3	3108	5 AAC90600	AAC90600 Rat sodiu
10	1024	91.1	1045	4 AAK52345	AAK52345 Human pol
11	1003	89.2	978	4 AAH98320	AAH98320 Human EST
12	1003	89.2	978	13 ADS11487	ADS11487 Human the
13	927.5	82.5	1195	5 AAS86764	AAS86764 DNA encod
14	886.5	78.9	953	13 ADS10151	ADS10151 Human the
15	742	66.0	471	2 AAV68895	AAV68895 EST clone
16	694	61.7	3531	5 AAS86763	AAS86763 DNA encod
17	477	42.4	657	5 AAC90603	AAC90603 Rabbit so
18	473	42.1	1335	10 ACES7868	ACES7868 Human SCN
19	473	42.1	1335	12 ADQ19428	ADQ19428 Human sof
20	473	42.1	1414	8 ABZ23837	ABZ23837 Human vol
21	472	42.0	1414	10 ADB78640	ADB78640 Human ion
22	472	42.0	1490	6 ABR63747	ABR63747 Rat seque
23	472	42.0	1490	6 ADS52855	ADS52855 Primary r
24	472	42.0	1490	12 ADQ09498	ADQ09498 Rat sodiu
25	465	41.4	1414	10 ADB78641	ADB78641 Human ion
26	408.5	36.3	621	5 AAS86762	AAS86762 DNA encod
27	262.5	23.4	850	4 AAF57675	AAF57675 Rat sodiu
28	262.5	23.2	850	4 AAF30669	AAF30669 Sodium ch
29	260.5	23.2	974	6 AAD29622	AAD29622 Human bet
30	234	20.8	407	4 ABA08942	ABA08942 Human vol
31	234	20.8	407	4 AAK53329	AAK53329 Human pol
32	230	20.5	855	10 ADG15041	ADG15041 Human SBC
33	218.5	19.4	358	10 ACP25382	ACP25382 Human col
34	167	14.9	1029	9 ACF25382	ACF25382 Rat schwa
35	165.5	14.7	3583	12 ADQ23651	ADQ23651 Human sof
36	163.5	14.5	777	6 ABA02395	ABA02395 Human mye
37	163.5	14.5	1693	12 ADP45442	ADP45442 Human vas
38	161.5	14.4	162	12 ADM66944	ADM66944 Human adl
39	160.5	14.3	970	4 AAF27741	AAF27741 Human tra
40	160.5	14.3	983	4 AAD02925	AAD02925 Human PRO
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42	160.5	14.3	983	8 ABR13481	ABR13481 Human DNA
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ALIGNMENTS

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ID AAC67837 standard; cDNA; 1261 BP.	
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AC AAC67837;	
DT 15-FEB-2001 (first entry)	
XX	
DE Human betac3 CDNA.	
XX	
KW Human: beta sub-unit; betac3; analgesic; anticonvulsant;	
KW cerebroprotective; vasotropic; cardiac; nootropic; cyclostatic;	
KW dermatological; gene therapy; voltage-gated sodium channel; pain;	
KW epilepsy; stroke; ischemia; heart disease; Jacobsen Syndrome;	
KW familial nonchromaffin paraganglioma; phenylketonuria;	
KW Charcot Marie Tooth disease; ss.	
XX	
OS Homo sapiens.	
XX	
PN W0200063367-A1.	
XX	
PD 26-OCT-2000.	
XX	
PF 24-FEB-2000; 2000MO-EP001783.	
XX	
PR 15-APR-1999; 99US-0129473P.	
XX	
PA (WARN) WARNER LAMBERT CO.	
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.	

XX Cox P, Dixon A, Jackson A, Morgan K;
 XX MPI; 2000-665241/64.
 DR P-PSDB; AAB36002.
 XX
 PT Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium
 PT channel, and their corresponding polypeptide, useful for detecting and
 PT treating sodium channel-associated conditions, e.g. pain, epilepsy and
 PT stroke.
 XX
 PS Claim 10; Page 70-71; 88pp; English.
 XX
 CC The present sequence is given in the claims of a specification relating
 CC to a novel family of beta sub-unit proteins from a voltage-gated sodium
 CC channel. Human and rat beta sub-units, which have been collectively
 CC identified as beta3, have been isolated. The polynucleotides and
 CC polypeptides are useful for screening for agonists and antagonists of
 CC sodium channels. The agonists, antagonists, proteins and nucleic acids
 CC may be used diagnosing of treating diseases or conditions associated with
 CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischemia,
 CC heart disease, Jacobson Syndrome, Familial Nonchromaffin Paraganglioma,
 CC Phenylketonuria and Charcot Marie Tooth disease
 CC
 SQ Sequence 1261 BP; 263 A; 366 C; 372 G; 260 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,336-124 Length: 1261
 Score: 1124.00 Matches: 215
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-09-977-579-2 (1-215) x AAC67837 (1-1261)

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 QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
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 Db ATGAGCTGGCTGCTGCTCTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 555
 QY 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
 Db GAATGGTTCACAGGCCCGAGGCGGGAAGATTCTTATTCAGATATCGAATGCG 615
 QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnIleTrpAsnGlySerLysAspLeu 100
 Db CACACAGAGAGTGAAGAGCCCTTTCAGGGCGGCTGAGAGATGAGATGAGCAAGACCTG 675
 QY 101 GluAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrTrpCys 120
 Db CAGAGAGTGTCTACACTGTGCTCAAGTCACTGACACACTGTGCTTACACCTGC 735
 QY 121 AsnValSerArgIlePheGluPheGluAlaHisArgProPheValIleThrTrpArgLeu 140
 Db AATGTGTCCCGGAGTGTGATTTGAGGCGCATCCGCTTGTGAAGAGAGAGCGGCTG 795
 QY 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
 Db ATCCCTTAAGATGACCCGAGGAGGCTGAGAGACTTCACTCTGTGCTCAGAAATC 855
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 Db ATATATGATCACTCTTCTGCTCTTCCACCTGTGGCTGCTCAATCGAGATGATATATG 915
 QY 181 TyrArgLysValSerLysAlaGluGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAla 200

Db 916 TACAGAAAGTCTCAAAAACCCAGAGGACGCCCAAGAAAAGCCGTCTACTACTTGGC 975
 QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
 Db ATCCCATCTGAGAACACAGAGAACTCTGCGTACCACTGAGAGGAA 1020
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 ID ADB78651 standard; cDNA, 1261 BP.
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 XX ADB78651;
 XX
 DT 04-DEC-2003 (first entry)
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 DE Human ion channel subunit cDNA mutant SCN1AR exon 1 SEQ ID NO:22.
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 KW ss; gene; mutant; ion channel; ion channel subunit; ICS; nocotropic;
 KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antidiarrhoeic;
 KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
 KW nephrotoxic; antidiabetic; ophthalmological; epilepsy;
 KW ion channel dysfunction; human.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN MO2003008574-A1.
 XX
 PD 30-JAN-2003.
 XX
 PF 08-JUL-2002; 2002WC-AU000910.
 XX
 PR 18-JUL-2001; 2001AU-00006452.
 PR 05-MAR-2002; 2002AU-00000910.
 PR 13-MAY-2002; 2002AU-00002292.
 XX
 PA (BION-) BIONOMICS LTD.
 PA (WALLACE R. WALLACE R. W.
 XX
 PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
 PI Berkovic SF, Scheffer IE;
 XX
 DR MPI; 2003-239332/23.
 XX
 PT Identifying predisposition to an ion channel dysfunction, such as
 PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
 PT schizophrenia, anxiety and depression, by detecting encoding-gene
 PT mutation events.
 XX
 PS Claim 6; SEQ ID NO 22; 106pp; English.
 XX
 CC The invention relates to a novel method for identifying a subject
 CC predisposed to a disorder associated with ion channel dysfunction. The
 CC method comprises ascertaining if at least one of the genes encoding ion
 CC channel subunits (ICS) has undergone a mutation event so that a cDNA
 CC derived from the subject has any of 134 nucleotide sequences. The method
 CC of the invention has nocotropic, neuroprotective, inotropic, antipyretic,
 CC antiarrhythmic, antidiarrhoeic, antidiabetic, antiparkinsonian,
 CC neuroleptic, tranquiliser, analgesic, nephrotoxic, antidiabetic, and
 CC ophthalmological activity. A polynucleotide of the invention acts as an
 CC ion channel agonist, or ion channel antagonist. The methods, isolated
 CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
 CC modulator of an ion channel, cells and genetically modified non-human
 CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
 CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
 CC kalemic periodic paralysis, myotonia, malignant hyperthermia,
 CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
 CC disease, Parkinson's disease, schizophrenia, hyperplexia, anxiety,
 CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
 CC pain, chronic/acute pain, Barter's syndrome, polycystic kidney disease,
 CC dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
 CC fibrosis, congenital stationary night blindness and total colour
 CC blindness. The present sequence represents a mutant cDNA of the

CC invention. The sequence data for this patent is not represented in the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 1261 BP; 263 A; 365 C; 372 G; 261 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,33e-124	Length:	1261
Score:	1124.00	Matches:	215
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-977-579-2 (1-215) x ADB78651 (1-1261)

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Db 376 ATGCTGCTCTTCAATAGATTGTTCCCTGGCTCTCTGCTGCTTACTGAGGTCACT 435
Qy 21 ValCysePheProValCyseValGluValProSerGluThrGluValGlnGlyAsnPro 40
Db 436 GTCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 495
Qy 41 MetIleLeuArgCyseIleSerCyseMetIleArgGluGluValGluAlaThrThrValVal 60
Db 496 ATGAGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 555
Qy 61 GluTrpPheTyrArgProGluGluGlyValAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 556 GAATGCTTCTCAAGCCCGAGGCGGCTAAAGATTCTTATTTCAGATTCGAAATGCC 615
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerIleAspLeu 100
Db 616 CACAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 675
Qy 101 GluAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 676 CAGAGCTGCTCACTGCTGCTCAAGCTCACTGCAAGCACTGCTGCTGCTTACACCTGC 735
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValIleTyrThrArgLeu 140
Db 736 AATGTCTCCCGAGAGTTGAGATTGAGCGCGATGCGCTTGTGGAAGACAGACCGGCTG 795
Qy 141 IleProLeuArgValThrGluGluAlaGlyIleAspPheThrSerValIleSerGluIle 160
Db 796 ATCCCCCTAAGAGTCACTGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 855
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Db 856 ATGATGTACATCTTCTGCTGCTTCTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 915
Qy 181 TyrArgIleValSerIleValGluGluAlaAlaGlnGluAsnIleAspTyrLeuVal 200
Db 916 TACGAAAGAGTCTTAAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 975
Qy 201 IleProSerGluLeuValGluAsnSerAlaValProValGluGlu 215
Db 976 ATCCATCTGAGAACAGAGAACTTGCCTTACAGTGAAGAGAA 1020

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RESULT 3

ACF57870
 ID ACF57870 standard; cDNA; 1261 BP.
 AC ACF57870;
 XX
 XX
 DT 15-JAN-2004 (first entry)
 DE Human SCN3B protein encoding cDNA.
 XX
 XX SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
 KM neuroprotective; anesthetic; cyostatic; cerebroprotective; cardiant;
 KM hypotensive; gene therapy; SCN3B; human; gene; ss.

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XX OS Homo sapiens.
XX Key Location/Qualifiers
XX Key 376..1023
XX CDS /*tag= a
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XX FT
XX MO2003072751-A2.
XX
XX 04-SEP-2003.
XX
XX 25-FEB-2003; 2003MO-US006010.
XX
XX 25-FEB-2002; 2002US-0359382P.
XX
XX (UVA-) UNIV VANDERBILT.
XX
XX George AL, Lossin C;
XX
XX WPI; 2003-712725/67.
XX
XX P-PSDB; ABR83183.
XX
XX Recombinantly expressed sodium channel type 1 alpha subunit, useful in
XX screening for modulators, for treating e.g. epilepsy.
XX
XX Disclosure; Page 145-147; 176pp; English.
XX
XX The invention relates to a recombinantly expressed and isolated human
XX SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
XX incorporated into a cell, is used to screen for specific modulators,
XX potentially useful as anticonvulsant, antiepileptic, neuroprotective,
XX analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
XX epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
XX motor endplate diseases, hypertension, congestive heart failure and
XX muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
XX and metastatic cancer cell lines). These activities can also be provided
XX by gene therapy vectors that express (I) or the modulators. The
XX modulators, also antibodies directed against (I), are used to detect
XX sodium channel polypeptides. The present sequence represents a human
XX SCN3B protein encoding cDNA
XX
XX Sequence 1261 BP; 263 A; 366 C; 372 G; 260 T; 0 U; 0 Other;

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Alignment Scores:

Pred. No.:	2,33e-124	Length:	1261
Score:	1124.00	Matches:	215
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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US-09-977-579-2 (1-215) x ACF57870 (1-1261)

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Qy 1 MeProAlaPheAenArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 376 ATGCTGCTCTTCAATAGATTGTTCCCTGGCTCTCTGCTGCTTACTGAGGTCACT 435
Qy 21 ValCysePheProValCyseValGluValProSerGluThrGluValGlnGlyAsnPro 40
Db 436 GTCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 495
Qy 41 MetIleLeuArgCyseIleSerCyseMetIleArgGluGluValGluAlaThrThrValVal 60
Db 496 ATGAGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 555
Qy 61 GluTrpPheTyrArgProGluGluGlyValAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 556 GAATGCTTCTCAAGCCCGAGGCGGCTAAAGATTCTTATTTCAGATTCGAAATGCC 615
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerIleAspLeu 100
Db 616 CACAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 675

```

QY 101 GlnAspValSerIleThrValIleuAsnValThrIleuAsnAspSerGlyLeuTyrThrCys 120
 DB 676 CAGGAGGTGCTCACTGTGCTCAACGTCATCTGAGACGCTGGCTCTACACCTGC 735
 QY 121 AsnValSerArgIlePheGluPheGluValAlaHisArgProPheValIleThrThrArgLeu 140
 DB 736 AATGTGTCCCGGAGTTTGAGTTTGAGGGCCATCGGCTTTTGAGAGAGACGGGGCTG 795
 QY 141 IleProLeuArgValThrGluValAlaGlyIleuAspPheThrSerValValSerGluIle 160
 DB 796 ATCCCTTAAGATCACCGAGGAGGCTGAGAGACTTCACCTGTGTCTCAGAAATC 855
 QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuThrLeuLeuIleGluMetIleTyrCys 180
 DB 856 ATGATGTACATCTTCTGTGCTCTTCTCCTCAGCTGTGGCTGCTCATCGAGATGATATTTGC 915
 QY 181 TyrArgIleValSerIleValAlaGluValAlaGlnGluAsnAlaSerAspTyrLeuAla 200
 DB 916 TACAGAAAGGTCTCAAAAGCCGAAAGGAGGAGCCCAAGAAACCGGTCTGACTACTTGGC 975
 QY 201 IleProSerGluAsnIleGluAsnSerAlaValProValGluGlu 215
 DB 976 ATCCCATCTGAGAACAGAGAACTGTGCGGTACAGTGGAGGAA 1020
 RESULT 4
 AAF84146
 ID AAF84146 standard; cDNA; 1510 BP.
 AC AAF84146;
 XX
 DT 07-SEP-2001 (first entry)
 DE Human novel sodium channel beta1-like subunit encoding cDNA.
 XX
 KW Sodium channel; sensory neurone specific channel; beta1-like subunit;
 KM SNS; therapeutic; pain; analgesic; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 213..860
 FT /*tag= a
 FT /product= "sodium channel beta1-like subunit"
 XX
 PN MO200144293-A2.
 XX
 PD 21-JUN-2001.
 XX
 PF 14-DEC-2000; 2000MO-GB004802.
 XX
 PR 17-DEC-1999; 99GB-00029970.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Plumptre M, Powell AJ, Sansau P;
 XX
 DR WPI; 2001-398129/42.
 DR P-PsDB; AAB85206.
 XX
 PT Novel sub-unit for voltage-gated sodium channel proteins for producing
 PT agents useful for treating pain.
 XX
 PS Claim 4; Page 29-30; 31pp; English.
 XX
 DE The invention provides a novel beta1-like sub-unit for voltage-gated
 CC sodium ion channel polypeptide, specifically a sensory neurone specific
 CC channel (SNS) subunit. The novel beta1-like subunit is useful for
 CC producing a therapeutic agent which is useful treating pain in a patient.
 CC The subunit can be expressed by standard recombinant methodology. The
 CC present sequence represents a human novel sodium channel beta1-like
 CC subunit encoding cDNA
 XX

SQ Sequence 1510 BP; 350 A; 410 C; 414 G; 336 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3,02e-124 Length: 1510
 Score: 1124.00 Matches: 215
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
 US-09-977-579-2 (1-215) x AAF84146 (1-1510)
 QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValIleTyrTrpValSer 20
 DB 213 ATCCCTGCTTCATATGATTTTCCCTGGCTTCTGTGCTTATCTACAGGTCAT 272
 QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGluAsnPro 40
 DB 273 GTCTGCTTCCCTGTGTGTGTGAGAGCCCTCGAGACGAGGCGCTGCAAGGCAACCC 332
 QY 41 MetIleLeuArgCysIleSerCysMetIleValArgGluValGluValAlaThrThrValVal 60
 DB 333 ATGAACTGCTGCTGATCTCTGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 392
 QY 61 GluTrpPheTyrArgProGluGlyIleValAspPheLeuIleTyrGluTyrArgAsnGly 80
 DB 393 GAATGTTTCTACAGGCGCCGAGGCGGTAAAGATTTCTTATTACAGATATGGAATGCG 452
 QY 81 HisGlnGluValGluSerProPheGlnGlyValGluGlnIleTrpAsnGlySerIleValAspLeu 100
 DB 453 CACAGAGAGGTGAG 512
 QY 101 GlnAspValSerIleThrValIleuAsnValThrIleuAsnAspSerGlyLeuTyrThrCys 120
 DB 513 CAGGAGGTGCTCACTGTGCTCAACGTCATCTGAGACGCTGTGGCTCTACACCTGC 572
 QY 121 AsnValSerArgIlePheGluPheGluValAlaHisArgProPheValIleThrThrArgLeu 140
 DB 573 AATGTGTCCCGGAGTTTGAGTTTGAGGGCCATCGGCTTGTGTGAAAGAGAGCGGCTG 632
 QY 141 IleProLeuArgValThrGluValAlaGlyIleuAspPheThrSerValValSerGluIle 160
 DB 633 ATCCCTTAAGATCACCGAGGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 692
 QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuThrLeuLeuIleGluMetIleTyrCys 180
 DB 693 ATGATGTACATCTTCTGTGCTTCTCCTCAGCTGTGGCTGCTCATCGAGATGATATTTGC 752
 QY 181 TyrArgIleValSerIleValAlaGluValAlaGlnGluAsnAlaSerAspTyrLeuAla 200
 DB 753 TACAGAAAGGTCTCAAAAGCCGAAAGGAGGAGCCCAAGAAACCGGTCTGACTACTTGGC 812
 QY 201 IleProSerGluAsnIleGluAsnSerAlaValProValGluGlu 215
 DB 813 ATCCCATCTGAGAACAGAGAACTGTGCGGTACAGTGGAGGAA 857
 RESULT 5
 ABA93727
 ID ABA93727 standard; cDNA; 4052 BP.
 XX
 AC ABA93727;
 XX
 DT 30-APR-2002 (first entry)
 XX
 DE Human signal transduction cDNA clone amy2_2f18.
 XX
 KW Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
 KM gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200198454-A2.
 XX

PD 27-DEC-2001.
 XX 25-APR-2001; 2001WO-IB002050.
 PF 25-APR-2001; 2000US-0199380P.
 PR 25-APR-2001; 2000US-0199380P.
 XX (GENU-) GERMAN HUMAN GENOME PROJECT.
 PA
 XX Wiemann S;
 PI
 DR WPI: 2002-055860/07.
 DR P-PSDB; ABB05689.
 XX
 PT Human cDNA sequences and clones derived from human fetal brain, fetal
 PT kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
 PT screening and therapy.
 PS
 PS Claim 1; Page 174-175; 611pp; English.
 CC The present invention describes assemblies and computer readable media
 CC comprising novel human cDNA sequences and clones derived from human
 CC foetal brain, foetal kidney, melanoma, testis and amygdala cDNA
 CC libraries. ABA93702 to ABA93766 represent human cDNA sequences from the
 CC present invention which encode the proteins given in ABB05662 to
 CC ABB05729. The human cDNA sequences and clones can be used in gene
 CC therapy. The clones may be used in a variety of applications, for example
 CC they may be used in profiling assays, for providing large arrays of human
 CC genetic material for implementing large-scale screening strategies and
 CC for treating diseases via gene therapy procedures
 CC
 SQ Sequence 4052 BP; 994 A; 1033 C; 1036 G; 989 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.23e-123 Length: 4052
 Score: 1124.00 Matches: 215
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-977-579-2 (1-215) x ABA93727 (1-4052)
 QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValIleTyrTyrValSer 20
 DB 804 ATGCTGCTTCAATAGATTGTTCCTCGCTTCTCGCTTATCTACTGGGTGCT 863
 QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
 DB 864 GTCTGCTTCTGCTGTGTGTGTGAAGTGCCTCGAGAGAGAGCGGTCAAGGCAACCC 923
 QY 41 MetIleuValArgCysIleSerCysMetIleValArgGluValGluAlaThrThrValVal 60
 DB 924 ATGAAGCGCGCTCATCTCTCGCATGAAGAGAGAGAGGTGAGGACCAACGCTGCTG 983
 QY 61 GluThrPheTyrArgProGluGluGlyIleValAspPheLeuIleTyrGluTyrArgAsnGly 80
 DB 984 GAAATGTTCTACAGCGCCGAGCGCGGTAAAGATTCTTATTATTCAGACTATTCGAAATGGC 1043
 QY 81 HisGlnGluValGluSerProPheGlnGlyValArgLeuGlnTyrPheGlnSerIleAspLeu 100
 DB 1044 CACGAGAGAGTGGAGAGAGCCCTTTCAGGGGCGCGCTCGCATGGAATGCAAGCAAGACTG 1103
 QY 101 GlnAspValSerIleThrValIleuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
 DB 1104 CAGACGCGTCAATCACTGCTCAACCTCACTGAGACGACTGCGCTCTACACCTGC 1163
 QY 121 AsnValSerArgGluPheGluPheGluValHisArgProPheValIleThrThrArgLeu 140
 DB 1164 AATGTCGCGGAGATTGAGTTGAGGCGCATCGCCCTTGTGAACAACAACGCGGCTG 1223
 QY 141 IleProLeuArgValThrGluGluValGlnGluValAspPheThrSerValValSerGluIle 160
 DB 1224 ATCCCTTAAGAGTCAACGAGAGAGGCTGAGAGAGACTTCACTCTGTGTCTCAGAAATC 1283

QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTyrLeuIleGluMetIleTyrCys 180
 DB 1284 ATGATGTACATCTTCTGCTGTCTTCTCTCACTTGTGGCTGCTCATCGAGATGATATATTGC 1343
 QY 161 TyrArgIleValSerIleValGluGluValAlaGlnGluAsnAlaSerAspTyrLeuAla 200
 DB 1344 TACAGAAAGTCTCAAAAGCCGAAAGAGCCCAAGAAAGCGCTGACTGACTTGGCC 1403
 QY 201 IleProSerGluAsnIleValAsnSerAlaValProValGluGlu 215
 DB 1404 ATCCATCTTGAGAACAGAGAACTCTGCGGTACCACTGAGAGAA 1448
 RESULT 6
 AAC90601
 ID AAC90601 standard; cDNA; 645 BP.
 AC AAC90601;
 AC
 DT 13-MAR-2001 (first entry)
 XX
 DE Rat sodium channel beta3 protein A1rx94h5 partial coding sequence.
 XX
 KW Rat: sodium channel beta3 protein; A1rx94h5; pain; sleep disorder;
 KW neurodegenerative disorder; mood disorder; muscle contraction; ss.
 OS Rattus sp.
 XX
 PN MO200069912-A1.
 XX
 PD 23-NOV-2000.
 XX
 PF 12-MAY-2000; 2000WO-US013144.
 XX
 PR 14-MAY-1999; 99US-0134198P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Curtis RAJ;
 DR WPI: 2001-122743/13.
 DR
 PT New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
 PT root ganglion cDNA library for use in chromosome mapping, forensic
 PT medicine, monitoring clinical trials and therapeutics.
 PS
 PS Claim 1; Page 40-41; 145pp; English.
 CC The present invention provides the protein and coding sequences of the
 CC rat sodium channel beta3 protein, designated A1rx94h5. This protein is
 CC involved in the generation of pain and other sensory or perceptible nerve
 CC impulses, in the establishment and endurance of mood, neurodegenerative
 CC and sleep disorders, and in the control of muscle contraction, including
 CC movements such as the heartbeat, digestion and vascular tone. The
 CC sequences can be used in predictive medicine, screening and diagnostic
 CC assays, and in pharmacogenomics
 CC
 SQ Sequence 645 BP; 155 A; 154 C; 181 G; 155 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.7e-122 Length: 645
 Score: 1105.00 Matches: 211
 Percent Similarity: 98.14% Conservative: 0
 Best Local Similarity: 98.14% Mismatches: 4
 Query Match: 98.31% Indels: 0
 DB: 5 Gaps: 0
 US-09-977-579-2 (1-215) x AAC90601 (1-645)
 QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValIleTyrTyrValSer 20
 DB 1 ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCAAGTGCATCTACTGGGTGCA 60

```

QY 21 ValCysePheProValCyseValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
DB 61 GTCTGCTCCCTGTGTGTGTGGAAGTCCCTCGAAGCACAAGCGGTGCGAATGCC 120
QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
DB 121 ATGAGCTGAGGTGCTACTCTCTGATGAGAGGAGGAGGTGAGGCGCACACTGTGTG 180
QY 61 GluTrpPheTyrArgProGluGluGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
DB 181 GAGTGTCTTACAGGCTTGAGGGGGGTAAGATTTCTTATATATGATGATCGAATGCG 240
QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
DB 241 CACGAGAACTGGAGAGCCCTTCCAAAGCGCTGTGCAGTGGAATGGAGCAAAAGCTG 300
QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrCys 120
DB 301 CAGGACGTATCCATCTCACTGATCTCAATGTCATTGATGATCACTTGCCCTCTACATGC 360
QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
DB 361 AATGTGTCCAGGAGTTTCAATTCAGAGGCAACAAGGCTTTGTGAAGACCAAGACTG 420
QY 141 IleProLeuArgValThrGluGluAlaGlyLysAspPheThrSerValLysGluIle 160
DB 421 ATACCTTTGGAGTCACTGAAAGGGCGGAGAAAGACTTCACTCCGTGCTCGGAATC 480
QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTyrLeuLeuIleGluMetIleTyrCys 180
DB 481 ATGATGTACATCTCTCTGCTGCTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnLysAspTyrLeuAla 200
DB 541 TACGAAAGGTCTCTTAAGGCCGAAAGGCGACACAGGAAATGCGTGACTACTTCT 600
QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
DB 601 ATCCCTTCAGAGAACAAAGAGAACTCTGTGTACTCTGTGAGGAA 645

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RESULT 7
AAC67836 standard; cDNA; 2220 BP.

AAC67836;
DT 15-FEB-2001 (first entry)

Rat beta3 subunit cDNA.
Rat; beta sub-unit; beta3; analgesic; anticonvulsant; cerebroprotective;
KM vasotropic; cardiant; nootropic; cytostatic; dermatological;
KM gene therapy; voltage-gated sodium channel; pain; epilepsy; stroke;
KM ischaemia; heart disease; Jacobsen Syndrome;
KM familial nonchromatin paraganglioma; phenylketonuria;
KM Charcot Marie Tooth disease; ss.

OS Rattus sp.
XX
XX MO200063367-A1.
XX
XX 26-OCT-2000.
XX
XX 24-FEB-2000; 2000MO-EP001783.
XX
XX 15-APR-1999; 99US-0129473P.
XX
XX (WARN) WARNER LAMBERT CO.
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
XX Cox P, Dixon A, Jackson A, Morgan K;
XX
XX WPI, 2000-665241/64.

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DR P-PSDB; AAB36001.
XX
XX Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium
PT channel, and their corresponding polypeptides, useful for detecting and
PT treating sodium channel-associated conditions, e.g. pain, epilepsy and
PT stroke.
XX
XX Claim 6; Page 69-70; 88pp; English.
PS
XX
XX The present sequence is given in the claims of a specification relating
CC to a novel family of beta sub-unit proteins from a voltage-gated sodium
CC channel. Human and rat beta sub-units, which have been collectively
CC identified as beta3, have been isolated. The polynucleotides and
CC polypeptides are useful for screening for agonists and antagonists of
CC sodium channels. The agonists, antagonists, proteins and nucleic acids
CC may be used diagnosing of treating diseases or conditions associated with
CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,
CC heart disease, Jacobsen Syndrome, familial Nonchromatin Paraganglioma,
CC Phenylketonuria and Charcot Marie Tooth disease
XX
SQ Sequence 2220 BP; 573 A; 557 C; 561 G; 529 T; 0 U; 0 Other;

```

Alignment Scores:

Pred. No.:	Length:	Score:
9, 88e-122	2220	1105.00

Percent Similarity: 98.14%
Best local Similarity: 98.14%
Query Match: 98.31%
DB: 3
Gaps: 0

US-09-977-579-2 (1-215) x AAC67836 (1-2220)

```

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
DB 363 ATGCTGCTTCAACAGATTTGCTTCCCTTACGCTTCTATATATGATGATCGAATGCC 422
QY 21 ValCysePheProValCyseValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
DB 423 GTCTGCTCCCTGTGTGTGTGGAAGTCCCTCGAAGACAAAGCGGTGCGAATGCC 482
QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
DB 483 ATGAACTGAGGTGATCTCTCTGATGAAAGGAGGAGAGGTGAGGCGCACACTGTGTG 542
QY 61 GluTrpPheTyrArgProGluGluGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
DB 543 GAGTGTCTTACAGGCTTGAGGGCGGTAAAGATTTCTTATATATGATGATCGAATGCC 602
QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
DB 603 CACGAGAACTGGAGAGCCCTTCCAAAGCCGCTGCAGTGGAATGGAGCAAAAGACTG 662
QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrCys 120
DB 663 CAGGAGGTATCCATCTCACTGATCAATGTCATTGAAATGACTTGGCTCTTACATGCG 722
QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
DB 723 AATGTGTCCAGGAGTTTCAATTCAGAGGCAACAAGGCTTTGTGAAGCACAGACTG 782
QY 141 IleProLeuArgValThrGluGluAlaGlyLysAspPheThrSerValLysGluIle 160
DB 783 ATACCTTTGGAGTCACTGAAAGGGGGGAGAAAGACTTCACTCCGTGCTCGGAATC 842
QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTyrLeuLeuIleGluMetIleTyrCys 180
DB 843 ATGATGTACATCTCTCTGCTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
QY 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnLysAspTyrLeuAla 200
DB 903 TACGAAAGGTCTCTTAAGGCCGAAAGGCGACACAGGAAATGCGTCTTACACTTCTGCT 962
QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215

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Db 963 ATCCCTTCAAGAGACAGAGAACTCTGTGTTACTGTGAGAGAA 1007

RESULT 8
AAC90602
ID AAC90602 standard; DNA; 2632 BP.

XX AAC90602;
AC AAC90602;
DT 13-MAR-2001 (first entry)

XX Rat sodium channel beta3 protein Alrx94h5 related sequence.
DE
XX Rat; sodium channel beta3 protein; Alrx94h5; pain; sleep disorder;
KW neurodegenerative disorder; mood disorder; muscle contraction; ds.
XX
OS Rattus sp.
XX
PN WO20069912-A1.
XX
PD 23-NOV-2000.
XX
PF 12-MAY-2000; 2000WO-US013144.
XX
PR 14-MAY-1999; 99US-0134198P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Curtis RAJ;
XX
XX WPI; 2001-122743/13.
XX
PT New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
PT root ganglion cDNA library for use in chromosome mapping, forensic
PT medicine, monitoring clinical trials and therapeutics.
XX
XX Claim 1; Page 41-42; 145pp; English.

XX The present invention provides the protein and coding sequences of the
CC rat sodium channel beta3 protein, designated Alrx94h5. This protein is
CC involved in the generation of pain and other sensory or perceptive nerve
CC impulses, in the establishment and endurance of mood, neurodegenerative
CC and sleep disorders, and in the control of muscle contraction, including
CC movements such as the heartbeat, digestion and vascular tone. The
CC sequences can be used in predictive medicine, screening and diagnostic
XX assays, and in pharmacogenomics
XX
SQ Sequence 2632 BP; 693 A; 636 C; 611 G; 692 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.26e-121 Length: 2632
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservative: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 5 Gaps: 0

US-09-977-579-2 (1-215) x AAC90602 (1-2632)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 78 ATGCTGCTTCAACAGATGCTTCCCTAGCTTCTAGAGCTCATCTACTGGGTCA 137
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 138 GTCCTGCTTCCCTGCTGTGTGTGGAAGTGCCTCGAGACAGAAACGCTCAGGGCAATGCC 197
Qy 41 MetValLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThraVal 60
Db 198 ATGAAGCTGAGGTGATCTCCGCAATGAAGAGGGAGGTGAGGCCACCACTGTGTG 257
Qy 61 GluTrpPheTyrArgProGluGluGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80

Db 258 GAGTGTCTTCAAGGCTGAGGGGGTAAAGATTTCCTATATATAGATATCGAATG 317
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 318 CACAGAGAGTGAAGAGCCCTTCCAAAGCCGCTCGAGTGAATGGAGCAAGACCTG 377
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 378 CAGACGATCATCATCTACTGATCAATGTCATTGAAATGACTGTGGCTTACACATGC 437
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 438 AATGTGTCCAGAGGATTCGATTCGAGGCACAGAGCCTTTTGAAGACCAAGAGACTG 497
Qy 141 IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 498 ATACCTTTCAGAGTCACTAGGAAGAGCGGAGAAACCTTCACTCGGTCTCCGAAATC 557
Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db 558 ATGATGTACATCTCTGCTGCTTCTCTCCTGAGCTGTATTGATGATGATCTATTGC 617
Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 618 TACAGAAAGTCTCTAAGGCCGGAAGAGGCACACAGAAATGCGTGTGACTACTTCT 677
Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 678 ATCCCTTCAAGAAACAGAGAACTCTGTGTTACTGTGAGAGAA 722

RESULT 9
AAC90600
ID AAC90600 standard; cDNA; 3108 BP.
XX
AC AAC90600;
XX
DT 13-MAR-2001 (first entry)

XX Rat sodium channel beta3 protein Alrx94h5 coding sequence.
DE
XX Rat; sodium channel beta3 protein; Alrx94h5; pain; sleep disorder;
KW neurodegenerative disorder; mood disorder; muscle contraction; ss.
XX
OS Rattus sp.
XX
PN WO20069912-A1.
XX
PD 23-NOV-2000.
XX
PF 12-MAY-2000; 2000WO-US013144.
XX
PR 14-MAY-1999; 99US-0134198P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Curtis RAJ;
XX
XX WPI; 2001-122743/13.
XX
DR P-PSDB; AAB50243, AAB50245.
XX
PT New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
PT root ganglion cDNA library for use in chromosome mapping, forensic
PT medicine, monitoring clinical trials and therapeutics.
XX
PS Claim 1; Fig 1; 145pp; English.

XX The present invention provides the protein and coding sequences of the
CC rat sodium channel beta3 protein, designated Alrx94h5. This protein is
CC involved in the generation of pain and other sensory or perceptive nerve
CC impulses, in the establishment and endurance of mood, neurodegenerative
CC and sleep disorders, and in the control of muscle contraction, including
CC movements such as the heartbeat, digestion and vascular tone. The
CC sequences can be used in predictive medicine, screening and diagnostic

CC assays, and in pharmacogenomics
 XX Sequence 3108 BP; 830 A; 748 C; 727 G; 803 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.ee-121	Length:	3108
Score:	1105.00	Matches:	211
Percent Similarity:	98.14%	Conservative:	0
Best Local Similarity:	98.14%	Mismatches:	4
Query Match:	98.31%	Indels:	0
DB:	5	Gaps:	0

US-09-977-579-2 (1-215) x AAC90600 (1-3108)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
 Db 78 ATGCTGCTCCCTTCAACATATGCTTCCCTAGCTTCTTACGCTCATCTGAGTACA 137
 Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
 Db 138 GTCTGCTTCCCTGCTGTGTGTGGAAGTCCCTCGAGACAGAAAGCGTGCAGGGCAATCCC 197
 Qy 41 MetLeuLeuArgCysIleSerCysMetLeuArgGluGluValGluAlaThrThrValVal 60
 Db 198 ATGAAGCTGAGGTGCATCTCTGCTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 257
 Qy 61 GluTrpPheTyrArgProGluGluGlyValAspPheLeuIleTyrGluTyrArgAsnGly 80
 Db 258 GAGTGTCTTCAACAGGCTGAGGGGGGTAAAGATTTCTTATATATGAGTATCGAATGGC 317
 Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLeuAspLeu 100
 Db 318 CACGAGAGATGAGAGAGCCCTTCAAGGCGCTGCGAGTGGATGGAGCAAAAGACTTG 377
 Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrCys 120
 Db 378 CAGACCTATCCATCCTGCTACTCAATGATCACTTGTATGATCACTGCGCTCTACACATGC 437
 Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValIysThrThrArgLeu 140
 Db 438 AATGTGTCGAGGAGGATTCGAAATTCGAGGACACAGGCTTTGTGAAGACACAGAGCTG 497
 Qy 141 IleProLeuArgValThrGluGluAlaGlyLeuAspPheThrSerValIleSerGluLe 160
 Db 498 ATACCTTTGCGAGTCACTGAAAGAGGCGGAGAAAGACTTCACTCCGCGCTCGGAATC 557
 Qy 161 MetMetCysIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
 Db 558 ATGATGTACATCTCTCTGCTGCTTCTTCACTTGTGCTGTTTATGATGATCTATTCG 617
 Qy 181 TyrArgIleValSerIleValGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
 Db 618 TACGAAAGGCTCTTAAGGCGGAGAGGACGACAGCAAAATTCGCTGCTACCTTCTGCT 677
 Qy 201 IleProSerGluAsnIleGluAsnSerAlaValProValGluGlu 215
 Db 678 ATCCCTTCAAGAAACAAGAGAACTGTGTGTAACCTGTGAGGAA 722
 RESULT 10
 AAK52345
 ID AAK52345 standard; cDNA; 1045 BP.
 XX AAK52345;
 AC AAK52345;
 XX AAK52345;
 DT 06-NOV-2001 (first entry)
 XX Human polynucleotide SEQ ID NO 890.
 DE Human polynucleotide SEQ ID NO 890.
 XX Human cytokine; cell proliferation; cell differentiation; gene therapy;
 KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KM tissue growth factor; immunomodulatory cancer; leukaemia;
 KM nervous system disorder; arthritis; inflammation; ss.
 XX

OS Homo sapiens.

PN W0200157190-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US004098.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00620325.

PR 01-SEP-2000; 2000US-00654936.

PR 15-SEP-2000; 2000US-00663561.

PR 20-OCT-2000; 2000US-00693325.

PR 30-NOV-2000; 2000US-00728422.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao Q, Wang D, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue H, Yang Y, Weinman T, Goodrich R;
 DR WPI; 2001-476283/51.
 DR P-PSDB; AAM79212.

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.

PS Claim 1; Page 2934-2935; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78823-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides have useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX

SO Sequence 1045 BP; 222 A; 289 C; 314 G; 220 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.72e-112	Length:	1045
Score:	1024.00 <td>Matches:</td> <td>195 </td>	Matches:	195
Percent Similarity:	100.00% <td>Conservative:</td> <td>0 </td>	Conservative:	0
Best Local Similarity:	100.00% <td>Mismatches:</td> <td>0 </td>	Mismatches:	0
Query Match:	91.10% <td>Indels:</td> <td>0 </td>	Indels:	0
DB:	4	Gaps:	0

US-09-977-579-2 (1-215) x AAK52345 (1-1045)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
 Db 302 ATGCTGCTCCCTTCAATGATTTGTTCCCTGCTTCTCTGCTTATCTACGAGTCACT 361
 Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
 Db 362 GTCTGCTTCCCTGCTGTGTGTGGAAGTCCCTCGAGACGAGAGGCGCTGCAGGCAATCCC 421
 Qy 41 MetLeuLeuArgCysIleSerCysMetLeuArgGluGluValGluAlaThrThrValVal 60
 Db 422 ATGAAGCTCGCGTGCATCTCTGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 481
 Qy 61 GluTrpPheTyrArgProGluGluGlyValAspPheLeuIleTyrGluTyrArgAsnGly 80
 Db 482 GAGTGTCTTCAACAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 541

QY 81 HieglngluValIGluserProphengluValrgleugInttpaanglYserIyAspleu 100
 DB 542 CACCAGAGGTGAGAGCCCTTCAGGGGCGCTGAGTAATGGCAGACGACCTG 601
 QY 101 GlnAspValSerIleThrValIleuAsnValThrlenuAspSerGlyLeuYThrCys 120
 DB 602 CAGACGTGTCCATCAGCTGCTCACTGCTGAGACGCTGAGCTGCTTACACCTGC 661
 QY 121 AsnValSerArgGluPheGluPheGluValHisArgProPheValIystrThrArgleu 140
 DB 662 AATGTGTCCCGGAGTTGAGTTGAGGCGCATCGGCTTGTGAGAGACGACGCGCTG 721
 QY 141 IleProleuArgValIThrGluGluValAGlyGluAspPheThrSerValIleSerGluIle 160
 DB 722 ATCCCTTAAGAGTACCGAGAGGCTGAGAGACCTGCTGCTGCTGAGAAATC 781
 QY 161 MetMetTyrlleleuValIlePheIleuThrlenuThrlenuIleGluMetIleTyrcys 180
 DB 782 ATGATGTACATCTTCTGCTCTTCTCTCACTTGTGCTGCTCATGAGATATATATTC 841
 QY 181 TyrArgLyValSerIyValAGluGluValAGluGluValAGluGluValAGluGluVal 195
 DB 842 TACAGAAAGGTCTCAAAAGCCGAGAGGACGCCCAAGAAACGCG 886
 RESULT 11
 ID AAH98320 standard; cDNA; 978 BP.
 XX AAH98320;
 DE 12-OCT-2001 (first entry)
 XX Human EST-derived coding sequence SEQ ID NO: 177.
 KM Human; sheep; pig; cow; fruit fly; Yeast; hamster; macaque; horse;
 KM tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KM diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
 KM gene therapy; nutrition; ss.
 XX Homo sapiens.
 XX WO200154477-A2.
 DB 02-AUG-2001.
 XX 25-JAN-2001; 2001WO-US002687.
 XX 25-JAN-2000; 2000US-00491404.
 PR 17-JUL-2000; 2000US-00617746.
 PR 03-AUG-2000; 2000US-00631451.
 PR 15-SEP-2000; 2000US-0063870.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Auendi V;
 PI Cao Y, Drmanac RA, Zhang J, Wehrman T;
 DR WPI; 2001-476164/51.
 DR P-PSDB; AAM23661.
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use.
 PS Claim 1; Page 299-300; 1275pp; English.
 XX The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA
 CC of the invention

XX SQ Sequence 978 BP; 193 A; 283 C; 293 G; 209 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5,14e-110 Length: 978
 Score: 1003.00 Matches: 196
 Percent Similarity: 93.46% Conservative: 4
 Best Local Similarity: 91.59% Mismatches: 12
 Query Match: 89.23% Indels: 2
 DB: 4 Gaps: 0
 US-09-977-579-2 (1-215) x AAH98320 (1-978)
 QY 1 MetProAlaPheAsnArgLeuPheProleuAlaSerIleValIleuIleYThrValSer 20
 DB 295 ATGCTTCTCTTCAATATAGATTGTTCCCTGCTTCTCTGCTTCACTGCTGCTGCTGCT 354
 QY 21 ValCysPheProValCysValAGluValProSerGluThrGluValAGluValAGluVal 40
 DB 355 GTCGCTTCCCTGTGTGTGTGAAAGTCCCTCGAGAGAGGCGGTGCAAGGCAACCC 414
 QY 41 MetIySeruArgCysIleSerCysMetIyArgGluGluValAGluValAGluValAGluVal 60
 DB 415 ATGAGCTGGGCTGCTCATCTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474
 QY 61 GluTrpPheTyArgProGluGluGlyIyAspPheIleuIleTyGluTyArgAsnGly 80
 DB 475 GAATGTTCTTACAGGCCCGAGGCGGTAAAGATTCTCTTATTAAGGTATCGGAATGCG 534
 QY 81 HieglngluValIGluserProphengluValrgleugInttpaanglYserIyAspleu 100
 DB 535 CACCAGAGGTGAGAGCCCTTCAGGGGCGCTGAGTAATGGCAGACGACCTG 594
 QY 101 GlnAspValSerIleThrValIleuAsnValThrlenuAspSerGlyLeuYThrCys 120
 DB 595 CAGACGTGTCCATCAGCTGCTCACTGCTGAGACGCTGAGCTGCTTACACCTGC 654
 QY 121 AsnValSerArgGluPheGluPheGluValHisArgProPheValIystrThrArgleu 140
 DB 655 AATGTGTCCCGGAGTTGAGTTGAGGCGCATCGGCTTGTGAGAGACGACGCGCTG 714
 QY 141 IleProleuArgValIThrGluGluValAGlyGluAspPheThrSerValIleSerGluIle 160
 DB 715 ATCCCTTAAGAGTACCGAGAGGCTGAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTG 774
 QY 161 MetMetTyrlleleuValIlePheIleuThrlenuThrlenuIleGluMetIleTyrcys 180
 DB 775 ATGATGTACATCTTCTGCTCTTCTCTCACTTGTGCTGCTCATGAGATGATGATGCTG 834
 QY 181 -TyrArgLyValSerIyValAGluGluValAGluGluValAGluGluValAGluGluVal 200
 DB 835 CTACAGAACGCTGTATCAGACGACGAGCGGCCCAAGAAACCGAGTGGCTACCTTTG 894
 QY 200 laileProserGluAsnLyGluAsnSerAlaValPro 212
 DB 895 CGATTCATTGTGAGACAGGAAAATTCTTGGTACT 932
 RESULT 12
 ID ADS11487 standard; DNA; 978 BP.
 XX ADS11487;
 DE 16-DEC-2004 (first entry)
 XX Human therapeutic config DNA - SEQ ID 1724.
 XX antiinflammatory; neuroprotective; antianemic; cytostatic; vulnerary;
 KM inflammatory; haemotopoleis; immunity; neurodegenerative; stem cell;
 KM aplastic anemia; cancer; wound healing; gene therapy; ds; gene.
 XX Homo sapiens.

PN WO2004080148-AZ.
 XX
 PD 23-SEP-2004.
 XX
 PF 30-SEP-2003; 2003WO-US030720.
 XX
 PR 02-OCT-2002; 2002US-0416186P.
 XX
 PA (NUVE-) NUVELO INC.
 XX
 PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y,
 PI Wang D, Chen R, Zhao Qa, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P,
 PI
 DR WPI; 2004-668857/55.
 DR P-PSDB; ADS12085.
 XX
 XX New polynucleotide, useful in preparing a composition for diagnosing or
 PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
 PT aplastic anemia or cancer for promoting wound healing.
 XX
 PS Example 2; SEQ ID NO 1724; 718bp; English.
 CC
 CC The invention relates to a novel isolated polynucleotide and the encoded
 CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
 CC neuroprotective, anti-naemic, cytostatic and vulnerary activities and may
 CC be useful in preparing a composition for diagnosing or treating
 CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
 CC disorders, such as aplastic anaemia or cancer, as well as for promoting
 CC wound healing. The molecules may also be utilised during gene therapy
 CC procedures. The current sequence is that of a human therapeutic contig
 CC DNA of the invention. The current sequence is not shown explicitly within
 CC the specification but can be accessed from the WIPO web-site.
 XX
 SO Sequence 978 BP; 193 A; 283 C; 293 G; 209 T; 0 U; 0 Other:
 Alignment Scores:
 Pred. No.: 5.14e-110 Length: 978
 Score: 1003.00 Matches: 196
 Percent Similarity: 93.46% Conservative: 4
 Best Local Similarity: 91.59% Mismatches: 12
 Query Match: 89.23% Indels: 2
 DB: Gaps: 0
 US-09-977-579-2 (1-215) x ADS11487 (1-978)
 QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTPValSer 20
 DB 295 ATGCTGCTGCTTCAATAGATTGTTCCCTGCTTCTCTGCTTATCTAGTGGTCACT 354
 QY 21 ValCyPheProValCyValAlaGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
 DB 355 GTCTGCTTCCCTGTGTGTGTGGAAGTCCCTCGAAGACGAGCCGCTGACGGCAACCCC 414
 QY 41 MetLeuLeuArgCysIleSerCysMetLeuArgGluGluValGlnAlaThrThrValVal 60
 DB 415 ATGAACTCGGCTGCAATCTCTCTCAAGAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474
 QY 61 GluThrPheTyrArgProGluGluGlyValAspPheLeuIleTyrGluTyrArgAsnGly 80
 DB 475 GAATGGTCTTACAGGCGCCGAGGGCGGGAAGATTCTTATTTACAGATTCGGAATGGC 534
 QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnIleTyrPheGlnIleSerLeu 100
 DB 535 CACCAAGAGGTGAGAGAGCCCTTTCAGGGGCGCTCGAAGTGAAGATGAGCAAGAGACTCG 594
 QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
 DB 595 CAGGAGGTGCTTCACTGCTCAACGTCACCTCTGACCACTCTGCTCTCACTGCTGCTG 654
 QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValIleThrThrArgLeu 140
 DB 655 AATGTGTCCTGGGAGTTGATTTGAGGCGCATGCGCCCTTGTGAAAGACAGACGCGGCTG 714

QY 141 IleProLeuArgValThrGluGluAlaGlyIleAspPheThrSerValValSerGluIle 160
 DB 715 ATCCCCCTAAGAGTCAACGAGAGGCTGAGAGGACTTCACTCTGTGTCTTCAGAAATC 774
 QY 161 MetMetTyrIleLeuLeuValPheLeuThrIleTyrPheLeuIleGluMetIleTyrCys 180
 DB 775 ATGATGTACATCTCTTGTGCTTCTCTCACTGCTGCTGCTCTCATGAGATGATACATTGC 834
 QY 181 -TyrArgLysValSerLeuAlaGluGluAlaValGlnGluAlaSerAspTyrLeu-A 200
 DB 835 CTACAGAACGGTATCAGACAGAACCGCCCAACGAAACCGGATGGTACTCTTGG 894
 QY 200 1a1leProSerGluAsnLysGluAsnSerAlaValPro 212
 DB 895 CGATTCCATTGAGAACGAGAAATTTCTCGTACT 932
 RESULT 13
 AAS86764
 ID AAS86764 standard; cDNA; 1195 BP.
 XX
 AC AAS86764;
 XX
 DT 13-FEB-2002 (first entry)
 DT
 DE DNA encoding novel human diagnostic protein #22568.
 XX
 XX Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US008631.
 XX
 PF 31-MAR-2000; 2000US-00540217.
 PR 23-APR-2000; 2000US-00649167.
 XX
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 XX
 PI WPI; 2001-639362/73.
 DR P-PSDB; ABG22577.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 1; SEQ ID NO 22568; 103bp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probe, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS864197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pat_sequences

XX Sequence 1195 BP; 253 A; 356 C; 381 G; 205 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.64e-101	Length:	1195
Score:	927.50	Matches:	184
Percent Similarity:	94.42%	Conservative:	2
Best Local Similarity:	93.40%	Mismatches:	9
Query Match:	82.52%	Indels:	2
DB:	5	Gaps:	1

US-09-977-579-2 (1-215) x AAS86764 (1-1195)

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QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 463 ATGCCTGCTTCAATAGATTGTTTCCCTGGCTTCTCGGCTTATCTAGTCACTAGT 522
QY 21 ValCysPheProValCysValGluValProSerGluThrGluAla--ValGlnGlyAs 39
Db 523 GTCGCTTCCCTGCTGGGAGAAAGTCCCTTAGAAAAAGGCGGCGGCGGCGGCTAA 582
QY 39 nProMetLeuAsnArgCysIleSerCysMetLeuArgGluGluValGluAlaThrThrVa 59
Db 583 CCCATGAAGCTGGGCTGATCTCTGATGAAGAAGAGAGAGAGGCGGCGGCGGCGGCTAA 642
QY 59 lValGluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAs 79
Db 643 GGTGAATGCTTCTTAACAGCCCGAGGCGGCTTAAGATTCTTATTATTCGAGTATCGGA 702
QY 79 nGlyHisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAs 99
Db 703 TGGCCACAGAGAGGTGAGAGCCCTTTCAGGGGCGCTGAGTGAATGACAGCAAGGA 762
QY 99 PLeuGluAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrTrh 119
Db 763 CCTGAGAGAGCTGGCTGATCTCTGATGAAGAAGAGAGAGGCGGCGGCGGCTTAC 822
QY 119 rCysAsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrAr 139
Db 823 CTGCAATGTCCTGGGAGTTTGAAGTTCAGGCGGATGGCCCTTGTGGAAGAGAGCGG 882
QY 139 GluLeuLeuProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValLysSerG 159
Db 883 GCTGATCCCTTAAGAGTCAACGAGAGGCTGAGAGAGACTTCACTCTGCTGCTCAGA 942
QY 159 uIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyr 179
Db 943 AATCATGATGATACATCTTCTGCTTCTTCTCACTTGTGCTGCTCATCGAGATGATATA 1002
QY 179 rCysTyrArgLysValSerLysValaGluGluAlaAlaGlnLysAsnAla 195
Db 1003 TTGCTACAGACAGGCTCTCAAAAGCCGAAGAGGAGCCCAAAAGAGCGG 1051

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RESULT 14
ADSI0151
ID ADSI0151 standard; DNA; 953 BP.

AC ADSI0151;
XX 16-DEC-2004 (first entry)
XX Human therapeutic DNA - SEQ ID 388.
DE
XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
KM inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
XX aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
OS Homo sapiens.
XX WO2004080148-A2.
XX

PD 23-SEP-2004.
XX
XX 30-SEP-2003; 2003WO-US030720.
XX
XX 02-OCT-2002; 2002US-0416186P.
XX

PA (NUVE-) NUVELO INC.

XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y,
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX WPI: 2004-668857/65.
DR P-PSDB; ADSI0835.
XX

PT New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.

PS Claim 1; SEQ ID NO 388; 718bp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic DNA of
CC the invention. The current sequence is not shown explicitly within the
XX specification but can be accessed from the WIPO web-site.

XX Sequence 953 BP; 180 A; 279 C; 290 G; 204 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.53e-96	Length:	953
Score:	886.50	Matches:	174
Percent Similarity:	84.91%	Conservative:	6
Best Local Similarity:	82.08%	Mismatches:	19
Query Match:	78.87%	Indels:	13
DB:	13	Gaps:	1

US-09-977-579-2 (1-215) x ADSI0151 (1-953)

```

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 327 ATGCCTGCTTCAATAGATTGTTTCCCTGGCTTCTCGGCTTATCTAGTCACTAGT 386
QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValaGlnGlyAsnPro 40
Db 387 GTCGCTTCCCTGCTGGGAGTTTGAAGTCCCTCGAGAGCGAGGCGGCGGCGGCAACCCC 446
QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrVala 60
Db 447 ATGAGCTGGGCTGATCTCTGATGAAGAAGAGAGAGAGTGAAGGCGGCGGCTG 506
QY 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 507 GAATGCTTCTTAACAGCCCGAGGCGGCTTAAGATTCTTATTATTCGAGTATCGGAATG 566
QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 567 CACGAGAGGTGAGAGCCCTTTCAGGGGCGGCTGAGTGAATGAGAGAGAGAGGACCTG 626
QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrTrhCys 120
Db 627 CAGAGCTGTCATCACTGATCTCTGATGAAGAAGAGAGAGTGAAGGCGGCGGCTG 686
QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 687 AATGTCCTGGGAGTTTGAAGTTCAGGCGGCTTGTGAGAGAGAGAGCGGCGGCTG 746
QY 141 lLeuProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValLysSerGluIle 160

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Db 747 ATCCCCTAAGTACACCGAGAGGCTGAGAGACTTCACTCTGTGCTTAACACTTC 806
 QY 161 MetMetTyrTlleLeuLeuValPheLeuThrLeuTyrLeuLeuIleGluMetIleTyrCys 180
 Db 807 ATGATGACATCCTCTGTGCTTCCACCTT----- 839
 QY 181 TyrArgValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
 Db 840 -----GTGACCAACCGCACCGCTCCAGAGCAGCATCTACTGCTCCACACAGT 887
 QY 201 IleProSerGluAsnLysGluAsnSerAlaValPro 212
 Db 888 GCTCTGATAGTCATCTGGGCTTCCAGCATCCCT 923
 RESULT 15
 AAV86895
 ID AAV86895 standard; cDNA; 471 BP.
 AC AAV86895;
 XX
 XX 27-APR-1999 (first entry)
 DT
 DE EST clone BM4.
 XX
 KM Expressed sequence tag; secreted protein; haematopoiesis regulator;
 KM tissue growth; activating; inhibin; tumour invasion suppressor; EST; human;
 KM chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
 KM receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
 XX
 OS Homo sapiens.
 XX
 PN MO845435-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 10-APR-1998; 98MO-US006954.
 XX
 PR 10-APR-1997; 97US-00835913.
 XX
 PA (GEMV) GENETICS INST INC.
 XX
 XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Werberg D, Treacy M;
 PI Spaulding V, Agostino MJ;
 XX
 DR WPI; 1999-070076/06.
 XX
 PT New polynucleotides encoding human secreted proteins - derived from e.g.
 PT human blood, kidney, foetal lung, placenta, testes, brain, ovary,
 PT pituitary, retina and colon cDNA libraries.
 PS
 PS Claim 1; Page 383-384; 633pp; English.
 XX
 CC This sequence represents an expressed sequence tag (EST), and is a
 CC polynucleotide of the invention. The polynucleotides of the invention are
 CC all secreted EST sequences isolated from a variety of human tissue
 CC sources. The EST sequences and proteins encoded by them are predicted to
 CC have useful biological activities which would make them suitable for
 CC treating, preventing or ameliorating medical conditions in humans and
 CC animals, although no supporting data is given. Suggested activities
 CC include nutritional activity, immune stimulating or suppressing activity,
 CC haematopoiesis regulating activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
 CC activity. The EST sequences are also stated to be useful for gene therapy
 XX
 SQ Sequence 471 BP; 93 A; 126 C; 143 G; 108 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 3,44e-79 length: 471
 Score: 742.00 Matches: 143
 Percent Similarity: 98.62% Conservative: 0
 Best Local Similarity: 98.62% Mismatches: 2

Query Match: 66.01% Indels: 1
 DB: 2 Gaps: 0
 US-09-977-579-2 (1-215) x AAV86895 (1-471)
 QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
 Db 29 ATGCTGCGCTTAATATGATTTGTTCCCTGGCTTCTCGTGCTTATCTACGGGTCAGT 88
 QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
 Db 89 GTCTGCTTCCCTGTGTGTGTGAAGCCCTCGAGACGAGGCC-GTGCANGGCAACCCC 147
 QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
 Db 148 ATGAACTCGCGCTGCATCTCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207
 QY 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
 Db 208 GAATGTTCTACAGGCCCGAGGGCGGTAAAGATTCTTATTTCAGATATCGAATGAGC 267
 QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
 Db 268 CACCAAGAGGTGAGAGGCCCTTCAGGGCCGCTGCAAGTGAATGCGACAGAGACCTG 327
 QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
 Db 328 CAGAGCTGCTCATCTGCTGCTCAACGTCATCTGTAAGATGACTTGCCCTACACTTCG 387
 QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValIleThrThrArgLeu 140
 Db 388 AATGTGTCCCGGAGATTGAGTTGAGCGGCATCGGCCCTTGTGAAAGACGACGCGCTG 447
 QY 141 IleProLeuArgVal 145
 Db 448 ATCCCTTAAGAGTC 462

Search completed: April 7, 2005, 15:26:59
 Job time : 437 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2005, 15:00:45 ; Search time 162 Seconds
(without alignments)
2171.602 Million cell updates/sec

Title: US-09-977-579-2

Perfect score: 1124

Sequence: 1 MPANRLPLASLVLIYVWS.....SDYLAIPSENKENSAPVVEE 215

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool_p/US09977579/runat_06042005_163457_23620/app_query.fasta_1.391
-DB=issued Patents NA -Qfmt=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=pt0 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USR=US09977579@cgn_1_1_105@runat_06042005_163457_23620 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	470	41.8	617	4	US-09-949-016-2369
2	165.5	14.7	11174	4	Sequence 14111, A
3	165.5	14.7	30337	4	Sequence 12053, A
4	147	13.1	1342	4	Sequence 787, App
5	147	13.1	1708	4	Sequence 4948, App
6	131	11.7	1121	4	Sequence 5103, App
7	131	11.7	1151	3	Sequence 1, Appli
8	131	11.7	1151	3	Sequence 3, Appli
9	131	11.7	1151	3	Sequence 5, Appli
10	131	11.7	1151	3	Sequence 7, Appli
11	129	11.5	600	3	Sequence 43, Appl
12	129	11.5	600	3	Sequence 47, Appl

13	127	11.3	600	3	US-09-430-503-41	Sequence 41, Appl
14	127	11.3	600	3	US-09-430-503-45	Sequence 45, Appl
15	127	11.3	752	3	US-09-430-503-17	Sequence 17, Appl
16	127	11.3	752	3	US-09-430-503-19	Sequence 19, Appl
17	127	11.3	752	3	US-09-430-503-21	Sequence 21, Appl
18	127	11.3	752	3	US-09-430-503-23	Sequence 23, Appl
19	125	11.1	1073	3	US-09-430-503-25	Sequence 25, Appl
20	125	11.1	1073	3	US-09-430-503-27	Sequence 27, Appl
21	125	11.1	1073	3	US-09-430-503-29	Sequence 29, Appl
22	125	11.1	1073	3	US-09-430-503-31	Sequence 31, Appl
23	124.5	11.1	1060	4	US-09-799-451-222	Sequence 222, App
24	118	10.5	480	3	US-09-430-503-33	Sequence 33, Appl
25	118	10.5	480	3	US-09-430-503-35	Sequence 35, Appl
26	118	10.5	480	3	US-09-430-503-37	Sequence 37, Appl
27	118	10.5	480	3	US-09-430-503-39	Sequence 39, Appl
28	112.5	10.0	1592	3	US-09-656-952-1	Sequence 1, Appli
29	110.5	9.8	1111	4	US-09-949-016-4949	Sequence 4949, App
30	110.5	9.8	1113	4	US-09-949-016-652	Sequence 652, App
31	109	9.7	1207	4	US-09-023-655-131	Sequence 131, App
32	109	9.7	1561	3	US-09-656-952-18	Sequence 18, Appl
33	109	9.7	1591	3	US-09-656-952-17	Sequence 17, Appl
34	109	9.7	1751	4	US-09-855-323-11	Sequence 11, Appl
35	108.5	9.7	2184	3	US-09-484-970B-161	Sequence 161, App
36	108	9.6	8083	3	US-09-383-630-4	Sequence 4, Appli
37	108	9.6	8083	3	US-09-383-630-5	Sequence 5, Appli
38	106	9.4	1557	3	US-08-996-138-2	Sequence 2, Appli
39	106	9.4	1557	4	US-09-556-972-2	Sequence 2, Appli
40	106	9.4	2830	1	US-08-604-333-3	Sequence 3, Appli
41	106	9.4	2830	3	US-09-110-618-3	Sequence 3, Appli
42	106	9.4	2830	3	US-09-578-178-3	Sequence 3, Appli
43	106	9.4	2830	4	US-09-577-806-3	Sequence 3, Appli
44	106	9.4	2830	4	US-09-621-502-7	Sequence 7, Appli
45	99.5	8.9	2079	4	US-09-949-016-3171	Sequence 3171, Ap

ALIGNMENTS

RESULT 1

US-09-949-016-2369
; Sequence 2369, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: CL001307
; FILE REFERENCE: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2369
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-2369

Alignment Scores:
Pred. No.: 1.36e-53 Length: 617
Score: 470.00 Matches: 101
Percent Similarity: 66.16% Conservative: 30
Best Local Similarity: 51.01% Mismatches: 59
Query Match: 41.81% Indels: 8
DB: 4 Gaps: 5

US-09-977-579-2 (1-215) x US-09-949-016-2369 (1-617)

QY 26 CysaValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCys 45

```

Db      21  TGGTGGAGTGGACCTCGGAGCCGAGCGGTGATGGATGACCTTCAAAATCTTTCG 80
QY      46  ILeSerCysMetLysArgGluGluValGluAlaThrThrValValGluTrpPheTyArg 65
Db      81  ATCTCTGCAAGCGCGCAGCAGACCAAGCTTGACACCTTACCAGTGGACCTTCGCG 140
QY      66  ProGluGlyGlyLysAspPheLeu-----IleTyrgluTyArgAsnGlyHisGlnGluVal 84
Db      141  CAGAAGGCACGTAGGAGGTTGTCAAGATCTCGCGCTATGAGATGAGGTGTGCAAGTCG 200
QY      85  GluSerPro-----PheGlnGlyArgLeuGlnTrpAsnGlySer-----LysAsp 99
Db      201  GAGGAGGATGAGCGCTTCGAGGCGCGGTGGTGGATGGCAGCGCGGCCACCAAGAC 260
QY      100  LeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyThr 119
Db      261  CTGCAGGATCTGTATCTTTCATCCATGTCACCTACACCACTCGCGGCGACTACGAG 320
QY      120  CysAsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArg 139
Db      321  TGCCAGCTTACCGCTGCTCTTCTTCGAAAACTACGAGCACAACACCAAGCGCTCGTCAAG 380
QY      140  LeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu 159
Db      381  AGATCCACATGAGTGTGAGAAAGCCACAGACATGGCATCCATCGTGTCTGAG 440
QY      160  IleMetMetTyrlleLeuLeuValPheLeuThrLeuTrpLeuLeuGluMetIleTy 179
Db      441  ATCATGATGTATGTCTCATTTGTTGGTGGTACCATATGCTGTCGACAGATGATTAC 500
QY      180  CysTyArgLysValSerLysAla---GluGluAlaAlaGlnGluAsnAlaSerAspTy 198
Db      501  TGCTACAGAAGATCGCTCGCGCCAGGAGACTGCTGCACAGAGAAATCGCTCGGAATAC 560
QY      199  LeuAlaIleProSerGluAsnLysGluAsn---SerAlaValProValGluGlu 215
Db      561  CTGGCCATCACCTCTGAAAGAAAGAAAGAACTGCACGCGGTCCAGGTGCCGAA 614

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RESULT 2

```

US-09-949-016-14111
; Sequence 14111, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14111
; LENGTH: 11174
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(11174)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14111

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Alignment Scores:
Pred. No.: 1.5e-10 Length: 11174
Score: 165.50 Matches: 56
Percent Similarity: 47.13% Conservative: 26
Best Local Similarity: 32.18% Mismatches: 45

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Query Match: 14.72% Indels: 48
DB: 4 Gaps: 7
US-09-977-579-2 (1-215) x US-09-949-016-14111 (1-11174)
QY      67  GluGlyGlyLysAspPheLeuIleTyrglu-TyrArgAsnGlyHisGlnGluValGluSe 86
Db      8220  GAAGAGGTATTTCATTTTACAAATTCGAAGAAACAGAGG-----CCTAGAGACATTGAGTC 8273
QY      86  rProPheGlnGlyArgLeu-----GlnTrp-----AsnGlySerLysAs 99
Db      8274  ACTTCGCAAGGTCCACAGCTGGCGAGTGGCAGAGCCAGCCCTTTGAACCTGAGCCTTCT 8333
QY      99  pleuGlnAspValSerIle-----ThrValLeuAsnValThrLeuAsnAspSerGlyLe 117
Db      8334  GGTTCAGAGCTACCGCTTTTAGGCACCGTGTGAGGGCGCTCCAG-AATGACACAGATGT 8392
QY      117  uTyThrCysAsnValSerArgGluPheGluPheGluAlaHisArg-----132
Db      8393  GGCCTCGAGTTACACAGGGAGCGAGTTGAGGGTGACCCCGCCAGGCGCTACCAAGGCT 8452
QY      133  -----ProPheValLysThrThrArgLeuIleProLeu-----143
Db      8453  GGGTATTAAATACACAGTGCATACACAGCGCCAGGAGGTTGAGCCACTCATCCAAGC 8512
QY      143  -----143
Db      8513  TCACACAGCAAGCTCACAGCACACTCAGGCTGTCTCATGAGCGCTGGGCTACCCCTTAACC 8572
QY      144  -ArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIleMetMetTy 163
Db      8573  CTGCTTGGCCCCCTGCGCCACACAGAGATGGCATCCATCGTGTCTGAGATCATGATGA 8632
QY      163  rIleLeuLeuValPheLeuThrLeuTrpLeuLeuGluMetIleTyCysTyArgLys 183
Db      8633  TGTGCTCATTTGTGGTGTGACCATATGCTGTCGACAGAGATGATTACTGCTCAAGAA 8692
QY      183  sValSerLysAla---GluGluAlaAlaGlnGluAsnAla 195
Db      8693  GATCGCTCGCGCCAGGAGACTGCTGCACAGAGAAATCGG 8732

```

RESULT 3

```

US-09-949-016-13053
; Sequence 13053, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13053
; LENGTH: 30337
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(30337)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13053

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Alignment Scores:
Pred. No.: 7.24e-10 Length: 30337
Score: 165.50 Matches: 56

Percent Similarity: 47.13% Conservative: 26
 Best Local Similarity: 32.18% Mismatches: 45
 Query Match: 14.72% Indels: 48
 DB: 4 Gaps: 7

US-09-977-579-2 (1-215) x US-09-949-016-13053 (1-30337)

QY 67 GluGlyValysAspPheLeuLeuTyrGlu-TyrArgAsnGlyHisGlnGluValGluSe 86
 DB 242 GAGGAGGTATTCATTTCATATGAGAAACAGAGG-----CCTAGACATTTAGTC 235
 QY 86 rPropheGlnGlyArgLeu-----GlnTrp-----AsnGlySerLyAs 99
 DB 296 ACTTGCGCAAGGTACACAGCTGCGCAGTGGCAGAGCCAGCCCTTTGAACCTGAGCCTTCT 355
 QY 99 pLeuGlnAspValSerIle-----ThrValLeuAsnValThrLeuAsnAspSerGlyLe 117
 DB 356 GGTTCGACAGTACCGGCTTTTGGCACCCTGCTGAGGGCCCTCAG-AATGACACAGATGT 414
 QY 117 uTyrThrCysAsnValSerArgGluPheGluPheGluAlaHisArg-----132
 DB 415 GGCTCGAGTTACACAGGAGGAGGTTGAGGGTGACCCACACAGCCCTACCAAGGCT 474
 QY 133 -----ProPheValLysThrThrArgLeuLeuProLeu-----143
 DB 475 GGGTATTATTAATACAGTGCATACACAGCCAGGCGGAGGTTGAGCCACTCATCCAAGC 534
 QY 143 -----143
 DB 535 TCACACAGCAAGCTCAGACACACTCAGCGTGTCTATGACAGCCCTGGGCTTAAACC 594
 QY 144 -ArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluLeuMetMetTy 163
 DB 595 CTGCTGGCCCTGCACCCACAGACATGGCATCATCTCTGAGATCATATGTA 654
 QY 163 rLeuLeuValPheLeuThrLeuTrpLeuLeuLeuGluMetIleTyrCysTyrArgly 183
 DB 655 TGTGCTCATTTGCTGTGACCATATGCTGCTGCGGACAGATGATTTACTGCTACAAGAA 714
 QY 183 sValSerLyAla---GluGluAlaAlaGlnGluAla 195
 DB 715 GATGCTGCGCCGACGAGAGACTGCTGCACAGGAGAAATGCG 754

RESULT 4

US-09-949-016-787
 ; Sequence 787, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 787
 ; LENGTH: 1342
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-787

Alignment Scores:
 Pred. No.: 1.64e-09 Length: 1342
 Score: 147.00 Matches: 57
 Percent Similarity: 41.44% Conservative: 35
 Best Local Similarity: 25.68% Mismatches: 80

Query Match: 13.08% Indels: 50
 DB: 4 Gaps: 9

US-09-977-579-2 (1-215) x US-09-949-016-787 (1-1342)

QY 7 LeuPheProLeuAlaSerLeuValLeuLeuTyrTrpValSerValCysPheProValCys 26
 DB 180 CTTTGGCCTATAGCAGCT--GTGGAATTTATACCTCCCGGTG-----221
 QY 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
 DB 222 -----CTGGAGGCTGTTAATGGGACAGATGCTCGGTTAAATGCACT 263
 QY 47 SerCysMetLysArgGluGluValGluAlaThrThrValValGluTrpPheTyrArgPro 66
 DB 264 TTTCTCAGCTTTGCCCTCTGGGTGATGCTCTAACAGTGACC---TGGAATTTTCGTCT 320
 QY 67 ---GluGlyGly---LysAspPheLeuLeuTyrGluTyrArgAsnGlyHisGlnGluVal 84
 DB 321 CTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCATAGATCCCTTCCAACCATG 380
 QY 85 GluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeuGlnAspValSer 104
 DB 381 AGTGGCGGCTTTAAGGACCGGCTCTCTGGGATGGGAATCTCGAGCGGTACGATGCTCC 440
 QY 105 IleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSerArg 124
 DB 441 ATCTTCTCTGGAACTGCAGTTCGACGACATGGACATACACCTGCCAGGTGAAGAAC 500
 QY 125 GluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeuLeuProLeuArg 144
 DB 501 -----CCACCTGAT 509
 QY 145 ValThrGluGluAlaGlyGluAspPheThrSerValVal-----SerGlu 159
 DB 510 GTTGATGGGTGATAGGGGAGATCCGGCTCAGCGCTGTCACACTGTACCTCTCTCGAG 569
 QY 160 IleMetMetTyrIleLeuLeuVal-----PheLeuThrLeuTrpLeu 173
 DB 570 ATCCACTTCTGGCTCTGGCCATGGCTCTGCTGTGCATGATGATCATTAATGTAAT 629
 QY 174 LeuLeuGluMetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaGlnGlu 193
 DB 630 GTAGTGTCTCTTCCAGCATTTACCGGAAAAAGCGATGGGCCGAAAGAGCT-----680
 QY 194 AsnAlaSerAspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProVal 213
 DB 681 -----CATAAAGTGGTGGAGATAAATCAAAAGAGAGAGAAAGGCTCAACCAA 728
 QY 214 GluGlu 215
 DB 729 GAGAAA 734

RESULT 5

US-09-949-016-4948
 ; Sequence 4948, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4948

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; LENGTH: 1708
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4948

Alignment Scores:
Pred. No.:          2,41e-09          Length:          1708
Score:             147.00           Matches:          57
Percent Similarity: 41.44%           Conservative:    35
Best Local Similarity: 25.68%          Mismatches:     80
Query Match:       13.08%             Indels:         50
DB:                4                 Gaps:           9

US-09-977-579-2 (1-215) x US-09-949-016-4948 (1-1708)

QY 7 LeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCys 26
DB 225 CTTTGGCCTATAGCAGCT---GTGGAAATTTATACCTCCCGGGTG-----266
QY 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
DB 267 -----CTGGAGGCTGTAAATGGGACAGATGCTCGGTAAATGCACT 308
QY 47 SerCysMetLysArgGluGluValGluAlaThrThrValValGluTrpPheTyrArgPro 66
DB 309 TTCTCCAGCTTTGGCCCTGTGGGTGATGCTCTAACAGTGACC---TGGAAATTTTCGTCT 365
QY 67 ---GluGlyGly---LysAspPheLeuIleTyrGluTyrArgAsnGlyHisGlnGluVal 84
DB 366 CTAGACGGGGGACCTGAGCAGTTGTATTCTACTACACATAGATCCCTTCCAAACCCATG 425
QY 85 GluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeuGlnAspValSer 104
DB 426 AGTGGCGGCTTTAAGGACCGGCTGTCTTGGGATGGGAATCCTGAGCGGTACGATGCTCTC 485
QY 105 IleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSerArg 124
DB 486 ATCCTTCTCTGGAACTCGAGTCGACGACAAATGGGACATACACCTGCCAGGTGAAGAAC 545
QY 125 GluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeuIleProLeuArg 144
DB 546 -----CCACCTGAT 554
QY 145 ValThrGluGluAlaGlyGluAspPheThrSerValVal-----SerGlu 159
DB 555 GTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTGTGCACACTGTACGCTTCTCTGAG 614
QY 160 IleMetMetTyrIleLeuLeuVal-----PheLeuThrLeuTrpLeu 173
DB 615 ATCCACTTCTGGCTCTGCCCATTTGGCTGTGCTGTGCACTGATGATCATATAGTAAT 674
QY 174 LeuIleGluMetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaGlnGlu 193
DB 675 GTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGCGCGAAAGACT-----725
QY 194 AsnAlaSerAspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProVal 213
DB 726 -----CATAAAGTGGTGGGATAAAATCAAAAGAGAGAAAGGCTCAACCAA 773
QY 214 GluGlu 215
DB 774 GAGAAA 779

RESULT 6
US-09-949-016-5103
; Sequence 5103, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
```

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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5103
; LENGTH: 1121
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5103

Alignment Scores:
Pred. No.:          1.78e-07          Length:          1121
Score:             131.00           Matches:          51
Percent Similarity: 37.39%           Conservative:    32
Best Local Similarity: 22.97%          Mismatches:     81
Query Match:       11.65%             Indels:         58
DB:                4                 Gaps:           9

US-09-977-579-2 (1-215) x US-09-949-016-5103 (1-1121)

QY 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
DB 250 GTATATACGCCAAAAGAAATCTTCGTGCAATGGTACACAAAGGGAAGCTGACCTGC---306
QY 47 SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe 63
DB 307 -----AGTTCAAGTCTACTAGTAGCAGCTGGCGGGTTGACCTCAGTCTCTGGAGC 357
QY 64 TyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln 82
DB 358 TTCCAGCCAGAGGGGGCGCACACTACTGTGCTGTTTTTCCACTACTCCCAAGGCAAGTG 417
QY 83 GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
DB 418 TACCTTGGGAATTTATCCACCATTTAAAGACAGATCAGCTGGCTGGAGACCTTGACAG 477
QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
DB 478 AAAGATGATCATCATCAACATAGAAATATGCAAGTTTATACACATGGCACCTATATCTGT 537
QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
DB 538 GATGTCAAAAAC-----549
QY 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu---159
DB 550 ---CCTCTGACATCGTTGTCAGCTGACACATAGAGCTCTATGTCTGTAAGAAAGAG 606
QY 160 -----IleMetMetTyrIleLeuLeuValPheLeuThr 170
DB 607 AATTTGCTGTGTTTCCAGTTTGGTAGTGGTGGGCATAGTTACTGCTGTGCTCTAGCT 666
QY 171 LeuTrpLeuLeuIleGluMetIleTyrCys-----TyrArgLys-----183
DB 667 CTCACCTGCTCATCAGCATGATTCCTGCTGCTCTATAGAAGGAAAAAAGCTCTAAACGG 726
QY 184 -----ValSerLysAlaGluGluAlaGlnGlu 193
DB 727 GATTACACTGGCTGCAGTACATCAGAGAGTTTGTCCACCATTTAGCAGCTCTCTCGAAG 786
QY 194 AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer 209
DB 787 TCCCCCTCCGACACTGAGGGTCTTTGTAAGAGTCTGCTCTCTGGATCTCTCACCAGGGCCCA 846
QY 210 AlaVal 211
DB 847 GTCAT 852
```

Db 727 GATTACACGGCTGCAGTACATACAGAGAGTTTGTTCACCAAGTAAAGCAGGCTCCTCGGAAG 78
 Qy 194 AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer 209
 Db 787 TCCCTCCGACACTGAGGCTTGTAAAGAGTCTGCTTCTTGGATCTCACCAGGGCCCA 846
 Qy 210 AlaVal 211
 Db 847 GTCATA 852
 RESULT 8
 US-09-430-503-3
 ; Sequence 3, Application US/09430503
 ; Patent No. 6355786
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhao, Zhizhuang
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
 ; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
 ; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
 ; CURRENT APPLICATION NUMBER: US/09/430,503
 ; CURRENT FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 1151
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: gene
 ; LOCATION: (1)..(1151)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (133)..(939)
 US-09-430-503-3
 Alignment Scores:
 Pred. No.: 1.85e-07 Length: 1151
 Score: 131.00 Matches: 51
 Percent Similarity: 37.39% Conservative: 32
 Best Local Similarity: 22.97% Mismatches: 81
 Query Match: 11.65% Indels: 58
 DB: Gaps: 9
 US-09-977-579-2 (1-215) x US-09-430-503-1 (1-1151)
 Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
 Db 250 GTATATACGCCAAAGAAATCTTCGTGGCAAAATGGTACACAAGGGAAGCTGACCTGC--- 306
 Qy 47 SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe 63
 Db 307 -----AAGTTCAAGTCTACTAGTACAGCTGGCGGTTGACCTCAGTCTCCCTGGAGC 357
 Qy 64 TyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln 82
 Db 358 TTCAGCCAGAGGGGCCGACACTACTGTGCTGTTTTTCCACTACTATCCCAAGGCAAGTG 417
 Qy 83 GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
 Db 418 TACCTTGGGAATTTATCCACCATTTAAAGACAGAAATCAGCTGGGCTGGAGACCTTGACAAG 477
 Qy 101 GluAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
 Db 478 AAAGATGCATCAATCAACATAGAAAAATATGCAAGTTTATACAAATGGCACCCTATATCTGT 537
 Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
 Db 538 GATGTCAAAAC----- 549
 Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu--- 159
 Db 550 ---CCTCCTGACATCGTTGCCAGCTCGACACATATAGGCTCTATGCTGTAGAAAAAGAG 606
 Qy 160 -----IleMetMetTyrIleLeuLeuValPheLeuThr 170
 Db 607 AATTGCTGCTGTTTCCAGTTGGGTAGGTGGGCATAGTTACTGCTGTGCTCCTAGGT 666
 Qy 171 LeuTrpLeuLeuIleGluMetIleTyrCys-----TyrArgLys----- 183
 Db 667 CTACTCTGCTATCAGCATGATCTGCTGCTGCTCTATAGGAAGGAAAACTCTAAACGG 726
 Qy 184 -----ValSerLysAlaGluGluAlaGlnGlu 193
 US-09-430-503-1
 Alignment Scores:
 Pred. No.: 1.85e-07 Length: 1151
 Score: 131.00 Matches: 51
 Percent Similarity: 37.39% Conservative: 32
 Best Local Similarity: 22.97% Mismatches: 81
 Query Match: 11.65% Indels: 58
 DB: Gaps: 9
 US-09-977-579-2 (1-215) x US-09-430-503-1 (1-1151)
 Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
 Db 250 GTATATACGCCAAAGAAATCTTCGTGGCAAAATGGTACACAAGGGAAGCTGACCTGC--- 306
 Qy 47 SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe 63
 Db 307 -----AAGTTCAAGTCTACTAGTACAGCTGGCGGTTGACCTCAGTCTCCCTGGAGC 357
 Qy 64 TyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln 82
 Db 358 TTCAGCCAGAGGGGCCGACACTACTGTGCTGTTTTTCCACTACTATCCCAAGGCAAGTG 417
 Qy 83 GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
 Db 418 TACCTTGGGAATTTATCCACCATTTAAAGACAGAAATCAGCTGGGCTGGAGACCTTGACAAG 477
 Qy 101 GluAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
 Db 478 AAAGATGCATCAATCAACATAGAAAAATATGCAAGTTTATACAAATGGCACCCTATATCTGT 537
 Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
 Db 538 GATGTCAAAAC----- 549
 Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu--- 159
 Db 550 ---CCTCCTGACATCGTTGCCAGCTCGACACATATAGGCTCTATGCTGTAGAAAAAGAG 606
 Qy 160 -----IleMetMetTyrIleLeuLeuValPheLeuThr 170
 Db 607 AATTGCTGCTGTTTCCAGTTGGGTAGGTGGGCATAGTTACTGCTGTGCTCCTAGGT 666
 Qy 171 LeuTrpLeuLeuIleGluMetIleTyrCys-----TyrArgLys----- 183
 Db 667 CTACTCTGCTATCAGCATGATCTGCTGCTGCTCTATAGGAAGGAAAACTCTAAACGG 726
 Qy 184 -----ValSerLysAlaGluGluAlaGlnGlu 193

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QY 160 -----lleMetMetTyrIleLeuLeuValPheLeuThr 170
Db 607 AATTGTCCTGTGTTCCAGTTGGGTAGTGGGCATAGTTACTGCTGTGCTCCTAGGT 666
QY 171 LeuTrpLeuLeuIleLeuMetIleTyrCys-----TyrArgLys----- 183
Db 667 CTCACCTGCTCATCAGCATGATTCTGGCTGTGCTCTATAGAGGAAACTCTTAACGG 726
QY 184 -----ValSerLysAlaGluGluAlaAlaGlnGlu 193
Db 727 GATTACACTGGCTGCAGTACATCAGAGAGTTTGTCCACAGTTAAGCAGGCTCTCGGAAG 786
QY 194 AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer 209
Db 787 TCCCTCCGACACTGAGGCTCTTGTAAAGAGTGTGCTTCTGGATCTCACCAGGGGCCA 846
QY 210 AlaVal 211
Db 847 GTCATA 852

RESULT 9
US-09-430-503-5
; Sequence 5, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1151)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (133)..(939)
US-09-430-503-5

Alignment Scores:
Pred. No.: 1.85e-07 Length: 1151
Score: 131.00 Matches: 51
Percent Similarity: 37.39% Conservative: 32
Best Local Similarity: 22.97% Mismatches: 81
Query Match: 11.65% Indels: 58
DB: 3 Gaps: 9

US-09-977-579-2 (1-215) x US-09-430-503-5 (1-1151)
QY 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 250 GTATATACGCCAAAAGAAATCTTCGTGGCAAAATGGTACACAAGGGAAGCTGACCTGC--- 306
QY 47 SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe 63
Db 307 -----AAGTTCAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTCTCTCGGAGC 357
QY 64 TyrArgProGluGlyClyLysAspPheLeu-----lleTyrGluTyrArgAsnGlyHisGln 82
Db 358 TTCCAGCCAGAGGGGGCCGACACTACTGTGTGCTGTTTTCACACTACTCCCAAGGGCAAGTG 417
QY 83 GluValGluSer-----ProPheGlnGlyArgLeuGlnTyrAsnGlySerLysAspLeu 100
Db 418 TACCTTGGGAATATCCACCATTTAAAGACAGAAATCAGCTGGGCTGGAGACCTTGACACAG 477
QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db -----AAGTTCAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTCTCTCGGAGC 357
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Db 478 AAGATGTCATCATCAATACATAGAAAATATGAGTTTATACAAATGGCCATATATCTGT 537
QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 538 GATGTCAAAAAC----- 549
QY 141 lleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu--- 159
Db 550 ---CCTCCTGACATCGTTGTCAGCTGCACACATTAGGCTCTATGTCGTGTAAGAAAGAG 606
QY 160 -----lleMetMetTyrIleLeuLeuValPheLeuThr 170
Db 607 AATTGTCCTGTGTTCCAGTTGGGTAGTGGGCATAGTTACTGCTGTGCTCCTAGGT 666
QY 171 LeuTrpLeuLeuIleLeuMetIleTyrCys-----TyrArgLys----- 183
Db 667 CTCACCTGCTCATCAGCATGATTCTGGCTGTGCTCTATAGAGGAAACTCTTAACGG 726
QY 184 -----ValSerLysAlaGluGluAlaAlaGlnGlu 193
Db 727 GATTACACTGGCTGCAGTACATCAGAGAGTTTGTCCACAGTTAAGCAGGCTCTCGGAAG 786
QY 194 AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer 209
Db 787 TCCCTCCGACACTGAGGCTCTTGTAAAGAGTGTGCTTCTGGATCTCACCAGGGGCCA 846
QY 210 AlaVal 211
Db 847 GTCATA 852

RESULT 10
US-09-430-503-7
; Sequence 7, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1151)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (133)..(939)
US-09-430-503-7

Alignment Scores:
Pred. No.: 1.85e-07 Length: 1151
Score: 131.00 Matches: 51
Percent Similarity: 37.39% Conservative: 32
Best Local Similarity: 22.97% Mismatches: 81
Query Match: 11.65% Indels: 58
DB: 3 Gaps: 9

US-09-977-579-2 (1-215) x US-09-430-503-7 (1-1151)
QY 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 250 GTATATACGCCAAAAGAAATCTTCGTGGCAAAATGGTACACAAGGGAAGCTGACCTGC--- 306
QY 47 SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe 63
Db 307 -----AAGTTCAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTCTCTCGGAGC 357
```

Qy	64	Tyr	Arg	Pro	Glu	Gly	Gly	Lys	Asp	Phe	Leu	---	Ile	Tyr	Glu	Tyr	Arg	Asn	Gly	His	Gln	82
Db	358	TT	CAG	CC	CAG	AGG	GGG	GGC	CC	CA	CT	ACT	GT	GT	CG	T	T	T	T	T	T	417
Qy	83	Glu	Val	Glu	Ser	---	Pro	Phe	Gln	Arg	Leu	Gln	Trp	Asn	Gly	Ser	Lys	Asp	Leu	100		
Db	418	TAC	CTT	TGG	GA	ATT	TCC	ACC	ATT	AA	GAC	AGA	ATC	AGC	TGG	CGT	GG	AGC	CTT	TGC	AA	477
Qy	101	Gln	Asp	Val	Ser	Ile	Thr	Val	Leu	Asn	Val	Thr	Leu	Asn	Asp	Ser	Gly	Leu	Tyr	120		
Db	478	AA	GAT	GCA	TCA	ATCA	ACAT	AGAAA	TAT	GCA	GT	TAT	TAT	ACA	ATG	GC	CA	CT	TAT	ATC	GT	537
Qy	121	Asn	Val	Ser	Arg	Lys	Phe	Glu	Ala	His	Arg	Pro	Phe	Val	Lys	Thr	Thr	Arg	Leu	140		
Db	538	GAT	GTCA	AAAA	AC	-----															549	
Qy	141	Ile	Pro	Leu	Arg	Val	Thr	Glu	Clu	Ala	Gly	Glu	Asp	Phe	Thr	Ser	Val	Ser	Glu	---	159	
Db	550	--	CCT	CTG	ACAT	CGT	TGT	CTC	AGC	CTG	GC	AC	AT	TAG	GC	TCT	AT	TGT	CGT	AGAAA	AG	606
Qy	160	---	Ile	Met	Met	Tyr	Ile	Leu	Leu	Val	Phe	Leu	Thr	170								
Db	607	AAT	TTC	CTG	TGT	TCC	AGT	TTC	GGT	TGG	TGG	CGC	AT	AGT	TAC	TCT	GTG	TCT	CT	AGT	666	
Qy	171	Leu	Trp	Leu	Leu	Ile	Glu	Met	Ile	Tyr	Cys	---	Tyr	Arg	Lys	---					183	
Db	667	CTC	ACT	TCT	GTCT	CAT	CAG	CAT	GAT	TCT	GGCT	GTCT	CT	TAT	AGA	AGG	AAAA	AACT	CT	AAAA	CG	726
Qy	184	---	Val	Ser	Lys	Ala	Glu	Glu	Ala	Ala	Gln	Glu	193									

```

RESULT 11
US-09-430-503-43
; Sequence 43, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(597)
US-09-430-503-43

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Alignment Scores:		
Pred. No.:	1.23e-07	Length:
Score:	129.00	Matches:
Percent Similarity:	37.57%	Conservative:
Best Local Similarity:	25.97%	Mismatches:
Query Match:	11.48%	Indels:
DB:	3	Gaps:
		7
		600

US-09-977-579-2 (1-215) x US-09-430-503-43 (1-600)

QY 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46

	118	GTATATACGCCAAAGAAATCTTCGTGGCAATGGTACACAAGGAGAGCTGACCTGC---	174
Db			
	47	SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe	63
Qy			
	175	-----AGTTCAAGTCTACTAGTACAGCTGGCGGGTGGACCTCAGTCTCTCTGGAGC	225
Db			
	64	TyrArgProGluGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln	82
Qy			
	226	TTCCAGCCAGAGGGGCGGCACACTACTGTGTCGTTTTTCCACTACTCCCAAGGCAAGTG	288
Db			
	83	GluValGluSer-----ProPheGlnIleValGluClnTrpAsnGlySerLysAspLeu	100
Qy			
	286	TACATTGGGAATATTCACCATTTTAAAGACAGAATCAGCTGGCGTGAGACCTTGACAA	345
Db			
	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys	120
Qy			
	346	AAAGATCATCATCAATCAGATAGAAAATATGCAGTGTATACACAATGSCACCTATATCTGT	405
Db			
	121	AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu	140
Qy			
	406	GATGTCAAAAAC-----	417
Db			
	141	IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu---	159
Qy			
	418	---CCTCTGCATCGTTGTCCAGCTGGACACATTAGGCTCTATGCTGTAGAAAAGAG	474
Db			
	160	-----IleMetMetTyrIleLeuLeuValPheLeuThr	170
Qy			
	475	AAATTGCTGTTGTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTGCTGTGGTCCTAGGT	534
Db			
	171	LeuTrpLeuLeuIleGluMetIleTyrCysTyr-----ArgLysValSerLysAla	187
Qy			
	535	CTCACTCTGCTCATCAGCATGATCTGGCTGCTCTATATAGAGGAAAAAAGCTTAAACGG	594
Db			
	188	Glu	188
Qy			
	595	GAT	597
Db			

RESULT 12

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US-09-430-503-47
; Sequence 47, Application US/09430503
; Patent No. 635786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOMERIZED
; TITLE OF INVENTION: THERAPEUTIC AND ISOMERIZED
; FILE REFERENCE: Attorney Docket No. 09-09-0000
; CURRENT APPLICATION NUMBER: US/09/430-503-47
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(597)
US-09-430-503-47

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Alignment Scores:	
Pred. No.:	1,23e-07
Score:	129.00
Percent Similarity:	37.5%
Best Local Similarity:	25.97%
Query Match:	11.48%
DB:	3
Length:	600
Matches:	47
Conservative:	21
Mismatches:	73
Indels:	40
Gaps:	7

US-09-977-579-2 (1-215) x US-09-430-503-47 (1-600)

Qy 27 vaGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46

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Db 118 GTATATACGCCAAAGAAATCTTCGTGGCAATGGTACACAAGGGAGCTGACCTGC--- 174
QY 47 SerCysMetLysArgGluValGluAlaThr-----ThrValValGluTrpPhe 63
Db 175 -----AAGTTCAAGTCTACTAGTACGACTGGGGGTTGACCTCAGCTCCTCGGAGC 225
QY 64 TyrArgProGluGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln 82
Db 226 TTTCCAGCCAGAGGGGGCCGACACTACTGTGTGCTGTTTTTCCACTACTCCCAAGGGCAAGTG 285
QY 83 GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 286 TACATTGGGAATATATCCACCAATTTAAAGACAGATCAGCTGGCTGGAGACCTTGACAAG 345
QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 346 AAAGATGCATCAATCAACATAGAAAATATGCAAGTTTATACAAATGGCACCTATATCTGT 405
QY 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 406 GATGTCAAAAAC----- 417
QY 141 IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValValSerGlu--- 159
Db 418 ---CCTCTGACATCGTTGCCAGCTGGACACATTAGGATCTATGTCGTAGAAAAAGAG 474
QY 160 -----IleMetMetTyrIleLeuLeuValPheLeuThr 170
Db 475 AATTTGCCCTGTGTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTGTGCTGCTTAGGT 534
QY 171 LeuTrpLeuLeuIleGluMetIleTyrCysTyr-----ArgLysValSerLysAla 187
Db 535 CTCACCTCTGCATCAGCATGATTCCTGCTGCTCTATAGAGGAAAAAACTCTAAACGG 594
QY 188 Glu 188
Db 595 GAT 597

RESULT 13
US-09-430-503-41
; Sequence 41, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(597)
US-09-430-503-41

Alignment Scores:
Pred. No.: 2,29e-07 Length: 600
Score: 127.00 Matches: 47
Percent Similarity: 37.57% Conservatives: 21
Best Local Similarity: 25.97% Mismatches: 73
Query Match: 11.30% Indels: 40
DB: 3 Gaps: 7

US-09-977-579-2 (1-215) x US-09-430-503-41 (1-600)
QY 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 118 GTATATACGCCAAAGAAATCTTCGTGGCAATGGTACACAAGGGAGCTGACCTGC--- 174
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QY 47 SerCysMetLysArgGluValGluAlaThr-----ThrValValGluTrpPhe 63
Db 175 -----AAGTTCAAGTCTACTAGTACGACTGGGGGTTGACCTCAGCTCCTCGGAGC 225
QY 64 TyrArgProGluGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln 82
Db 226 TTTCCAGCCAGAGGGGGCCGACACTACTGTGTGCTGTTTTTCCACTACTCCCAAGGGCAAGTG 285
QY 83 GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 286 TACCTTGGGAATATATCCACCAATTTAAAGACAGATCAGCTGGCTGGAGACCTTGACAAG 345
QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 346 AAAGATGCATCAATCAACATAGAAAATATGCAAGTTTATACAAATGGCACCTATATCTGT 405
QY 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 406 GATGTCAAAAAC----- 417
QY 141 IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValValSerGlu--- 159
Db 418 ---CCTCTGACATCGTTGCCAGCTGGACACATTAGGCTCTATGTCGTAGAAAAAGAG 474
QY 160 -----IleMetMetTyrIleLeuLeuValPheLeuThr 170
Db 475 AATTTGCCCTGTGTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTGTGCTGCTTAGGT 534
QY 171 LeuTrpLeuLeuIleGluMetIleTyrCysTyr-----ArgLysValSerLysAla 187
Db 535 CTCACCTCTGCATCAGCATGATTCCTGCTGCTCTATAGAGGAAAAAACTCTAAACGG 594
QY 188 Glu 188
Db 595 GAT 597

RESULT 14
US-09-430-503-45
; Sequence 45, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(597)
US-09-430-503-45

Alignment Scores:
Pred. No.: 2,29e-07 Length: 600
Score: 127.00 Matches: 47
Percent Similarity: 37.57% Conservatives: 21
Best Local Similarity: 25.97% Mismatches: 73
Query Match: 11.30% Indels: 40
DB: 3 Gaps: 7

US-09-977-579-2 (1-215) x US-09-430-503-45 (1-600)
QY 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 118 GTATATACGCCAAAGAAATCTTCGTGGCAATGGTACACAAGGGAGCTGACCTGC--- 174
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Qy 47 SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe 63
Db 175 -----AAGTTCAAGTCTACTAGTACGACTGGCGGTTGACCTCAGTCTCTCTGGAGC 225
Qy 64 TyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln 82
Db 226 TCCAGCCAGAGGGGGCCGACACTACTGTGTGCGTTTTTCCACTACTCCCAAGGGCAAGTG 285
Qy 83 GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 286 TACCTGGGAATATATCCACATTTAAAGACAGAAATCAGCTGGGCTGGAGACCTTGACAAG 345
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 346 AAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACAAATGCGCACCTATATCTGT 405
Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 406 GATGTCAAAAAC----- 417
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu--- 159
Db 418 ---CCTCCTGACATCGTTGTCAGCCTGGACACATTAGGATCTATGTCGTAGAAAAGAG 474
Qy 160 -----IleMetMetTyrIleLeuLeuValPheLeuThr 170
Db 475 AATTGCTGCTGTTTCCAGTTTGGGTAGTGGTGGCATAGTACTGCTGTGGTCTTAGGT 534
Qy 171 LeuTrpLeuLeuIleGluMetIleTyrCysTyr-----ArgLysValSerLysAla 187
Db 535 CTCACCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAGGAAAAAACTCTAAACGG 594
Qy 188 Glu 188
Db 595 GAT 597

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RESULT 15

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US-09-430-503-17
; Sequence 17, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(627)
US-09-430-503-17

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Alignment Scores:

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Pred. No.: 3.28e-07 Length: 752
Score: 127.00 Matches: 47
Percent Similarity: 37.57% Conservative: 21
Best Local Similarity: 25.97% Mismatches: 73
Query Match: 11.30% Indels: 40
DB: 3 Gaps: 7

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US-09-977-579-2 (1-215) x US-09-430-503-17 (1-752)

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Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 118 GTATATACGCCAAAGAAATCTTCGTGGCAATGTTACACAGGGAAAGCTGACCTGC--- 174
Qy 47 SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe 63

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Search completed: April 7, 2005, 17:12:30
Job time : 172 secs

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Db 175 -----AAGTTCAAGTCTACTAGTACGACTGGCGGTTGACCTCAGTCTCTCTGGAGC 225
Qy 64 TyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln 82
Db 226 TCCAGCCAGAGGGGGCCGACACTACTGTGTGCGTTTTTCCACTACTCCCAAGGGCAAGTG 285
Qy 83 GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 286 TACCTGGGAATATATCCACATTTAAAGACAGAAATCAGCTGGGCTGGAGACCTTGACAAG 345
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 346 AAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACAAATGCGCACCTATATCTGT 405
Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 406 GATGTCAAAAAC----- 417
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu--- 159
Db 418 ---CCTCCTGACATCGTTGTCAGCCTGGACACATTAGGCTCTATGTCGTAGAAAAGAG 474
Qy 160 -----IleMetMetTyrIleLeuLeuValPheLeuThr 170
Db 475 AATTGCTGCTGTTTCCAGTTTGGGTAGTGGTGGCATAGTACTGCTGTGGTCTTAGGT 534
Qy 171 LeuTrpLeuLeuIleGluMetIleTyrCysTyr-----ArgLysValSerLysAla 187
Db 535 CTCACCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAGGAAAAAACTCTAAACGG 594
Qy 188 Glu 188
Db 595 GAT 597

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: April. 7, 2005, 15:19:45 ; Search time 502 Seconds
(without alignments)
2595.420 Million cell updates/sec

Title: US-09-977-579-2
Perfect score: 1124
Sequence: 1 MPANRLPLASLVIYWS.....SDYLAIPSENKENSAPVVEE 215

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09977579 @CGN 1 1 723 @runat 06042005 163458 23652
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- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
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- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1105	98.3	2220	11	US-09-977-579-3
4	1105	98.3	2632	13	US-10-029-191-22
5	1105	98.3	3108	13	US-10-029-191-1
6	477	42.4	657	13	US-10-029-191-23
7	473	42.1	1335	18	US-10-723-860-2247
8	473	42.1	1414	18	US-10-477-272-1
9	472	42.0	1490	9	US-09-917-800A-1654
10	260.5	23.2	974	17	US-10-401-916-13
11	258.5	23.0	807	17	US-10-401-916-12
12	234	20.8	407	17	US-10-276-774-718
13	167	14.9	1029	17	US-10-205-331-111
14	165.5	14.7	3583	18	US-10-723-860-6471
15	163.5	14.5	1929	10	US-09-960-706-472
16	160.5	14.3	970	19	US-10-874-706-84
17	160.5	14.3	983	13	US-10-053-107-11
18	160.5	14.3	983	14	US-10-227-884-237
19	160.5	14.3	983	14	US-10-230-163-237
20	160.5	14.3	983	14	US-10-230-338-237
21	160.5	14.3	983	14	US-10-218-631-237
22	160.5	14.3	983	14	US-10-230-414-237
23	160.5	14.3	983	14	US-10-213-145-11
24	160.5	14.3	983	14	US-10-232-224-237
25	160.5	14.3	983	14	US-10-216-159A-237
26	160.5	14.3	983	14	US-10-218-849-237
27	160.5	14.3	983	14	US-10-227-873-237
28	160.5	14.3	983	14	US-10-227-883-237
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30	160.5	14.3	983	14	US-10-230-434-237
31	160.5	14.3	983	14	US-10-213-199-11
32	160.5	14.3	983	14	US-10-219-003-237
33	160.5	14.3	983	14	US-10-219-075-237
34	160.5	14.3	983	14	US-10-219-464-237
35	160.5	14.3	983	14	US-10-219-466-237
36	160.5	14.3	983	14	US-10-219-479-237
37	160.5	14.3	983	14	US-10-219-481-237
38	160.5	14.3	983	14	US-10-230-260-237
39	160.5	14.3	983	14	US-10-232-231-237
40	160.5	14.3	983	14	US-10-232-233-237
41	160.5	14.3	983	14	US-10-216-165-237
42	160.5	14.3	983	14	US-10-218-956-237
43	160.5	14.3	983	14	US-10-219-468-237
44	160.5	14.3	983	14	US-10-219-478-237
45	160.5	14.3	983	14	US-10-219-536-237

ALIGNMENTS

RESULT 1

US-09-977-579-4
; Sequence 4, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated so
; TITLE OF INVENTION: channel
; FILE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977,579
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1261

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-977-579-4

Alignment Scores:
Pred. No.: 2,02e-143 Length: 1261
Score: 1124.00 Matches: 215
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-977-579-2 (1-215) x US-09-977-579-4 (1-1261)

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QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
DB 376 ATGCCTGCTCAATAGATTGTTCCCTGGCTTCTCTCGTCTTATCTAGTGGTCACT 435

QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
DB 436 GTCTGCTCCCTGTGTGTGGAGTGCCTCGAGACGGAGCGCGTGCAGGGCAACCCC 495

QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
DB 496 ATGAAGCTGGCTGCATCTCTGTCATGAAGAGAGAGAGGTGGAGGCCACCCAGGTGGT 555

QY 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
DB 556 GAATGTTCTCAGAGCCCGAGGCGGTAAGATTTCCTTATTACGAGTATCGGAATGCG 615

QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
DB 616 CACCAGGAGGTGGAGAGCCCTTTCAGGGCGCCTGCAGTGAATGGCAGACGACCTG 675

QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
DB 676 CAGGAGCTGTCATCTGTCTCACTGTCATCTGAGAGCATCTGGCCCTCTACACCTGC 735

QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
DB 736 AATGTGTCGGGAGTTTGAGTTGAGGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 795

QY 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
DB 796 ATCCCCCTAAGAGTCAACGAGGAGGTGGAGAGGACTTCACTCTGTGTGCTCAGAAATC 855

QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
DB 856 ATGATGTATACCTTCTGTCTTCTCTCACCTGTGGCTGCTCATCGAGATGATATATTGC 915

QY 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
DB 916 TACAGAAAGGTCTCAAAAGCCGAAGAGGAGCCCAAGAAACCGCTCTGACTACCTTGGC 975

QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
DB 976 ATCCCATCTGAGAACAAAGGAGAACTCTGCGTACCGAGTGGAGAA 1020
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RESULT 2

US-10-029-191-21
; Sequence 21, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, Rory A. J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14

; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-21

Alignment Scores:

Pred. No.: 2,91e-141 Length: 645
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservative: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 13 Gaps: 0

US-09-977-579-2 (1-215) x US-10-029-191-21 (1-645)

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DB 1 ATGCCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTCTCATCTACTTGGGTGAGA 60

QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
DB 61 GTCTGCTCCCTGTGTGTGGAGTGCCTCGAGACAGAGCGGTGCAGGGCAATCCC 120

QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
DB 121 ATGAAGCTGAGTGCATCTCTGTCATGAAGAGGAGGAGGTGGAGGCCACCTCTGTGTG 180

QY 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
DB 181 GAGTGGTGTCTACAGGCTGAGGCGGTAAAGATTTCCTTATATATAGATATCGGAATGCG 240

QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
DB 241 CACCAGGAGGTGGAGAGCCCTTTCAGGCCCTGTCAGTGAATGGGAGCAAGACCTG 300

QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
DB 301 CAGGAGCTATCATCTGCTACTCAATGTCACTTGAATGACTCTGGCCCTCTACACATGC 360

QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
DB 361 AATGTGTCCAGGAGTTCGAATTCAGGCACACAGGCCCTTTGTGAAGACCAAGAGACTG 420

QY 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
DB 421 ATACCTTTGGAGTCACTGAAGAGCGGGAGAGACTTCACCTCGTGTGCTCGGAAATC 480

QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
DB 481 ATGATGTATACCTCTCTGTCTTCTCTCACCTGTGGCTGTTTATTGAGATGATCATTTGC 540

QY 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
DB 541 TACAGAAAGGTCTCAAGGCCGAAGAGGAGCAGCAGGAAATGCGTCTGACTACCTTGTCT 600

QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
DB 601 ATCCCTTCAGAGAACAGAGGAGAACTCTGTGTACCTGTGGAGGAA 645
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RESULT 3

US-09-977-579-3
; Sequence 3, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodi
; TITLE OF INVENTION: channel
; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses th
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977,579

; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: rat
US-09-977-579-3

Alignment Scores:
Pred. No.: 1.98e-140 Length: 2220
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservative: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 11 Gaps: 0

US-09-977-579-2 (1-215) x US-09-977-579-3 (1-2220)

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QY	21	ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro	40
DB	423	GTCTGCTTCCCTGTGTGTGGAGTGCCTTCGGAGACAGAGCGGTGCGGCAATCCC	482
QY	41	MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrValVal	60
DB	483	ATGAAGCTGAGGTGCATCTCTGCATGAAGAGGAGGAGGTGGAGCCACCATCTGTGTG	542
QY	61	GluTrpPheTyrArgProGluGlyGlyAspPheLeuIleTyrGluTyrArgAsnGly	80
DB	543	GAGTGTGTTCTACAGGCTGAGGCGGTAAAGATTTCCTATATAGTATCGGAATGGC	602
QY	81	HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu	100
DB	603	CACAGGAAGTGGAGAGCCCTTCCAAAGGCCGTCTGCAGTGGAAATGGGAGCAAGACCTG	662
QY	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys	120
DB	663	CAGACGTATCCATCACTGACTCAATGTCAATTTGAATGACTCTGGCCTCTACACATGC	722
QY	121	AsnValSerArgGluPheGluAlaHisArgProPheValIleThrArgLeu	140
DB	723	AATGTGTCCAGGAGTTCGAATTCGAGGCACACAGGCTTTTGTGAAGACCACGAGACTG	782
QY	141	IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle	160
DB	783	ATACCTTTGGAGTCACTGAAGAGCGGGAGAGACTTCACCTCCGCTGGGTCTCGGAATC	842
QY	161	MetMetTyrIleLeuLeuValPheLeuThrLeuTyrLeuIleGluMetIleTyrCys	180
DB	843	ATGATGTACATCTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	902
QY	181	TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla	200
DB	903	TACAGAAAGGTCTCTAAGCCGGAAGAGGAGCAGCAAGAAATGCGTCTGACTACCTTGCT	962
QY	201	IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu	215
DB	963	ATCCCTTTCAGAGAACAGGAGAACTCTGTGTGTACCTCTGTGAGGAA	1007

RESULT 4

US-10-029-191-22

; Sequence 22, Application US/10029191

; Publication No. US20020160453A1

; GENERAL INFORMATION:

; APPLICANT: CURTIS, RORY A.J.

; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2632
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-22

Alignment Scores:
Pred. No.: 2.57e-140 Length: 2632
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservative: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 13 Gaps: 0

US-09-977-579-2 (1-215) x US-10-029-191-22 (1-2632)

QY	1	MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer	20
DB	78	ATGCTGCTCCCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGTCTCATCTACTGGGTGAGA	137
QY	21	ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro	40
DB	138	GTCTGCTTCCCTGTGTGTGGAGTGCCTTCGGAGACAGAGCGGTGCGGCAATCCC	197
QY	41	MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrValVal	60
DB	198	ATGAAGCTGAGGTGCATCTCTGCATGAAGAGGAGGAGGTGGAGCCACCATCTGTGTG	257
QY	61	GluTrpPheTyrArgProGluGlyGlyAspPheLeuIleTyrGluTyrArgAsnGly	80
DB	258	GAGTGTGTTCTACAGGCTGAGGCGGTAAAGATTTCCTATATAGTATCGGAATGGC	317
QY	81	HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu	100
DB	318	CACAGGAAGTGGAGAGCCCTTCCAAAGGCCGTCTGCAGTGGAAATGGGAGCAAGACCTG	377
QY	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys	120
DB	378	CAGACGTATCCATCACTGACTCAATGTCAATTTGAATGACTCTGGCCTCTACACATGC	437
QY	121	AsnValSerArgGluPheGluAlaHisArgProPheValIleThrArgLeu	140
DB	438	AATGTGTCCAGGAGTTCGAATTCGAGGCACACAGGCTTTTGTGAAGACCACGAGACTG	497
QY	141	IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle	160
DB	498	ATACCTTTGGAGTCACTGAAGAGCGGGAGAGACTTCACCTCCGCTGGGTCTCGGAATC	557
QY	161	MetMetTyrIleLeuLeuValPheLeuThrLeuTyrLeuIleGluMetIleTyrCys	180
DB	558	ATGATGTACATCTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	617
QY	181	TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla	200
DB	618	TACAGAAAGGTCTCTAAGCCGGAAGAGGAGCAGCAAGAAATGCGTCTGACTACCTTGCT	677
QY	201	IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu	215
DB	678	ATCCCTTTCAGAGAACAGGAGAACTCTGTGTGTACCTCTGTGAGGAA	722

RESULT 5

US-10-029-191-1

```

1  Sequence 1, Application US/10029191
2  Publication No. US20020160453A1
3  GENERAL INFORMATION:
4
5  APPLICANT: CURTIS, ROY A.J.
6
7  TITLE OF INVENTION: NOVEL GENE ENCODED BY THE
8  TITLE OF INVENTION: NOVEL GENE ENCODED BY THE
9  TITLE OF INVENTION: NOVEL GENE ENCODED BY THE
10  FILE REFERENCE: 210147.00XX/SU1
11  CURRENT APPLICATION NUMBER: US/10/12-20
12  CURRENT FILING DATE: 2001-12-20
13  PRIOR APPLICATION NUMBER: 09/569,912
14  PRIOR FILING DATE: 2000-05-12
15  PRIOR APPLICATION NUMBER: US 60/133
16  PRIOR FILING DATE: 1999-05-14
17  NUMBER OF SEQ ID NOS: 23
18  SOFTWARE: PatentIn Ver. 2.1
19  SEQ ID NO 1
20  LENGTH: 3108
21  TYPE: DNA
22  ORGANISM: Rattus sp.
23  US-10-029-191-1

```

Alignment Scores:	
Pred. No.:	3,328-140
Score:	1105.00
Percent Similarity:	99.14%
Best Local Similarity:	99.14%
Query Match:	98.31%
DB:	13
Length:	3108
Matches:	211
Conservative:	0
Mismatches:	4
Indels:	0
Gaps:	0

US-09-977-579-2 (1-215) x US-10-029-191-1 (1-3108)

Qy	1	MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrThrValSer	20
Db	78	ATGCGCTCGCCTTCAACAGAAATGCTTCCCTACGCTTCTAGTGTCTACATCTGGGTGACA	137
Qy	21	ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro	40
Db	138	GTCTGCTTCCCTGTGTGTGTGGAGTGGCCCTCGAGACAGAGCGGTGACGGCAATCCC	197
Qy	41	MetLysLeuArgCysIleSerCysMetLysbArgGluGluValGluAlaThrThrValVal	60
Db	198	ATGAAGACTGAGGTGATCTCTCGCATGAAGAGGAGGAGGTGGAGGCCACCACTGTGGTG	257
Qy	61	GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly	80
Db	258	GAGTGGTCTACAGAGCCTGAGGCGGTAAAGATTTCCTATATATGATATCGGAATGGC	317
Qy	81	HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu	100
Db	318	CACCAAGAGTGGAGAGCCCTTCCAAGGCCGCTCGCAGGTGGAATGGAGCAAGAAGACCTG	377
Qy	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys	120
Db	378	CAGGACGTATCCATCAGTGTACTCAATGTCACTTTGATGACTCTGGCCCTTACACATGC	437
Qy	121	AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu	140
Db	438	AATGTGTCCAGGCGATTCCGAATTCGAGGCACACAGGCGCTTTGTGAAGACACACGAGACTG	497
Qy	141	IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValSerValSerGluIle	160
Db	498	ATACCTTTGCGAGTCACTGAAGAGCGGGAGAAGACTTCACCTCCGCGGTCTCGGAATC	557
Qy	161	MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys	180
Db	558	ATGATGTACATCCTCCTGGTCTTCCTCACCTTGTGGCTGTATTATGAGATGATATATTGC	617
Qy	181	TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla	200
Db	618	TACAGAAGGTCTTAAGGCCGAGAGGACGACAGGAAATGGCTCTGACTACCTTGCT	677
Qy	201	IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu	215

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Db      678  ATCCCTTCAGACAACAGAGAACTCTGTGTGTACCTGTGGAGGAA  722
      RESULT 6
      US-10-029-191-23
      ; Sequence 23, Application US/10029191
      ; Publication No. US20020160453A1
      ; GENERAL INFORMATION:
      ; APPLICANT: CURTIS, RORY A.J.
      ; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA
      ; TITLE OF INVENTION: PROTEIN
      ; FILE REFERENCE: 210147.00XX/5U1
      ; CURRENT APPLICATION NUMBER: US/10/029,191
      ; CURRENT FILING DATE: 2001-12-20
      ; PRIOR APPLICATION NUMBER: 09/569,978
      ; PRIOR FILING DATE: 2000-05-12
      ; PRIOR APPLICATION NUMBER: US 60/134,198
      ; PRIOR FILING DATE: 1999-05-14
      ; NUMBER OF SEQ ID NOS: 23
      ; SOFTWARE: PatentIn Ver. 2.1
      ; SEQ ID NO 23
      ; LENGTH: 657
      ; TYPE: DNA
      ; ORGANISM: Lepus Sp.
      US-10-029-191-23

```

Alignment Scores:		
Pred. No.:	5,438-55	Length:
Score:	477.00	Matches:
Percent Similarity:	64.49%	Conservative:
Best Local Similarity:	49.53%	Mismatches:
Query Match:	42.44%	Indels:
DB:	13	Gaps:
		5
		5

US-09-977-579-2 (1-215) x US-10-029-191-23 (1-657)

Qy	2	LeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCysValGluVal	23
Db	13	CTGGCTTCGTGGTCCGGCCCGCGCTGGTTCCTCGGCCCTGGGGGGCTCGTGGAGGTG	72
Qy	30	ProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIleSerCysMet	49
Db	73	GACTCGGAGACCGACCGTGTACGGGATGACCTTCAAAATTCGTGCATCTCTCTCAAG	132
Qy	50	LysArgGluGluValGluAlaThrThrValValGluTrpPheTyrArgProGluGlyGly	69
Db	133	CGCCGACGACGACCAACCGCCGACACTTACCGAGTGGACCTTCCGCCAAGAGGGCACT	192
Qy	70	LysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGlnGluValGluSerPro---	87
Db	193	GAGGAGTTTCGTACAGATCTCGGCTATGAGAAACAGAGGTGTCAGCTGGAGGAAGACGAG	252
Qy	88	---PheGlnGlyArgLeuGlnTrpAsnGlySer-----LysAspLeuGlnAspVal	103
Db	253	CGCTTTGAGGGCCGGCTGTGGAAACGGCAGCCGGGGCACCAAGGACCTGCAGGACCTG	312
Qy	104	SerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSer	123
Db	313	TCCATCTTCATCACCAAATGTCACTTACAACCACTCGGGCGACTACCAAGTCCCATGTCTAC	372
Qy	124	ArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeuIleProLeu	143
Db	373	CGCGCTGCTCTCTTCGAAAATACGACGACAAACACCGAGCTCGTCAAGAGATCCACCTG	432
Qy	144	ArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIleMetMetTyr	163
Db	433	GAGGTGGTGGACAGCCAAACAGAGACATGGCATCCATCTGTGTCGGAGATCATGATGTAC	492
Qy	164	IleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCysTyrArgLys	183
Db	493	GTGCTCATCTGGTGTGAACATCTGGCTCTGTGGCGGAGATGGTGTACTGCTACAGAG	552
Qy	184	ValSerLysAla---GluGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAlaIlePro	202

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Db 553 ATCGCGCGCCACGAGGAGCGCGCGAGAGAACGCTCGGAATATTGGCCATCAC 612
Qy 203 SerGluAsnLysGluAsn---SerAlaValProValGluGlu 215
Db 613 TCAGAAAGCAAGAAATTCACGGCGCTCAGGTGGCTGAA 654

RESULT 7
US-10-723-860-2247
; Sequence 2247, Application US/10723860
; Publication No. US2004025360A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2247
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2247

Alignment Scores:
Pred. No.: 5,77e-54 Length: 1335
Score: 473.00 Matches: 109
Percent Similarity: 63.35% Conservative: 31
Best Local Similarity: 49.32% Mismatches: 71
Query Match: 42.08% Indels: 10
DB: 18 Gaps: 6

US-09-977-579-2 (1-215) x US-10-723-860-2247 (1-1335)
Qy 3 AlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuLeuTyrTrpValSerValCys 22
Db 22 GCCATGGGGAGGCTG-----CTGGCTTAGTGTGGCGCGGCGACTGGTGCTCTACGCC 75
Qy 23 PheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLys 42
Db 76 TCGGGGGCTCGGTGGAGGTGGACTCGAGACCGGCGCGCTGTATGGGATGACCTTCAA 135
Qy 43 LeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValGluTrp 62
Db 136 ATTCCTTGCATCTCTCGAAGCGCGCGAGACCAACGCTGAGACCTTTCACCGAGTGG 135
Qy 63 PheTyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHis 81
Db 196 ACCTTCGCCAGAGGCGACTGAGAGTGTTCAGATCTCGCGCTATGAGATGAGGTG 255
Qy 82 GlnGluValGluSerPro-----PheGlnGlyArgLeuGlnTrpAsnGlySer----- 97
Db 256 TTGCAGCTGGAGGAGGATGAGCGCTTCAGGGCGCGGTGGTGGTGAATGCGACCGGGGC 315
Qy 98 ---LysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db 316 ACCAAAGACCTCGCAGGATCTGTCTATCTCATCAACCAATGTCACCTACCAACCACTCGGC 375
Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluPheGluAlaHisArgProPheValLys 136
Db 376 GACTACGAGTGCCACGTCTACCGCTCTCTTCGAAAACCTACGAGCACAACACGAGC 435
Qy 137 ThrThrArgLeuLeuProLeuArgValThrGluAlaGlyGluAspPheThrSerVal 156
Db 436 GTCGTCAGAGAGATCCACATTGAGTAGTGACAAAGCCAAACAGAGACATGGCATCCATC 495
Qy 157 ValSerGluLeuMetMetTyrIleLeuLeuValPheLeuLeuThrLeuTrpLeuLeuGlu 176
Db 157 ValSerGluLeuMetMetTyrIleLeuLeuValPheLeuLeuThrLeuTrpLeuLeuGlu 176
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Db 496 GTGCTCTGAGATCATGTATGTATGTCTATTGTGTGTGTGACCATATGGCTGTGGCAGAG 555
Qy 177 MetIleTyrCysTyrArgLysValSerLysAla---GluGluAlaAlaGlnGluAsnAla 195
Db 556 ATGATTATTACTGTACTAAGAAGATCGCTGCGCGCGCACGAGACTGCTGCACAGAGAAATGCC 615
Qy 196 SerAspTyrLeuAlaIleProSerGluAsnLysGluAsn---SerAlaValProValGlu 214
Db 616 TCGGAATACCTGGCCATCACCCTCTGAAGACCAAGAGAACTGCACGGCGCTCCAGGTGCC 675
Qy 215 Glu 215
Db 676 GAA 678

RESULT 8
US-10-477-272-1
; Sequence 1, Application US/10477272
; Publication No. US20040191791A1
; GENERAL INFORMATION:
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: P12
; FILE REFERENCE: SCN1B (R85C)
; CURRENT APPLICATION NUMBER: US/10/477,272
; CURRENT FILING DATE: 2003-11-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-272-1

Alignment Scores:
Pred. No.: 6.3e-54 Length: 1414
Score: 473.00 Matches: 109
Percent Similarity: 63.35% Conservative: 31
Best Local Similarity: 49.32% Mismatches: 71
Query Match: 42.08% Indels: 10
DB: 18 Gaps: 6

US-09-977-579-2 (1-215) x US-10-477-272-1 (1-1414)
Qy 3 AlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuLeuTyrTrpValSerValCys 22
Db 98 GCCATGGGGAGGCTG-----CTGGCTTAGTGTGGCGCGGCGACTGGTGCTCTACGCC 151
Qy 23 PheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLys 42
Db 152 TCGGGGGCTCGCTGGAGGTGGACTCGGAGACCGGCGCGTGTATGGGATGACCTTCAA 211
Qy 43 LeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValGluTrp 62
Db 212 ATTCCTTGCATCTCTCGAAGCGCGCGAGACCAACGCTGAGACCTTTCACCGAGTGG 271
Qy 63 PheTyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHis 81
Db 272 ACCTTCGCCAGAGGCGACTGAGAGTGTTCAGATCTCGCGCTATGAGATGAGGTG 331
Qy 82 GlnGluValGluSerPro-----PheGlnGlyArgLeuGlnTrpAsnGlySer----- 97
Db 332 TTGCAGCTGGAGGAGGATGAGTGTTCGAGGGCGCGGTGGTGGTGAATGCGACCGGGGC 391
Qy 98 ---LysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db 392 ACCAAAGACCTCGCAGGATCTGTCTATCTCATCAACCAATGTCACCTACCAACCACTCGGC 451
Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluPheGluAlaHisArgProPheValLys 136
Db 452 GACTACGAGTGCCACGTCTACCGCTCTCTTCGAAAACCTACGAGCACAACACGAGC 511
Qy 137 ThrThrArgLeuLeuProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156
Db 512 GTCGTCAGAGAGATCCACATTGAGTAGTGACAAAGCCAAACAGAGACATGGCATCCATC 571
```

QY 157 ValSerGluLeuMetTyrIleLeuValPheLeuThrLeuTrpLeuLeuGlu 176
DB 572 GTGCTCAGATCATGATGATGCTCAATGCTGTTGATGCTGCTGCGCAGAG 631
QY 177 MetIleTyrCysTyrArgLysValSerLysAla---GluGluAlaGlnGluAla 195
DB 632 ATGATTACTGTACAAAGAGATCGCTGCGGCCACGAGACTGCTGCAGAGAAATGCC 691
QY 196 SerAspTyrLeuAlaIleProSerGluAenLysGluAsn---SerAlaValProValGlu 214
DB 692 TCGGAATACCTGGCCATCACTCTGAAGCAAGAGAACTGCACGGGGCTGCCAGGTGGCC 751
QY 215 Glu 215
DB 752 GAA 754

RESULT 9

US-09-917-800A-1654
; Sequence 1654, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; PRIORITY FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1654
; LENGTH: 1490
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_017288
US-09-917-800A-1654

Alignment Scores:
Pred. No.: 9,38e-54 Length: 1490
Score: 472.00 Matches: 105
Percent Similarity: 64.49% Conservative: 33
Best Local Similarity: 49.07% Mismatches: 68
Query Match: 41.99% Indels: 8
DB: 9 Gaps: 5

US-09-977-579-2 (1-215) x US-09-917-800A-1654 (1-1490)

QY 10 LeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCysValGluVal 29
DB 232 CTGGCTCTCGTGGCGGGTGTGCTGATCTCAGCGTGGGGGGCTGCGTGGAGGTG 291

QY 30 ProSerGluThrGluAlaValGlnGlyAenProMetLysLeuArgCysIleSerCysMet 49
DB 292 GATTCTGACCGAGCGAGTGTATGGATGACCTCTTAAATCCTGTGTATCTCTCTTAAG 351
QY 50 LysArgGluGluValGluAlaThrThrValValGluTyrPheTyrArgProGluGlyGly 69
DB 352 COTCTGTAGTGAGCACCGCCGAGACCTTCACGGAGTGGACCTTCGCCAGAGGGGCACA 411
QY 70 LysAspPheLeu---IleTyrGluTyrArgAenGlyHisGlnGluValGluSerPro--- 87
DB 412 GAGGAATTGTCAAGATCCTACGCTATGAGATAGGTGCTGCAGCTGGAGGAAGATGAG 471
QY 88 ---PheGlnGlyArgLeuGlnTrpAenGlySer-----LysAspLeuGlnAspVal 103
DB 472 CGCTTTGAGGGCGGTGTGGTGTGGAACGGTAGTTCGGGGGCACCAAGGACCTGCAGGACCTG 531
QY 104 SerIleThrValLeuAenValThrLeuAenAspSerGlyLeuTyrThrCysAenValSer 123
DB 532 TCCATCTTCATCACCATGTACCTACACCACTCTGGCGACTAGCATGTACGTCTTAC 591
QY 124 ArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeuIleProLeu 143
DB 592 CGTCTCTCTTCTTGTGATAATTACGAGCACACACCGCGTCTCAAGAAGATCCACCTG 651
QY 144 ArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIleMetTyr 163
DB 652 GAGGTGGTGGCAAGGCCAACAGAGATATGGCATCCATCGTGTCAAGATCATGTATG 711
QY 164 IleLeuLeuValPheLeuLeuTrpLeuLeuIleGluMetIleTyrCysTyrArgLys 183
DB 712 GTGCTCATGTGTGTAAACCATATGGCTCGTGGCGGAGATGGTGTACTGTCTACAAGAG 771
QY 184 ValSerLysAla---GluGluAlaGlnGluAenAlaSerAspTyrLeuAlaIlePro 202
DB 772 ATTGTGCTGCCAGGAGTGTGCACAAGAGATGCTCGGAATACCTCGGAATACCTGCCCATCT 831
QY 203 SerGluAenLysGluAen---SerAlaValProValGluGlu 215
DB 832 TCCGAGACCAAGAGAACTGTACAGCGCTCCAGGTGGGTGAA 873

RESULT 10

US-10-401-916-13
; Sequence 13, Application US/10401916
; Publication No. US20040002439A1
; GENERAL INFORMATION:
; APPLICANT: Qin, Ning
; APPLICANT: Codd, Ellen
; APPLICANT: D'Andrea, Michael
; TITLE OF INVENTION: DNAs encoding human betala sodium channel subunit
; FILE REFERENCE: ORT-1221
; CURRENT APPLICATION NUMBER: US/10/401,916
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/875,456A
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-401-916-13

Alignment Scores:
Pred. No.: 5,45e-25 Length: 974
Score: 260.50 Matches: 67
Percent Similarity: 56.13% Conservative: 20
Best Local Similarity: 43.23% Mismatches: 59
Query Match: 23.18% Indels: 9
DB: 17 Gaps: 5

US-09-977-579-2 (1-215) x US-10-401-916-13 (1-974)

Qy 3 AlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCys 22
Db 1 GCCATGGGGAGGCTG-----CTGGCTTAGTGTGGCGGGGCACTGCTCTCAGCC 54
Qy 23 PheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLys 42
Db 55 TGGCGGGGCTGCGTGGAGGTGGACTCGGAGACCGAGGCGGTGTATGGGATGACCTTCAAA 114
Qy 43 LeuArgCysIleSerCysMetLysArgGluValGluAlaThrValValGluTrp 62
Db 115 ATTCTTTGATCTCTCGAAGCGCGGAGGAGACCAACGCTGAGACCTTCCACGAGTGG 174
Qy 63 PheTyrArgProGluGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHis 81
Db 175 ACCTTCCGCCAGAGGCACTGAGAGTTTGTCAAGATCTCGCGCTATGAGATGAGGTG 234
Qy 82 GlnGluValGluSerPro-----PheGlnGlyArgLeuGlnTrpAsnGlySer----- 97
Db 235 TTGCAGCTGGAGGAGGATGAGCGCTTCGAGGGCGCGTGTGGAATGGCAGCGGGGC 294
Qy 98 ---LysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db 295 ACCAAGACCTTGCAGGATCTGTCTATCTTATCACCACCAATGTACCTACACCACTCGGGC 354
Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgProPheValLys 136
Db 355 GACTACGAGTGCCAGCTACCGCGCTGCTCTTCTCGAAGAACTACGAGCACACACCGAGC 414
Qy 137 ThrArgLeuIleProLeuArgValThrGluAlaGlyGlu 151
Db 415 GTCTCAAGAAGATCCACATTTAGGTAGTGACAAA---GGTGAG 456

RESULT 11

US-10-401-916-12
; Sequence 12, Application US/10401916
; Publication No. US20040002439A1
; GENERAL INFORMATION:
; APPLICANT: Qin, Ning
; APPLICANT: Codd, Ellen
; APPLICANT: D'Andrea, Michael
; TITLE OF INVENTION: DNAs encoding human betala sodium channel subunit
; FILE REFERENCE: ORT-1221
; CURRENT APPLICATION NUMBER: US/10/401.916
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/875,456A
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-401-916-12

Alignment Scores:

Pred. No.:	7.67e-25	Length:	807
Score:	258.50	Matches:	64
Percent Similarity:	56.76%	Conservative:	20
Best Local Similarity:	43.24%	Mismatches:	57
Query Match:	23.00%	Indels:	7
DB:	17	Gaps:	4

US-09-977-579-2 (1-215) x US-10-401-916-12 (1-807)

Qy 10 LeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCysValGluVal 29
Db 13 CTGGCTTAGTGTGGCGGCGGCACTGTGTCTCTCAGCGCGGGCTCGGTGGAGGTG 72
Qy 30 ProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIleSerCysMet 49
Db 73 GACTCGAGACCGAGGCGGTATGGATGACCTTCAAAATCTTTTCATCTCTCTGCAAG 132
Qy 50 LysArgGluValGluAlaThrThrValValGluTrpPheTyrArgProGluGlyGly 69

Db 133 CGCGCAGCGAGACCAACGCTGAGACCTTCCACGAGTGGACCTTCCGCCAGAGGGCACT 192
Qy 70 LysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGlnGluValGluSerPro--- 87
Db 193 GAGGAGTTTGTCAAGATCTCTGCGCTATGAGATGAGGTGTTCAGCTGGAGGAGGATGAG 252
Qy 88 ---PheGlnGlyArgLeuGlnTrpAsnGlySer-----LysAspLeuGlnAspVal 103
Db 253 CGCTTCGAGGCGCGGTGTGTGGAATGGACCGGGGCGACCAAGACCTTGCAGATCTG 312
Qy 104 SerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSer 123
Db 313 TCTATCTTTCATCACCACCAATGTCACTACACCACTCGGGCGGACTACGAGTGCCAGTCTAC 372
Qy 124 ArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeuIleProLeu 143
Db 373 CGCTGTCTCTTCTTCAAAACTACGAGCACACACCGCGTGTCAAGAAGATCCACATT 432
Qy 144 ArgValThrGluGluAlaGlyGlu 151
Db 433 GAGGTAGTGACAAA---GGTGAG 453

RESULT 12

US-10-276-774-718/c
; Sequence 718, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21273-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 718
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-718

Alignment Scores:

Pred. No.:	6.16e-22	Length:	407
Score:	234.00	Matches:	47
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	20.82%	Indels:	0
DB:	17	Gaps:	0

US-09-977-579-2 (1-215) x US-10-276-774-718 (1-407)

Qy 149 AlaGlyGluAspPheThrSerValSerGluIleMetMetTyrIleLeuValPhe 168
Db 230 GCTGGAGAGGACTTCACCTCTGTGGTCTCAGAATCATGATGATACCTCTCTGTCTTC 171
Qy 169 LeuThrLeuTrpLeuLeuIleGluMetIleTyrCysTyrArgLysValSerLysAlaGlu 188
Db 170 CTCACCTTGTGGTGTCTCATCGAGATGATATATTGCTACAGAAAGGTCTCAAAAGCGAA 111
Qy 189 GluAlaAlaGlnGluAsnAla 195
Db 110 GAGGACGCCCAAGAAAACGCG 90
RESULT 13
US-10-205-331-111
; Sequence 111, Application US/10205331
; Publication No. US20040058326A1
; GENERAL INFORMATION:

```
/ APPLICANT: Warner-Lambert Company
/ APPLICANT: Lee, Kevin
/ APPLICANT: Dixon, Alistair
/ APPLICANT: Brooksbank, Robert
/ APPLICANT: Pincock, Robert
/ TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
/ FILE REFERENCE: WL-A-018199
/ CURRENT APPLICATION NUMBER: US/10/205,331
/ CURRENT FILING DATE: 2002-07-24
/ PRIOR APPLICATION NUMBER: GB 0118354.0
/ PRIOR FILING DATE: 2001-07-27
/ NUMBER OF SEQ ID NOS: 117
/ SOFTWARE: Patent in Ver. 2.1
/ SEQ ID NO 111
/ TYPE: DNA
/ LENGTH: 1029
/ ORGANISM: Rattus norvegicus
/ FEATURE:
/ OTHER INFORMATION: Schwann cell peripheral myelin
US-10-205-331-111

Alignment Scores:
Pred. No.: 4,13e-12 Length: 1029
Score: 167.00 Matches: 58
Percent Similarity: 43.81% Conservative: 34
Best Local Similarity: 27.62% Mismatches: 100
Query Match: 14.86% Indels: 18
DB: 17 Gaps: 7

US-09-977-579-2 (1-215) x US-10-205-331-111 (1-1029)
QY 11 AlaSerLeuValLeuLeuTyrTrpValSerValCysPheProValCysValGluValPro 30
DB 89 TCTTCTTGGTGTG-----TCCCAACCCCTGGCCATTGGTTTACACGGAC 136
QY 31 SerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIleSerCysMetLys 50
DB 137 AGGGAAGTCTATGGTCTGGCTGCCCTCCAGGTCACCTGCACATGC---TCTTCTGGTCC 193
QY 51 ArgGluGluValGluAlaThrThrValValGluTrpPheTyrArgProGluGlyLys 70
DB 194 AGTGAATGGTCTCAGATCAGATCTCTTTTACCTGGCGCTACAGCTGAAGAGGCCGA 253
QY 71 AspPheLeu---IleTyrGluTyrArgAsnGlyHisGlnGluValGlu-----SerPro 87
DB 254 GATGCCATTTCATCTTCCACTATGCCAAGGGTCAACCTTACATCGATGAGTGGGGACC 313
QY 88 PheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeuGluAspValSerIleThrVal 107
DB 314 TTCAGAGCGCATCCAGTGGGTAGGGACCCCTAGCTGGAGGATGGCTCCATTGTCTATA 373
QY 108 LeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSerArgGluPheGlu 127
DB 374 CACAACCTAGACTACAGTCACAAGGCACTTTCACATGTGATGTCAAAAACCCACCGGAC 433
QY 128 PheGluAlaHisArgProPheValLysThrThrArgLeuLeuProLeuArgValThrGlu 147
DB 434 -----ATAGTGGGCAAGACGCTCTCAGGTCAAGCTCATGTCTATGTCTTTGAA 475
QY 148 GluAlaGlyGluAspPheThrSerValValSerGluLeuMetMetTyrIleLeuLeuVal 167
DB 476 AAAGTGCCCACTAGGTATGGGTGGTGGTGGAGCGGTGATCGGTGGCATCTCTGGGGTG 535
QY 168 PheLeuThrLeuTrpLeuLeuLeuGluMetile---TyrCysTyrArgLysValSerLys 186
DB 536 GTGCTGTTCGTGTGTCTTCTTCTACCTGATCCGGTACTGTGGTGTGGTGGCAGGAGGCT 595
QY 187 AlaGluGlu-----AlaAlaGlnGluAsnAlaSerAspTyrLeuAlaIleProSer 203
DB 596 GCCCTGCAGAGGAGGCTCAGTGCCATGAGAGAGGGGAAATTTCAAGATCTTCTTAAGGAC 655
QY 204 GluAsnLysGluAsnSerAlaValProVal 213
DB 111
QY 111
DB 111

Db 656 TCCTCGAAGCGCGCGCGGCGGACGACGCGAGTG 685
RESULT 14
US-10-723-860-6471
/ Sequence 6471, Application US/10723860
/ Publication No. US20040253606A1
/ GENERAL INFORMATION:
/ APPLICANT: Aziz, Natasha
/ APPLICANT: Ginsburg, Wendy M.
/ APPLICANT: Zlotnik, Albert
/ TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
/ TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
/ FILE REFERENCE: 05882.0193.NPUS01
/ CURRENT APPLICATION NUMBER: US/10/723,860
/ CURRENT FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: 60/429,739
/ PRIOR FILING DATE: 2002-11-26
/ NUMBER OF SEQ ID NOS: 8393
/ SOFTWARE: Patent in version 3.2
/ SEQ ID NO 6471
/ LENGTH: 3583
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (294)..(315)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1696)..(1712)
/ OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-6471

Alignment Scores:
Pred. No.: 4,59e-11 Length: 3583
Score: 165.50 Matches: 56
Percent Similarity: 47.11% Conservative: 26
Best Local Similarity: 33.18% Mismatches: 45
Query Match: 14.72% Indels: 48
DB: 18 Gaps: 7

US-09-977-579-2 (1-215) x US-10-723-860-6471 (1-3583)
QY 67 GluGlyGlyLysAspPheLeuLeuTyrGlu-TyrArgAsnGlyHisGlnGluValGluSe 86
DB 1851 GAAGGAGGTATTTCATTTTACAAATTGAAGAAACAGAGG-----CCTAGAGACATTGAGTC 1904
QY 86 rPropheGlnGlyArgLeu-----GlnTrp-----AsnGlySerLysAs 99
DB 1905 ACTTGGGCAAGTCAACAGCTGGCGGAGGAGCCGCTTTCGAACCTGAGCCTTCT 1964
QY 99 pheuGlnAspValSerile-----ThrValLeuAsnValThrLeuAsnAspSerGlyLe 117
DB 1965 GGTTCGACAGGTACGGCTTTTAGGCACCGTGTGAGGGCTCCAG-AATGACACAGATGT 2023
QY 117 uTyrThrCysAsnValSerArgGluPheGluPheGluAlaHisArg-----132
DB 2024 GGCCTCGAGTTACACAGGAGCGGTTGAGGGTGACCCCGGAGGCTTACCAAGGCT 2083
QY 133 -----ProPheValLysThrThrArgLeuLeuProLeu-----143
DB 2084 GGGTATTATATACAGTGCATACACAGGCGGAGGAGGTGAGCCACTCATCCAAGC 2143
QY 143 -----143
DB 2144 TCACACAGCAAGCTCACACAGCACACTCAGGCTGTCTATGAGCCTGGGCTACCCCTTAAC 2203
QY 144 -ArgValThrGluGluAlaGlyLysPheThrSerValValSerGluLeuMetMetTy 163
DB 2204 CTGCTGGCGCCCTGAGGAGCAACAGAGACATGCCATCTCGTGTCTGAGTATGATGA 2263
QY 163 rIleLeuLeuValPheLeuThrLeuTrpLeuLeuLeuGluMetileTyrCysTyrArgLy 183
DB 111
QY 111
DB 111
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Db 2264 TGTGCTCATTGTGTGTGACATATGCTGTGGCAGAGATGATTTACTGTACAGAA 2323
 Qy 183 sValSerLysAla---GluGluAlaAlaGlnGluAsnAla 195
 Db 2324 GATCGCTGCCGCCACGAGACTGCTGCACAGGAGATGCG 2363
 RESULT 15
 US-09-960-706-472
 ; Sequence 472, Application US/09960706
 ; Publication No. US20030134280A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Munger, William B.
 ; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
 ; FILE OF INVENTION: Gene Expression Profiles
 ; FILE REFERENCE: 44921-5029-01US
 ; CURRENT APPLICATION NUMBER: US/09/960,706
 ; CURRENT FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: 60/223,323
 ; PRIOR FILING DATE: 2000-08-07
 ; PRIOR APPLICATION NUMBER: 09/873,319
 ; PRIOR FILING DATE: 2001-06-05
 ; NUMBER OF SEQ ID NOS: 1124
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 472
 ; LENGTH: 1929
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Genbank Accession No. US20030134280A1 D10537
 US-09-960-706-472

Alignment Scores:

Pred. No.:	3.31e-11	Length:	1929
Score:	163.50	Matches:	54
Percent Similarity:	45.55%	Conservative:	33
Best Local Similarity:	28.27%	Mismatches:	81
Query Match:	14.55%	Indels:	23
DB:	10	Gaps:	7

US-09-977-579-2 (1-215) x US-09-960-706-472 (1-1929)

Qy	11	AlaSerLeuValLeuLeuTyrTrpValSerValCysPheProValCysValGluValPro	30
Db	101	TCTTCTTTGGTGTG-----TCCCGCGCCCGAGCCCATCGTGGTTTACACCGAC	148
Qy	31	SerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIleSerCysMetLys	50
Db	149	AGGAGGTCCATGGTGTGGGCTCCCGGTGACCCCTGCACCTGC---TCCTTCTGTCTC	205
Qy	51	ArgGluGluValGluAlaThrThrValValGluTrpPheTyrArgProGluGlyGlyLys	70
Db	206	AGTGAGTGGGTCTCAGATGACATCTCTTCCCTGGCGCTACCGCCCGAGGAGGAGCAGA	265
Qy	71	AspPheLeu---IleTyrGluTyrArgAsnGlyHisGlnGluValGlu-----SerPro	87
Db	266	GATGCCATTTTCGATCTTCCACTATGCCAGGAGCAACCCCTACATTGACGAGGTGGGACC	325
Qy	88	PheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeuGlnAspValSerIleThrVal	107
Db	326	TTCAAAGAGCGCATCCAGTGGGTAGGGGACCTCTCGCTGGAGGATGGCTCCATTGTGCATA	385
Qy	108	LeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSerArgGluPheGlu	127
Db	386	CACAACTAGACTACAGTGACATGGCAGCTTCACTTGTGACGCTCAAAACCCCTCCAGAC	445
Qy	128	PheGluAlaHisArgProPheValLysThrArgLeuLeuProLeuArgValThrGlu	147
Db	446	-----ATAGTGGGCAAGACCTCTCAGGTACGCTGTATGCTTTTGA	487
Qy	148	GluAlaGlyGluAspPheThrSerValSerGluIleMetMetTyrIleLeuVal	167
Db	488	AAAGTGCCAACTAGGTACGGGGTGTCTTCTGGGAGCTGTGATCGGGGTGTCTCGGGGTG	547

Qy	168	PheLeuThrLeuTrpLeuLeuIleGluMetIle---TyrCysTyr-----	181
Db	548	GTGCTGTTGCTGCTGCTGCTTTTCTACGTGGTTCGGTACTGCTGGCTACGACGAGCG	607
Qy	182	-----ArgLysValSerLysAlaGluGlu	189
Db	608	GCCCTGCAGAGAGGCTCAGTGTATGGAGAAG	640

Search completed: April 7, 2005, 17:21:00
 Job time : 508 secs

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<!--648
/locus_tag="HCM6793"

ORIGIN
Alignment Scores:
Pred. No.: 2,13e-126 Length: 648
Score: 1124.00 Matches: 215
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-977-579-2 (1-215) x AY419145 (1-648)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 1 ATGCCTGCCTTCAATAGATTGTTTCCCTGGCTTCTCTGCTTATCTACTGGGTCAGT 60

QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 61 GTCGTCTCCCTGTGTGTGTGAAGTCCCTCGAGACGGAGCCGTGAGGGCAACCC 120

QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 121 ATGAAGCTCGCTGCATCTCTCGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180

QY 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgGly 80
Db 181 GAATGTCTTACAGGCCCGAGGCGGTGAAGATTCTCTTATTACAGATCGGAATGCG 240

QY 81 HisGlnGluValIleSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 241 CACCAGAGGTGGAGAGCCCTTTCCAGGGCGCTGTCAGTGAATGGCAGAGACCTG 300

QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrCys 120
Db 301 CAGGACGTGTCCATCACTGTGTCACGTCACCTCTGAACGACTCTGGCCTCTACACCTG 360

QY 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 361 AATGTGTCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGGGCTG 420

QY 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 421 ATCCCCCTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACCTCTGTGTCTCAGAAATC 480

QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db 481 ATGATGTATACATCTTCTGTGCTCTCTCCCTGCTGCTGCTGCTCATCGAGATGATATTGC 540

QY 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 541 TACAGAAAGTCTCAAAACCGAGAGGCGGCCCAAGAAACCGCTCTGACTACCTTGCC 600

QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 601 ATCCCATCTGAGAACCAAGGAGAACTCTGGGTACCACTGAGGAA 645

RESULT 2
LOCUS CR609664 2555 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DF023YA09 of Fetal brain of Homo sapiens (human).
ACCESSION CR609664
VERSION CR609664.1 GI:50490471
KEYWORDS HTC; CNSLT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE 1 (bases 1 to 2555)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
JOURNAL
REMARK
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
Genoscope.
2 (bases 1 to 2555)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE [E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
Location/Qualifiers
source
1..2555
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF023YA09"
/tissue_type="Fetal brain"
/plasmid="pCMVSPORT_6"

ORIGIN
Alignment Scores:
Pred. No.: 1,52e-125 Length: 2555
Score: 1124.00 Matches: 215
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-09-977-579-2 (1-215) x CR609664 (1-2555)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 235 ATGCCTGCCTTCAATAGATTGTTTCCCTGGCTTCTCTGCTTATCTACTGGGTCAGT 294

QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 295 GTCGTCTCCCTGTGTGTGTGAAGTCCCTCGAGACGGAGCCGTGAGGGCAACCC 354

QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 355 ATGAAGCTCGCTGCATCTCTCGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 414

QY 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 415 GAATGTCTTACAGGCCCGAGGCGGTGAAGATTCTCTTATTACAGATCGGAATGCG 474

QY 81 HisGlnGluValIleSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 475 CACCAGAGGTGGAGAGCCCTTTCCAGGGCGCTGTCAGTGAATGGCAGAGACCTG 534

QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrCys 120
Db 535 CAGGACGTGTCCATCACTGTGCTCAACGTCACCTCTGACGACTCTGGCCTCTACACCTGC 594

QY 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 595 AATGTGTCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGGGCTG 654

QY 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 655 ATCCCCCTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACCTCTGTGTCTCAGAAATC 714

QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db 715 ATGATGTATACATCTTCTGTGCTCTCTCCCTGCTGCTCATCGAGATGATATATTGC 774

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Qy 181 TyArgLysValSerLysAlaGluAlaGlnGluAlaSerAspTyrLeuAla 200
Db 775 TACAGAAAGGCTCAAAAGCCAGAGAGCGCCCAAGAAACGGCTGTGACTACCTTGCC 834
Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 835 ATCCCATCTGAGAACAGGAGAACTCTGCGGTACCACTGGAGGAA 879

RESULT 3
HSM801563
LOCUS HSM801563 4052 bp mRNA linear HTC 22-SEP-2004
DEFINITION Homo sapiens mRNA; cDNA DKFZp761F182 (from clone DKFZp761F182).
ACCESSION AL136589
VERSION AL136589.1 GI:13276680
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4052)
Ostenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A.,
Mewes,H.W., Weil,B., Amid,C., Oeanger,A., Fobo,G., Han,M. and
Wiemann,S.
The German cDNA Consortium
Direct Submission
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinried/Germany) within the cDNA
sequencing consortium of the German Genome Project.
This clone (DKFZp761F182) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp761F182
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES             source
     source
1..4052
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/db_xref="RZPD:DKFZp761F182"
/db_xref="taxon:9606"
/clone="DKFZp761F182"
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/clone_lib="761 (synonym: hamy2). Vector pSport1; host
DH10B; sites NotI + SalI"
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1..4052
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804..1451
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/db_xref="GOA:Q9NY72"
/db_xref="UniProt/Swiss-Prot:Q9NY72"
/translations="MPAFNRLPFLASLIYWSVCFVPCVVEPSETEAVQGNPKMLR
CSIMGRKEVEATVYVWFYRPEGKDFLIYVRNGHQBVEPFGRLQWNGSKDLQD
VSTLVNLTNLSGLTYCNVSRFEFEHPRFPVKTTLLPLRTEAGEDFTSVSEI
MYTLLVFLTLWLLIEMIYCYRKVSKAEAAQENASDYLAIPSENKENSAPVEE"

Alignment Scores:
Pred. No.: 2,93e-125 Length: 4052
Score: 1124.00 Matches: 215
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

ORIGIN

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US-09-977-579-2 (1-215) x HSM801563 (1-4052)
Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 804 ATGCTCGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGCCTATCTACTGGTCACT 863
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 864 GTCTGCTTCCCTGTGTGTGGAGTGCCTTCGGAGAGCGGAGCGCGTGCAGGGCAACCCC 923
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 924 ATGAAGCTGCGCTGCATCTCTGCATCAGAGAGAGAGAGGTTGGAGGCCACACCGTGGTG 983
Qy 61 GluTrpPheTyrArgProGluGlyGlyAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 984 GAATGGTTCTACAGGCCCGAGGGCGGTAAGATTTCCTTATTTACGAGTATCGGAATGGC 1043
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 1044 CACCAGAGGTGGAGAGCCCTTTTCAGGGGCGCTTCAGTGGGAATGGCAGCAGGACCTG 1103
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 1104 CAGGACGTGTCCATCACTGTCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGC 1163
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 1164 AATGTGTCCCGGAGTTTGAAGTTTGAAGCGCATCGGCCCTTTGTGAAGACGACGCGGTG 1223
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 1224 ATCCCTTAAGATCACCGAGAGGCTGGAGAGACTTCACTCTGTGTCTCAGAAATC 1283
Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db 1284 ATGATGTACATCTTCTGTGTCTTCTTCCCTCACCTTGTGGCTGCTCATCGAGATGATATTCG 1343
Qy 181 TyrArgLysValSerLysAlaGluAlaGlnGluAlaSerAspTyrLeuAla 200
Db 1344 TACAGAAAGGCTCAAAAGCCAGAGAGCGCCCAAGAAACGGCTGTGACTACCTTGCC 1403
Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 1404 ATCCCATCTGAGAACAGGAGAACTCTGCGGTACCACTGGAGGAA 1448

RESULT 4
BX420015 1062 bp mRNA linear EST 01-MAY-2004
LOCUS BX420015 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF023YA09 5-PRIME, mRNA sequence.
ACCESSION BX420015
VERSION BX420015.2 GI:46929710
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1062)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30646738.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

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This sequence belongs to sequence cluster 6147.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODF023AA05QP1&c=6147.r.

FEATURES

Source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODF023YA09"
/tissue type="FETAL BRAIN"
/dev stage="fetal"
/clone lib="Homo sapiens FETAL BRAIN"
/notes="Organ: brain; Vector: pCMVSPORT.6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Alignment Scores:
Pred. No.: 5,42e-125 Length: 1062
Score: 1115.00 Matches: 214
Percent Similarity: 99.53% Conservative: 0
Best Local Similarity: 99.53% Mismatches: 1
Query Match: 99.20% Indels: 0
DB: 5 Gaps: 0

US-09-977-579-2 (1-215) x BX420015 (1-1062)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
DB 234 ATGCCTGCCCTCAATAGATTGTTCCCTCGGCTTCTCTGCTTATCTACTGGGTCAGT 293
QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
DB 294 GTCGTCTTCCCTGTGTGTGAGTGCCTCGGAGACGGAGCCGTGAGGGCAACCCC 353
QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal 60
DB 354 ATGAAGCTCGCTGCATCTCTCTCATGAAGAGAGAGAGGTGAGGCCACCGTGGTG 413
QY 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
DB 414 GAATGTTCTACAGGCCCGAGGCGGTAAAGATTCTCTTATTACGAGTATCGAATGCG 473
QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
DB 474 CACGAGGAGTGGAGAGCCCTTTTCAGGGCGGCTGCTGAGTGGAAATGGCAGGACCTG 533
QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
DB 534 CAGGACGTGTCCATCATCTGTCTCAACGTCATCTGAACGACTCTGGCCCTCTACACCTGC 593
QY 121 AsnValSerArgGluPheGluAlaHisAtgProPheValLysThrThrArgLeu 140
DB 594 ATGTGTCGGGAGTTGAGTTGAGGCGCATCGGCCCTTTGTGAAGACGACCGGCTG 653
QY 141 IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValValSerGluIle 160
DB 654 ATCCCTTAAAGATCAACGAGGAGGTGGAGGAGCTTCACTCTCTGTGCTCAGAAATC 713
QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTyrLeuIleGluMetIleTyrCys 180
DB 714 ATGATGTACATCTTCTGTCTTCTCTCACCTTGTGGCTCTCATCGAGATGATATTGC 773
QY 181 TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
DB 774 TACAGAAAGGTCTCAAAAGCCGAGGAGGAGCCCAAGAAAACCGCTCTGACTACCTTGGC 833
QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
DB 834 ATCSCATCTTGAGAACAGGAGAACTCTGGCGTACCAAGTGAGGAA 878

RESULT 5

AY419147

LOCUS

DEFINITION

AY419147

648 bp DNA linear

GSS 12-DEC-2003

Mus musculus HCM6793 gene, VIRTUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

ACCESSION

AY419147

VERSION

AY419147.1

GI:39775107

GSS.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 648)

Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Perriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,

Adams,M.D. and Cargill,M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

Science 302 (5652), 1960-1963 (2003)

PUBMED

14671302

REFERENCE

2 (bases 1 to 648)

Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Perriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,

Adams,M.D. and Cargill,M.

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Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Perriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,

Adams,M.D. and Cargill,M.

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Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Perriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,

Adams,M.D. and Cargill,M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

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PUBMED

14671302

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Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Perriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,

Adams,M.D. and Cargill,M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

Science 302 (5652), 1960-1963 (2003)

PUBMED

14671302

REFERENCE

2 (bases 1 to 648)

Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,


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Percent Similarity: 97.67%      Conservative: 0
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Query Match: 97.60%             Indels: 0
DB: 3                           Gaps: 0

US-09-977-579-2 (1-215) x AK049747 (1-3549)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
DB 232 ATGCCTGCCTTCACAGATTGCTCCCTAGCTCTCTAGTGTCTCATCTACTGGTTCAGA 291
QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
DB 292 GTCTGCTCCCTGCTGTGTAGAGTACCTCGGAGACAGAGCGGCGGCAATTC 351
QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrValVal 60
DB 352 ATGAAGCTGAGATGCATCTCTCGATGAAGAGGAGGAGGTGGAGGCCACCATGTAGTG 411
QY 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
DB 412 GAGTGGTCTACAGGCTGAGGCGGTAAAGATTCTTATATATAGTATCGAATGGC 471
QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
DB 472 CACCAGAGGTGGAGAGCCCTTCCAAGTGTCTGTCAGTGGAAATGGGAGCAAGACCTG 531
QY 101 GluAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
DB 532 CAGAGCGATTCATCACTGTTCTCAATGTCACTCTGAATCACTCTGGCCCTTACACATGT 591
QY 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
DB 592 AATGTCTCCAGGAGTTGATGTCGAGACACACGGCCCTTGTGAAGACACACAGACTA 651
QY 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
DB 652 ATACCCCTGCGAGTCACTGAAGAGCGGAGAGACTTCACCTCCGTGGTCTCGGAATC 711
QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
DB 712 ATGATGTACATCTCTCTGGTCTTCTCTCACCTGTGGCTGTTTATTGATGATGATCTATTGC 771
QY 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
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QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
DB 832 ATCCCTTCAGAGAACAGGAGAACTCTGTGTACCCGTGGAGGAA 876

RESULT 8
AK049286 4149 bp mRNA linear HTC 03-APR-2004
LOCUS Mus musculus ES cells cDNA, RIKEN full-length enriched library,
DEFINITION Clone:C330019103 product:VOLTAGE-GATED SODIUM CHANNEL BETA-3
SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog [Rattus
norvegicus], full insert sequence.
ACCESSION AK049286
VERSION AK049286.1 GI:26093400
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Carninci, P. and Hayashizaki, Y.
AUTHORS High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
AUTHORS

```

```

TITLE Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
JOURNAL Normalization and subtraction of cap-trapper-selected cDNAs to
MEDLINE prepare full-length cDNA libraries for rapid discovery of new genes
PUBMED Genome Res. 10 (10), 1617-1630 (2000)
REFERENCE 20499374
AUTHORS 11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Harada, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsui, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
JOURNAL sequencing pipeline with 384 multicapillary sequencer
MEDLINE Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 20530913
REFERENCE 11076861
AUTHORS 4

The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS 6

The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
JOURNAL of 60,770 full-length cDNAs
MEDLINE Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 4149)
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.

FEATURES
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ORIGIN
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Query Match: 96.44% Indels: 1
DB: 3 Gaps: 0

US-09-977-579-2 (1-215) x AK049286 (1-4149)
QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
DB 410 ATGCCTGCCCTTCAACAGATTGTTCCCTAGTCTTCTAGTGTCTATCTACTGGGTGAGA 469
QY 21 ValCysPhe-ProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPr 40
DB 470 GTCTGCTTCCCTGTGTGTAGAGTACCTTCGGAGACAGAGCCGTGCAGGGCAATTC 529
QY 40 oMetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVa 60
DB 530 CATGAAGCTGAGATGATCTCTCGCATGAAGAGGAGGAGGTGGAGGCCACCACTGTACT 589
QY 60 lGluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGl 80
DB 590 GGAGTGGTCTACAGCCCTGAGCGCGGTAAAGATTCTCTATATATATGATATCGAAATGG 649
QY 80 vHisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLe 100
DB 650 CCACAGAGGTGGAGAGCCCTTCAAGTGTCTGCAAGTGAATGGAGCAAGACCT 709
QY 100 uGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCy 120
DB 710 GCAGGAGGTATCCATCACTGTTCTCAATGTCATCTGTAATGACTCTGGCTCTACACATG 769
QY 120 sAsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLe 140
DB 770 TAAATGTGTCCAGGAGTTTGTAGTTCGAAGCACACCGCCCTTTGTGAAGACCAAGACT 829
QY 140 uIleProLeuArgValThrGluAlaGlyGluAspPheThrSerValValSerGluIle 160
DB 830 AATACCCCTGCGAGTCACTGAGAGCGGGAGAGACTTCACTCCGTGGTCTCGGAAT 889
QY 160 eMetMetTyrIleLeuLeuValPheLeuThrLeuThrLeuLeuIleGluMetIleTyrCy 180
DB 890 CATGATGATACATCTCTCTGCTCACTACCTTGTGGCTGTTATTAGATGATCTATTG 949
QY 180 sTyrArgLysValSerLysAlaGluGluAlaGlnGluAlaSerAspTyrLeuAl 200
DB 950 CTACGAAAGGTCTCTAAGCGCGAAGAGCGCTCAGGAAATGCGTCTGACTACCTTGC 1009
QY 200 alleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
DB 1010 TATCCCTTCAGAGACACAGAGACTCTGTGTACCCGTGGAGGA 1055

RESULT 9
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LOCUS
DEFINITION
UI-M-BH3-bseq-d-04-0-UI.r1 NIH BMAP M.S4 Mus musculus cDNA clone
BM933157 636 bp mRNA linear EST 13-MAR-2002
UI-M-BH3-bseq-d-04-0-UI 5', mRNA sequence.
ACCESSION
BM933157.1 GI:19392309
VERSION
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 636)
Bonaldo,M.P., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 REVERSE.

FEATURES
source

1. 636
Location/Qualifiers
/organism="Mus musculus"
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/db_xref="taxon:10090"
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/clone_lib="NIH_BMAP_M.S4"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; The
NIH_BMAP_M.S4 library is a subtracted library of a series,
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hippocampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: NIH_BMAP_M.S4,
NIH_BMAP_M.S3.3, NIH_BMAP_M.S3.2, NIH_BMAP_M.S3.1,
NIH_BMAP_M.S2, NIH_BMAP_M.S1. The subtracted library
(NIH_BMAP_M.S4) was constructed as follows: PCR amplified
cDNA inserts from NIH_BMAP_M.S3.3, NIH_BMAP_M.S3.2, and
NIH_BMAP_M.S3.1 clones from which 3' ESTs had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M.S3.3, NIH_BMAP_M.S3.2, and NIH_BMAP_M.S3.1
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
NIH_BMAP_M.S4 library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)"

ORIGIN

Alignment Scores:

Pred. No.: 5,82e-119 Length: 636
Score: 1063.00 Matches: 203
Percent Similarity: 97.13% Conservatives: 0
Best Local Similarity: 97.13% Mismatches: 6
Query Match: 94.57% Indels: 0
DB: 5 Gaps: 0

US-09-977-579-2 (1-215) x BM933157 (1-636)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
DB 7 ATGCCTGCCCTTCAACAGATTGTTCCCTAGTCTTCTAGTGTCTATCTACTGGGTGAGA 66

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
 Db 67 GTCTGCTTCCCTGCTGTGTAGTAGTACCTTCGAGACAGAGCGGTGCAGGGCAATCC 126
 Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
 Db 127 ATGAAGCTGATGATCATCTCTCTGATGAAGAGGAGGAGGTGGAGGCCACCACTGTAGTG 186
 Qy 61 GluTrpPheTyrArgProGluGluGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
 Db 187 GAGTGGTTCACAGCCTCAGGCGGTAAAGATTCTCTATATAGATATCGAAATGGC 246
 Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
 Db 247 CACCAGGAGGTGGAGAGCCCTTCCAAAGTCTGTCTGAGTGAATGGAGCAAGACCTG 306
 Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
 Db 307 CAGSACGTATCCATCACTCTCTCAATGTCACTCTGAATGACTCTGGCCTCTACACATGT 366
 Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
 Db 367 AATGTGTCAGGAGGTGTAGTTCGAAGCACACCGGCCCTTTTGAAGACCAAGACTA 426
 Qy 141 IleProLeuArgValThrGluGluAlaGlyLysPheThrSerValSerGluIle 160
 Db 427 ATACCCCTGCGAGTCACTGAAGAGCGGAGAGACTTCACTCCGTGGTCTCGGAATC 486
 Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCys 180
 Db 487 ATGATGTACATCTCTCTGCTCTCACTCTGGCTGTGTTATTTAGATGATCTATTTGC 546
 Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
 Db 547 TACAGAAAGTCTCTAGTTCGAGAGCGAGCTCAGGAAATGCTGTGACTACCTTGTCT 606
 Qy 201 IleProSerGluAsnLysGluAsnSer 209
 Db 607 ATCCCTTCAGAGAACACAGAGACTCT 633

RESULT 10
 BX445002
 LOCUS
 DEFINITION
 CS0DF023YA09 5-PRIME, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 975)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 15, 2003 this sequence version replaced gi:30782286.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
 This sequence belongs to sequence cluster 6147.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS1AF006ZE05QP1&c=6147.r.
 Location/Qualifiers
 1..975
 /organism="Homo sapiens"
 /mol_type="mRNA"

FEATURES
 source

/db xref="taxon:9606"
 /clone="CS0DF023YA09"
 /tissue_type="FETAL BRAIN"
 /dev_stage="fetal"
 /Clone_lib="Homo sapiens FETAL BRAIN"
 /notes="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 1.88e-118 Length: 975
 Score: 1061.00 Matches: 209
 Percent Similarity: 97.67% Conservative: 1
 Best Local Similarity: 97.21% Mismatches: 5
 Query Match: 94.40% Indels: 1
 DB: 5 Gaps: 0

US-09-977-579-2 (1-215) x BX445002 (1-975)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
 Db 235 ATGCCTGCCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTATCTACTGGTCACT 294
 Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
 Db 295 GTCTGCTTCCCTGCTGTGTGGAGTCCCTTCGGAGAGCGAGGCCGTGCAGGGCAACCCC 354
 Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
 Db 355 ATGAAGCTCGCTGCTATCTCTGCATGAGAGAGAGGAGGTGGAGGCCACCACTGGTGTG 414
 Qy 61 GluTrpPheTyrArgProGluGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
 Db 415 GAATGGTTCTACAGGCCCGGCGGTAAAGATTCTCTTATTACGAGTATCGGAATGGC 474
 Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
 Db 475 CACCAGGAGTGGAGAGCCCTTTCAGGGGGCGCTGCAGTGGATGGCAGCAAGGACCTG 534
 Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
 Db 535 CAGSACGTGTCCATCACTGTCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCAAC 594
 Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
 Db 595 AAWAAGTCCCGGAGTTTGTAGTTTGTAGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 654
 Qy 141 IleProLeuArgValThrGluGluAlaGlyLysPheThrSerValSerGluIle 160
 Db 655 ATCCCTTAAGATCACCAGGAGGCTGGAGAGACTTCACTCTGTGGTCTCAGAAATC 714
 Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCys 180
 Db 715 ATGATGTACATCTCTCTGCTCTCTCACTCTGGCTGTCTCATCGAGATGATATATTC 774
 Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
 Db 775 TACAGAAAGTCTCAAAAGCCGAGAGCGGCCCAAGAAACCGCTCTGACTACCTTGGCC 834
 Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
 Db 835 ATCCATCTGAGAACAGGAGAC-TCTTCGGGTAMCACTGGAGGAT 878

RESULT 11

BB614118

LOCUS

DEFINITION

ACCESSION

VERSION

BB614118 672 bp mRNA linear EST 26-OCT-2001
 BB614118 RIKEN full-length enriched, 0 day neonate head Mus
 musculus cDNA clone 4833414B02 5', mRNA sequence.

BB614118
 BB614118.1 GI:16454578

REFERENCE AUTHORS	1 (bases 1 to 4105) Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shennan,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,T.E., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.B., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullah,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.D., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL MEDLINE PUBMED	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 22388257
REFERENCE AUTHORS	2 (bases 1 to 4105) Strausberg,R. Direct Submission
JOURNAL	Submitted (08-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK COMMENT	NIH-MGC Project URL: http://mgi.nci.nih.gov Contact: MGC help desk Email: cgabs-rc@mail.nih.gov Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library Preparation: M. Bento Soares, University of Iowa cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcsc.bc.ca Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lilja Prabhu, Parvaneh Saedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Scott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
FEATURES source	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 126 Row: 1 Column: 19 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23943798 This clone has the following problem: frame shifted. Location/Qualifiers 1..4105 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6" /db_xref="taxon:10090" /clone="IMAGE:6826414" /tissue_type="Brain, mouse, 13.5,14.5,16.5,17.5 dpc" /clone_lib="NIH_BMAP_FY0" /lab_host="DH10B" /note="Vector: pYX-ASC"
ORIGIN	Alignment Scores: Pred. No.: 2,67e-115 Length: 4105 Score: 1042.50 Matches: 208 Percent Similarity: 96.74% Conservative: 0 Best Local Similarity: 96.74% Mismatches: 6
Query Match:	92.75% Indels: 3
DB:	3 Gaps: 1
US-09-977-579-2 (1-215) x BC058083 (1-4105)	
Qy	1 MetProAlaPheAenArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db	356 ATGCTGCTTCAACAGATTGCTTCCCTAGTCTCTCTAGTGTCTCATCTACTGGGA--- 411
Qy	21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db	412 GTCTGCTTCCCTGTGTGTAGTAAGTACCTTCGAGACAGAACCGGTGCGAGGCAATTC 471
Qy	41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db	472 ATGAGCTGAGATGCATCTCTCGATGAGAGGAGGAGGTGGAGGCCACCATCTGTAGTG 531
Qy	61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db	532 GAGTGGTCTTACAGGCTGAGGCGGTAAAGATTTCCTTATATATAGTAGTATCGAAATGGC 591
Qy	81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db	592 CACCAGAGGTGGAGAGCCCTTCCAGGTCGTCTGCAGTGGATGGAGCAA-GACCTG 650
Qy	101 GlnAspValSerIleThrValLeuAenValThrLeuAenAspSerGlyLeuTyrThrCys 120
Db	651 CAGAGCTATCCATCACTGTTCTCAATGTCATCTGANTGACTCTGGCCTCTACATGT 710
Qy	121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db	711 AATGTGTCCAGGCGAGTTTGAAGTTCGAAGCACACCGGCCCTTTGTGAAGACCACCAAGACTA 770
Qy	141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db	771 ATACCCCTCGAGTCACTGAAGAGCGGAGAGACTTCACCTCCGCGGTCTCGGAATC 830
Qy	161 MetMetTyrIleLeuLeuValPheLeuThrLeuTyrLeuLeuIleGluMetIleTyrCys 180
Db	831 ATGATGTACATCTCTCTGCTCTCTCCACCTTGTGGCTGTTTATGAGATGATCTATTGC 890
Qy	181 TyrArgLysValSerLysAlaGluAlaGlnGluAenAlaSerAspTyrLeuAla 200
Db	891 TACAGAAAGGTCTCTAAGGCGGAGAGGAGCTCAGGAAATGCGTCTGACTACCTTGTCT 950
Qy	201 IleProSerGluAsnLysGluAenSerAlaValProValGluGlu 215
Db	951 ATCCCTTCAGAGAACCAAGGAGAACTCTGTGTGTTACCCGTGGAGGAA 995
RESULT 13	
LOCUS	BG294174 950 bp mRNA linear EST 21-FEB-2001
DEFINITION	602391245F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4503250 5', mRNA sequence.
ACCESSION	BG294174
VERSION	BG294174.1 GI:13054543
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 950)
AUTHORS	NIH-MGC http://mgi.nci.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabs-rc@mail.nih.gov Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LAM10373 row: i column: 11
High quality sequence stop: 643.
Location/Qualifiers
1..950

FEATURES

source

/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:4503250"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: Noti;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 3,27e-108 Length: 950
Score: 977.00 Matches: 198
Percent Similarity: 93.95% Conservative: 4
Best Local Similarity: 92.09% Mismatches: 11
Query Match: 86.92% Indels: 4
DB: 4 Gaps: 2

US-09-977-579-2 (1-215) x BG294174 (1-950)

QY 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
DB 87 ATGCCTGCTTCAACAGATTGTTCCCTTAGCTTCTTAGTGTCTATCTACTGGGTGAGA 146
QY 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
DB 147 GTCGTCTCCCTGTGTGTAGAGTACCTCGGAGACAGAGCCGTGAGGCAATTCC 206
QY 41 MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrValVal 60
DB 207 ATGAAGCTGAGATGATCTCTCCGATGAAGAGGAGGAGGTGGAGGCCACCACTGTAGT 266
QY 61 GluTrpPheTyrArgProGluGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
DB 267 GAGTGGTCTACAGGCTGAGGCGGTAAAGATTTCCTTATATAGATATCGAATGGC 326
QY 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
DB 327 CACCAGAGGTGGAGAGCCCTTCCAAAGTCTGTGAGTGAATGGGAGCAAGACCTG 386
QY 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
DB 387 CAGGACGTATCCATCACTGTTCTCAATGTCATCTGGAATGACTGTGGCTCTACACATG 446
QY 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
DB 447 AATGTGTCAG-GAGTTTGAAGTTCGAGACACCGGCCCTTTGTGAGACCAAGACTA 505
QY 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
DB 506 ATACCCCTCGAGTCACTGAAGAGCGGAGAGAAGACTTCACCTCCGTGCTCGGAATC 565
QY 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTyrLeuIleGluMetIleTyrCys 180
DB 566 ATGATGTATACCTCTCTGCTCTCTCCATCTGTGGCTGTTTATTGAGATGATCTATTC 625
QY 181 TyrArgLysValSerLysAlaGluGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAla 200
DB 626 TACAGAAAGGTCTCTAGGCCCGAGAGGAGGT-CAGAGAAATGCGTCTACTACTTG--- 581
QY 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
DB 682 TATCCCTTAGAGAACAGGCAA---CCTGTGTACCGTGGGATAAG 723

RESULT 14

BP200910

LOCUS

DEFINITION

BP200910 Sugano cDNA library, amygdala Homo sapiens cDNA clone

AMR03894, mRNA sequence.

ACCESSION

BP200910

VERSION

BP200910.1 GI:52050356

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 582)

Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Suzuki, I., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES

source

1..582

/organism="Homo sapiens"

/mol_type="mRNA"

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/clone="AMR03894"

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ORIGIN

Alignment Scores:

Pred. No.: 1.1e-106 Length: 582

Score: 962.00 Matches: 182

Percent Similarity: 99.45% Conservative: 0

Best Local Similarity: 99.45% Mismatches: 1

Query Match: 85.59% Indels: 0

DB: 5 Gaps: 0

US-09-977-579-2 (1-215) x BP200910 (1-582)

QY 2 ProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerVal 21

DB 34 CTGCTCTTCAATAGATTGTTCCCTTGGCTTCTCTGCTTATCTACTGGGTGAGTGC 93

QY 22 CysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMet 41

DB 94 TGCTTCCCTGTGTGTGGAGTGCCTCGGAGACGGAGCGCTGCAGGCAACCCCATG 153

QY 42 LysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrValValGlu 61

DB 154 AAGCTCGCTGCATCTCTGTCATGAAGAGAGAGGAGGTGGAGGCCACCGGTGGTGA 213

QY 62 TrpPheTyrArgProGluGlyLysAspPheLeuIleTyrGluTyrArgAsnGlyHis 81

DB 214 TGGTCTACAGCCCGAGGCGGTAAAGATTTCCTTATTACAGTATCGAATGCCCAC 273

QY 82 GlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeuGln 101

DB 274 CAGGAGGTGGAGAGCCCTTTCAGGGCGCTTCAGTGAATGGCAGGACCTGCAG 333

QY 102 AspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsn 121

DB 334 GACGTGTCCATCACTGTGCTCAACGTCACCTCGAACGACTCTGGCTCTACACCTCAAT 393

QY 122 ValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeuIle 141

DB 394 GTGTCGGGAGTTGAGTTGAGGCGCATCGCCCTTTGTGAAGACGACGGGCTGATC 453

QY 142 ProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIleMet 161


```

Db 454 CCCTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACCTCTGTGGTCTCAGAAATCATG 513
Qy 162 MetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleLeuGluMetIleTyrCysTyr 181
Db 514 ATGTACATCTCTTGGTCTCCTCACCCTGTGGTCTCTCAGAGATGATATATTGCTAC 573
Qy 182 ArgLysVal 184
Db 574 AGAAGGTC 582

RESULT 15
CA749311 723 bp mRNA linear EST 09-JUL-2003
UI-M-FY0-cdd-k-17-0-UI.r1 NIH BMAP_FY0 Mus musculus cDNA clone
IMAGE:6831594 5', mRNA sequence.
CA749311
CA749311.1 GI:25570984
EST.
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 723)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cga@nci.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5,
Location/Qualifiers
1. 723
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/db_xref="taxon:10090"
/clone="IMAGE:6831594"
/tissue_type="whole brain"
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/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP FY0"
/notes="Organ: Brain; Vector: pYX- Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN
Alignment Scores:
Pred. No.: 1.7e-103 Length: 723
Score: 937.00 Matches: 180
Percent Similarity: 97.30% Conservative: 0
Best Local Similarity: 97.30% Mismatches: 4
Query Match: 83.36% Indels: 1
DB: 6 Gaps: 0

```

```

US-09-977-579-2 (1-215) x CA749311 (1-723)
Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 170 ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGTCTATCTACTGCGGTGAGA 229
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 230 GTCTGCTTCCCTGTGTGTAGAGTACCCTCCGAGACAGAGCCGCTGAGGGCAATTC 289
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 290 ATCAAGCTGAGATGCATCTCCTGCATGAAGAGGAGGAGGTGAGGCGCCACCCTGTAGTG 349
Qy 61 GluTrpPheTyrArgProGluGluGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 350 GAGTGGTCTTACAGGCTGAGGCGGTAAAGATTCTTATATATGATGATCGAAATGGC 409
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
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Db 650 CATGATGTACATCCTCTGCTGCTCTCCTCACCTTGTGGCTGTTTATTGAGATGATCTATTG 709
Qy 180 sTyrArgLysVal 184
Db 710 CTACAGAAAGGTC 722

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Search completed: April 7, 2005, 17:09:38
Job time : 3104 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 07:44:40 ; Search time 1135.27 Seconds
(without alignments)
10158.276 Million cell updates/sec

Title: US-09-977-579-4_COPY_1024_1261

Perfect score: 238

Sequence: 1 aacaggagcagtgtgacatg.....tgccagaactgagaagcgg 238

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	238	100.0	1261	6 AR359850	AR359850 Sequence
2	238	100.0	1261	6 AX039100	AX039100 Sequence
3	238	100.0	1261	9 HSA243396	AJ243396 Homo sapi
4	236	99.2	5306	9 AB032984	AB032984 Homo sapi
5	216	90.8	127347	2 AP000682	AP000682 Homo sapi
6	216	90.8	144833	2 AC063921	AC063921 Homo sapi
7	216	90.8	149800	2 AC021981	AC021981 Homo sapi
8	216	90.8	172546	2 AC024604	AC024604 Homo sapi
9	216	90.8	178169	9 AP002765	AP002765 Homo sapi
10	216	90.8	178431	2 AP002749	AP002749 Homo sapi
11	216	90.8	181471	9 AC069539	AC069539 Homo sapi
12	203.6	85.5	3296	9 AB097521	AB097521 Macaca fa
13	118	49.6	174285	2 AC145484	AC145484 Lemur cat
14	108	45.4	66980	2 AC013796	AC013796 Homo sapi
15	47.4	19.9	189486	2 AC114854	AC114854 Rattus no
16	44.2	18.6	175316	5 BX649282	BX649282 Zebrafish
17	44	18.5	182917	9 AL139383	AL139383 Human DNA
18	43.8	18.4	178225	5 BX005286	BX005286 Zebrafish
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C	20	43.2	18.2	139084	5	AL935332	AL935332	Zebrafish
	21	43.2	18.2	196687	10	AC122466	AC12466	Mus muscu
	22	43.2	18.2	199229	10	AC120004	AC120004	Mus muscu
	23	43.2	18.2	345383	2	AC149590	AC149590	Mus muscu
C	24	43.2	18.0	184751	5	BX571948	BX571948	Zebrafish
C	25	42.6	17.9	206768	2	AC125951	AC125951	Rattus no
C	26	42.6	17.9	228381	2	AC103262	AC103262	Rattus no
C	27	42.6	17.9	240645	2	AC126633	AC126633	Rattus no
C	28	42.4	17.8	61434	9	AC007366	AC007366	Homo sapi
	29	42.4	17.8	93599	2	AC084728	AC084728	Homo sapi
C	30	42.4	17.8	118674	2	AC023063	AC023063	Homo sapi
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	35	41.8	17.6	159084	9	AC138512	AC138512	Homo sapi
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	37	41.6	17.5	196341	2	BX293552	BX293552	Danio rer
	38	41.6	17.5	248002	5	BX323588	BX323588	Zebrafish
C	39	41.4	17.4	99961	9	AL606510	AL606510	Human DNA
	40	41.4	17.4	226950	10	AL671011	AL671011	Mouse DNA
C	41	41.2	17.3	151804	2	AC008161	AC008161	Mus muscu
	42	41.2	17.3	152684	2	BX897684	BX897684	Danio rer
C	43	41.2	17.3	157907	2	CR847996	CR847996	Danio rer
	44	41.2	17.3	180745	9	AL359183	AL359183	Human DNA
C	45	41.2	17.3	205379	10	AL591174	AL591174	Mouse DNA

ALIGNMENTS

RESULT 1	AR359850	Sequence 4 from patent US 6593565.	1261 bp	DNA	linear	PAT 17-AUG-2003
LOCUS	AR359850	Sequence 4 from patent US 6593565.	1261 bp	DNA	linear	PAT 17-AUG-2003
DEFINITION	AR359850	Sequence 4 from patent US 6593565.	1261 bp	DNA	linear	PAT 17-AUG-2003
ACCESSION	AR359850	Sequence 4 from patent US 6593565.	1261 bp	DNA	linear	PAT 17-AUG-2003
VERSION	AR359850.1	GI:33766660	1261 bp	DNA	linear	PAT 17-AUG-2003
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1261)					
AUTHORS	Heslin, P. and Lynam, N.R.					
TITLE	Vehicle interior rearview mirror assembly including an accessory-containing housing					
JOURNAL	Patent: US 6593565-A 4 15-JUL-2003;					
FEATURES	Location/Qualifiers					
source	1. .1261					
ORIGIN	/organism="unknown"					
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Gaps	0;						
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Qy	61	AGCAATGTCAATGGCATCAGGAGGGCGGCCCAAGGGCCCATCGCTTCCCTTCATGCATC	120				
Db	1084	AGCAATGTCAATGGCATCAGGAGGGCGGCCCAAGGGCCCATCGCTTCCCTTCATGCATC	1143				
Qy	121	CATTGTTCTGTTCAATTCATTCATCCATACATCCACCTGCCTCTGAGCTTTCACTCTGAC	180				
Db	1144	CATTGTTCTGTTCAATTCATTCATCCATACATCCACCTGCCTCTGAGCTTTCACTCTGAC	1203				
Qy	181	TCCTTAACCTCCATCAGACCTCTACGACCACTAAGACTCTGCCAGAACTGAGAGCCGG	238				
Db	1204	TCCTTAACCTCCATCAGACCTCTACGACCACTAAGACTCTGCCAGAACTGAGAGCCGG	1261				

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LOCUS	AX039100	Sequence 4 from Patent WO0063367.				REFERENCE	3 (bases 1 to 1261)
DEFINITION	AX039100					AUTHORS	Morgan,K.
ACCESSION	AX039100					TITLE	Direct Submission
VERSION	AX039100.1	GI:11229276				JOURNAL	Submitted (13-MAR-2000) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
KEYWORDS						COMMENT	On Mar 14, 2000 this sequence version replaced gi:7160974.
SOURCE	Homo sapiens (human)					FEATURES	Location/Qualifiers
ORGANISM	Homo sapiens					source	1. .1261
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					gene	/organism="Homo sapiens"
AUTHORS	Cox,P., Dixon,A., Jackson,A. and Morgan,K.					5'UTR	/mol_type="mRNA"
TITLE	A novel family of beta sub-unit proteins from a voltage-gated sodium channel, nucleic acids encoding them and therapeutic or diagnostic uses there of					CDS	/db_xref="taxon:9606"
JOURNAL	Patent: WO 0063367-A 4 26-OCT-2000; WARNER-LAMBERT COMPANY (US) ; Cambridge University Technical Services Limited (GB)						/tiissue_type="brain"
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ORIGIN							
Query Match	100.0%; Score 238; DB 9; Length 1261;						
Best Local Similarity	100.0%; Pred. No. 3.1e-59;						
Matches 238; Conservative	0; Mismatches 0; Indels 0; Gaps 0;						
QY	1 AACAGGACGAGTGTGACATGAGGTGGCTGAACACCTGAGGAGCTGACATCCCATGTTTC	60					
DB	1024 AACAGGACGAGTGTGACATGAGGTGGCTGNAACCTGAGGAGCTGACATCCATGTTTC	1083					
QY	61 AGCAATGTCAATGGCATCAGGAGGCGCCCAAGAGGCCCATCGTCTTCCTTCATGCATC	120					
DB	1084 AGCAATGTCAATGGCATCAGGAGGCGCCCAAGAGGCCCATCGTCTTCCTTCATGCATC	1143					
QY	121 CATTGTTCTGTTTCATTTCATTCATCATACATCCACCTGCTCTGAGCTTTTCACCTCTGAC	180					
DB	1144 CATTGTTCTGTTTCATTTCATTCATCATACATCCACCTGCTCTGAGCTTTTCACCTCTGAC	1203					
QY	181 TCCTTAATCCATCAGACTTACGACACATAAGACTTGCAGAACTGAGAGCCGG	238					
DB	1204 TCCTTAATCCATCAGACTTACGACACATAAGACTTGCAGAACTGAGAGCCGG	1261					
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LOCUS	HS243396	Homo sapiens mRNA for voltage-gated sodium channel beta-3 subunit (scn3b gene).					
DEFINITION	AJ243396						
ACCESSION	AJ243396.2	GI:7242612					
VERSION	scn3b gene; voltage-gated sodium channel beta-3 subunit.						
KEYWORDS	Homo sapiens						
SOURCE	Homo sapiens						
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1 Morgan,K., Stevens,E.B., Shaw,B., Cox,P., Dixon,A.K., Lee,K., Pinnoch,R.D., Hignes,J., Richardson,P.J., Mizuguchi,K. and Jackson,A.P.						
AUTHORS							
TITLE	beta 3: an additional auxiliary subunit of the voltage-sensitive sodium channel that modulates channel gating with distinct kinetics						
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (5), 2308-2313 (2000)						
MEDLINE	20160948						
PUBMED	10688874						
REFERENCE	2 Morgan,K.						
AUTHORS	Direct Submission						
TITLE	Submitted (28-JUN-1999) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM						
JOURNAL							

MEDLINE 20039618
PUBMED 10574461
REFERENCE 2 (bases 1 to 5306)
AUTHORS Ohara,O., Nagase,T. and Kikuno,R.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnaif@kazusa.or.jp.
URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)

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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.1e-58;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AACGAGGAGTGATGACATGAGTGGCTGAACACCTGAGGAGCTGACATCCCATGTTTC 60
Db 696 AACGAGGAGTGATGACATGAGTGGCTGAACACCTGAGGAGCTGACATCCCATGTTTC 755
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Db 756 AGCAATGTCATGTCATCAGAGGCGCCCGAGGGCCCATCGCTTCCTTCATGCATC 815
Qy 121 CATTTGTTCTGTTTCATTCATTCATCATCATCATCATCATCATCATCATCATCATCATC 180
Db 816 CATTTGTTCTGTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATC 875
Qy 181 TCCTTAACCTCATCAGACCTCTAGCGACCATATAGACTCTGCCAGAACTGAGAGCC 236
Db 876 TCCTTAACCTCATCAGACCTCTAGCGACCATATAGACTCTGCCAGAACTGAGAGCC 931

RESULT 5
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LOCUS Homo sapiens chromosome 11 clone CMB9-32A1 map 11q24, WORKING DRAFT
DEFINITION SSEQUENCE, 8 unordered pieces.
ACCESSION AP000682
VERSION AP000682.3 GI:9844967
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 127347)
REFERENCE
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens 127,347 genomic DNA of 11q24

JOURNAL
REFERENCE 2 (bases 1 to 127347)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-15-1 Kitasato, Sagami-hara, Kanagawa 228-8555, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-42-778-9923, Fax:81-42-778-9924)
On Aug 18, 2000 this sequence version replaced gi:8118870.
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDrafter11
Center clone name: CMB9-32A1
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 124981 bases at least Q40
Consensus quality: 125815 bases at least Q30
Consensus quality: 126286 bases at least Q20
Insert size: 126647; sum-of-contigs
Quality coverage: 12.71x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of
8 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
1 33532 contig of 33532 bp in length
33633 59223 contig of 25591 bp in length
59324 83007 contig of 23684 bp in length
83108 100196 contig of 17089 bp in length
100297 112313 contig of 12017 bp in length
112414 121413 contig of 8630 bp in length
121144 125917 contig of 4774 bp in length
126018 127347 contig of 1330 bp in length.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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33633 59223: contig of 25591 bp in length
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59324 83107: contig of 23684 bp in length
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112414 121413: contig of 8630 bp in length
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QY 201 CTACGCACCATTAAGACTCTGCCAGACTGAGAGCC 236
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RESULT 6
LOCUS AC063921 144833 bp DNA linear HTG 08-JAN-2003
DEFINITION Homo sapiens chromosome 3 clone RP11-142P10, WORKING DRAFT
SEQUENCE, 13 unordered pieces.
ACCESSION AC063921
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 144833)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Alsbrooks, S.L., Anarauge, H.C., Are, J.R., Ayale, M., Banks, T.,
Barbais, J., Benton, J., Bimge, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieva, M., Brown, B., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carton, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
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Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
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Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
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Li, J., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louissegh, H.,
Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapa, P., Martin, R., Martindale, A., Martinez, E.,
Massey, B., Mawhney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G.,
Oragunye, N., Oviado, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojebokan, I., Rolfe, M., Ruiz, S., Savary, G.,
Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I.,
Sodergren, B., Sonaite, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Taber, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telifrod, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczky, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 144833)
Worley, K.C.
Direct Submission
Submitted (22-APR-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 144833)
Worley, K.C.
Direct Submission
Submitted (08-JAN-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Apr 28, 2002 this sequence version replaced gi:16117924.
----- Genome Center of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HAXY
Center clone name: RP11-142P10
----- Summary Statistics
Sequencing vector: M13;
Chemistry: Dye-terminator Big Dye: 86% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 127260 bases at least Q40
Consensus quality: 132735 bases at least Q30
Consensus quality: 136183 bases at least Q20
Estimated insert size: 139078; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2437: contig of 2437 bp in length
* 2438 2537: gap of unknown length
* 2538 4812: contig of 2275 bp in length
* 4813 8488: gap of unknown length
* 4913 8488: contig of 3576 bp in length
* 8489 8589: gap of unknown length
* 8589 11163: contig of 2575 bp in length
* 11164 11263: gap of unknown length

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* 11264 16638: contig of 5375 bp in length
* 16639 gap of unknown length
* 16730 contig of 5132 bp in length
* 21870 gap of unknown length
* 21871 gap of unknown length
* 21970 gap of unknown length
* 30780 contig of 8810 bp in length
* 30880 gap of unknown length
* 30881 contig of 8387 bp in length
* 39267 gap of unknown length
* 39268 gap of unknown length
* 39368 gap of unknown length
* 46891 gap of unknown length
* 46991 gap of unknown length
* 59650 contig of 12666 bp in length
* 59657 gap of unknown length
* 59757 contig of 23553 bp in length
* 83310 gap of unknown length
* 83410 contig of 28448 bp in length
* 111858 gap of unknown length
* 111958 contig of 32876 bp in length.

FEATURES
    source
    1. 144833
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
    /chromosome="3"
    /clone="RP11-142P10"

ORIGIN
Query Match          90.88; Score 216; DB 2; Length 144833;
Best Local Similarity 100.0%; Pred. No. 6.9e-53;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AGGTGGCTCAACACCTGAGGAGCTGGACATCCCATGTTTCAGCAATGTCATGGCATCAG 80
Db 90523 AGTGGCTCAACACCTGAGGAGCTGGACATCCCATGTTTCAGCAATGTCATGGCATCAG 90582
QY 81 GAGGGCGCCCAAGGGCCCATCGTTCCTTCATGATCCATGTTCTGTTCAATTCATT 140
Db 90583 GAGGGCGCCCAAGGGCCCATCGTTCCTTCATGATCCATGTTCTGTTCAATTCATT 90642
QY 141 CATCCATACATCCACCTGCTGAGCTTTCACCTGATGCTCCCTCACTCCATCCATCAGACCT 200
Db 90643 CATCCATACATCCACCTGCTGAGCTTTCACCTGATGCTCCCTCACTCCATCCATCAGACCT 90702
QY 201 CTACGCACCAATAGACTCTGCCAGAACTGGAAGCC 236
Db 90703 CTACGCACCAATAGACTCTGCCAGAACTGGAAGCC 90738

RESULT 7
AC021981
LOCUS          149800 bp DNA linear HTG 19-JUL-2000
DEFINITION    Homo sapiens chromosome 11 clone RP11-11C15 map 11, WORKING DRAFT
SEQUENCE      29 unordered pieces.
AC021981
VERSION        AC021981.2 GI:9280747
KEYWORDS       HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 149800)
AUTHORS       Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE         Homo sapiens chromosome 11, clone RP11-11C15
JOURNAL       Unpublished
REFERENCE     2 (bases 1 to 149800)
AUTHORS       Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Bieda,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
Choepey,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferraira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Headford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K.,

```

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Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivier,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 19, 2000 this sequence version replaced gi:6731265.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1335
Center clone name: 11_C_15
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 135317 bases at least Q40
Consensus quality: 141872 bases at least Q30
Consensus quality: 144404 bases at least Q20
Insert size: 121000; agarose-fp
Insert size: 147000; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; agarose-fp
Quality coverage: 3.5 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1441: contig of 1441 bp in length
* 1442 1541: gap of 100 bp
* 1542 2883: contig of 1342 bp in length
* 2884 2983: gap of 100 bp
* 2984 4649: contig of 1666 bp in length
* 4650 4749: gap of 100 bp
* 4750 6112: contig of 1363 bp in length
* 6113 6212: gap of 100 bp
* 6213 7413: contig of 1201 bp in length
* 7414 7513: gap of 100 bp
* 7514 9050: contig of 1537 bp in length
* 9051 9150: gap of 100 bp
* 9151 10944: contig of 1794 bp in length
* 10945 11044: gap of 100 bp
* 11045 13203: contig of 2159 bp in length
* 13204 13303: gap of 100 bp
* 13304 16118: contig of 2815 bp in length
* 16119 16218: gap of 100 bp
* 16219 18673: contig of 2455 bp in length
* 18674 18773: gap of 100 bp
* 18774 21180: contig of 2407 bp in length
* 21181 21280: gap of 100 bp
* 21281 23200: contig of 1920 bp in length
* 23201 23300: gap of 100 bp
* 23301 26526: contig of 3226 bp in length
* 26527 26626: gap of 100 bp
* 26627 29655: contig of 3029 bp in length
* 29656 29755: gap of 100 bp
* 29756 34739: contig of 4983 bp in length
* 34739 34838: gap of 100 bp

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TITLE
JOURNAL
COMMENT

Center code: GTC
Web site: <http://www.genomecorp.com/>
Contact: gsc-seqcenter@genomecorp.com
----- Project Information -----
Center project name: hg202
----- Summary Statistics -----
Sequencing vector: N/A

Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 990315
Consensus quality: 152033 bases at least Q40
Consensus quality: 163535 bases at least Q30
Consensus quality: 165256 bases at least Q20
Insert size: 170446; sum-of-contigs
Quality coverage: 4.3x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1339: Contig of 1339 bp in length
1340 1439: Gap of unknown length
1440 2789: Contig of 1350 bp in length
2790 2889: Gap of unknown length
2890 4562: Contig of 1673 bp in length
4563 4662: Gap of unknown length
4663 6344: Contig of 1682 bp in length
6345 6444: Gap of unknown length
6445 9221: Contig of 2777 bp in length
9222 9321: Gap of unknown length
9322 11997: Contig of 2676 bp in length
11998 12097: Gap of unknown length
12098 14867: Contig of 2770 bp in length
14868 14967: Gap of unknown length
14968 19919: Contig of 4952 bp in length
19920 20019: Gap of unknown length
20020 24125: Contig of 4106 bp in length
24126 24225: Gap of unknown length
24226 29444: Contig of 5219 bp in length
29445 29544: Gap of unknown length
29545 34568: Contig of 5024 bp in length
34569 34668: Gap of unknown length
34670 39414: Contig of 4746 bp in length
39415 39514: Gap of unknown length
39515 45885: Contig of 6371 bp in length
45886 45985: Gap of unknown length
45986 50997: Contig of 5012 bp in length
50998 51097: Gap of unknown length
51098 59143: Contig of 8046 bp in length
59144 59243: Gap of unknown length
59244 67779: Contig of 8536 bp in length
67780 67879: Gap of unknown length
67880 76429: Contig of 8550 bp in length
76430 76529: Gap of unknown length
76530 86704: Contig of 10175 bp in length
86705 86804: Gap of unknown length
86805 103147: Contig of 16343 bp in length
103148 103247: Gap of unknown length
103248 116343: Contig of 13096 bp in length
116344 116443: Gap of unknown length
116444 135318: Contig of 18875 bp in length
135319 135418: Gap of unknown length
135419 172546: Contig of 37128 bp in length.

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="Chromosome 10"
/clone="RP11-331G19"

ORIGIN
/clone_lib="RPC1-11"
Query Match 90.8%; Score 216; DB 2; Length 172546;
Best Local Similarity 100.0%; Pred. No. 6.8e-53;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 AGGTGGCCTGAACACCTGAGGGACTGGACATCCCATGTTCCAGCAATGTCATGTCATCAG 80
DB 170778 AGGTGGCCTGAACACCTGAGGGACTGGACATCCCATGTTCCAGCAATGTCATGTCATCAG 170719
QY 81 GAGGCGGCCCAAGAGGCCCATCGCTTCCCTTCATGCATCCATTTGTTCTGTTTCATTCATT 140
DB 170718 GAGGCGGCCCAAGAGGCCCATCGCTTCCCTTCATGCATCCATTTGTTCTGTTTCATTCATT 170659
QY 141 CATCCATACATCCACCTGCTCTGAGCTTTCACCTCTGACTCCCTTAATCAGACCT 200
DB 170658 CATCCATACATCCACCTGCTCTGAGCTTTCACCTCTGACTCCCTTAATCAGACCT 170599
QY 201 CTACGCAACCAATAGACTCTGCCAGAACTGAGAAGCC 236
DB 170598 CTACGCAACCAATAGACTCTGCCAGAACTGAGAAGCC 170563
RESULT 9
AP002765/c 178169 bp DNA linear PRI 15-MAR-2003
LOCUS Homo sapiens genomic DNA, chromosome 11q clone:RP11-634B22,
DEFINITION complete sequence.
ACCESSION AP002765
VERSION AP002765.3 GI:16751488
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published Only in Database (2000)
REFERENCE 2 (bases 1 to 178169)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Nov 5, 2001 this sequence version replaced gi:12381934.
FEATURES
source
1. .178169
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q"
/clone="RP11-634B22"

ORIGIN
Query Match 90.8%; Score 216; DB 9; Length 178169;
Best Local Similarity 100.0%; Pred. No. 6.8e-53;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 AGGTGGCCTGAACACCTGAGGGACTGGACATCCCATGTTCCAGCAATGTCATGTCATCAG 80
DB 87137 AGGTGGCCTGAACACCTGAGGGACTGGACATCCCATGTTCCAGCAATGTCATGTCATCAG 87078
QY 81 GAGGCGGCCCAAGAGGCCCATCGCTTCCCTTCATGCATCCATTTGTTCTGTTTCATTCATT 140
DB 87077 GAGGCGGCCCAAGAGGCCCATCGCTTCCCTTCATGCATCCATTTGTTCTGTTTCATTCATT 87018

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QY      141  CATCCATACATCCACCTGCTCTGAGCTTTCACCTCTGACTCCCTAACTCCATCAGACCT 200
Db      87017 CATCCATACATCCACCTGCTCTGAGCTTTCACCTCTGACTCCCTAACTCCATCAGACCT 86958

QY      201  CTACGCACCATAGACTCTGCCAGAACTCAGAGAAGCC 236
Db      86957 CTACGCACCATAGACTCTGCCAGAACTCAGAGAAGCC 86922

RESULT 10
AP002749/c
LOCUS      178431 bp      DNA      linear      HTG 13-JUL-2000
DEFINITION Homo sapiens chromosome 11 clone RP11-158J21 map 11q24, WORKING
DRAFT SEQUENCE, 41 unordered pieces.
ACCESSION AP002749
VERSION   1
KEYWORDS  HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 178431)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 178,431 genomic DNA of 11q24
Published Only in DataBase (2000)
2 (bases 1 to 178431)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (10-JUL-2000) Masahira Hattori. The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-42-778-9923, Fax:81-42-778-9924)
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDraft11
Center clone name: RP11-158J21
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 155982 bases at least Q40
Consensus quality: 165758 bases at least Q30
Consensus quality: 170239 bases at least Q20
Insert size: 174431; sum-of-contigs
Quality coverage: 4.20x in Q20 bases; sum-of-contigs
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NOTE: This is a 'working draft' sequence. It currently consists of
41 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
1      13012 contig of 13012 bp in length
13113 24677 contig of 11565 bp in length
24778 34640 contig of 9863 bp in length
43297 50126 contig of 6830 bp in length
57725 57725 contig of 7499 bp in length
57826 57825 contig of 100 bp
64613 64612 contig of 6787 bp in length
64713 64712 contig of 100 bp
71000 70999 contig of 6287 bp in length
71000 70999 contig of 100 bp
71000 76188 contig of 5089 bp in length
76189 76288 contig of 100 bp
76289 83580 contig of 7292 bp in length
83581 83680 contig of 100 bp
83681 90511 contig of 6831 bp in length
90512 90511 contig of 100 bp
90612 95493 contig of 4882 bp in length
95494 95593 contig of 100 bp
95594 102262 contig of 6669 bp in length
102263 102362 contig of 100 bp
102363 105866 contig of 3504 bp in length
105867 105866 contig of 100 bp
111143 111142 contig of 5176 bp in length
111243 111242 contig of 100 bp
111243 115923 contig of 4681 bp in length
115243 116023 contig of 100 bp
116024 121747 contig of 5724 bp in length
121748 121847 contig of 100 bp
121848 125532 contig of 3685 bp in length
125533 125632 contig of 100 bp
125633 127927 contig of 2295 bp in length

```

```

103663 105866 contig of 3504 bp in length
105967 111142 contig of 5176 bp in length
111243 115923 contig of 4681 bp in length
121747 121747 contig of 5724 bp in length
121848 125532 contig of 3685 bp in length
125633 127927 contig of 2295 bp in length
128028 131184 contig of 3157 bp in length
131285 132725 contig of 1441 bp in length
132826 135566 contig of 2741 bp in length
135667 138000 contig of 2334 bp in length
138101 141194 contig of 3094 bp in length
141295 143619 contig of 2325 bp in length
143720 146448 contig of 2729 bp in length
146549 149531 contig of 2983 bp in length
149632 152157 contig of 2526 bp in length
152258 155623 contig of 3366 bp in length
155724 158334 contig of 2611 bp in length
158435 160509 contig of 2075 bp in length
160610 162343 contig of 1734 bp in length
162444 164809 contig of 2366 bp in length
164910 167036 contig of 2127 bp in length
167137 169169 contig of 2033 bp in length
169270 171052 contig of 1783 bp in length
171153 172933 contig of 1781 bp in length
171034 174180 contig of 1147 bp in length
174281 175729 contig of 1449 bp in length
175830 176905 contig of 1076 bp in length
177006 178431 contig of 1426 bp in length.

```

```

* NOTE: This is a 'working draft' sequence. It currently
* consists of 41 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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```

* 13012: contig of 13012 bp in length
* 13013 13112: gap of 100 bp
* 13113 24677: contig of 11565 bp in length
* 24678 34640: contig of 9863 bp in length
* 34641 34740: gap of 100 bp
* 34741 43196: contig of 8456 bp in length
* 43197 43296: gap of 100 bp
* 43297 50126: contig of 6830 bp in length
* 50127 50226: gap of 100 bp
* 50227 57725: contig of 7499 bp in length
* 57726 57825: gap of 100 bp
* 57826 64612: contig of 6787 bp in length
* 64613 64712: gap of 100 bp
* 64713 70999: contig of 6287 bp in length
* 71000 70999: gap of 100 bp
* 71000 76188: contig of 5089 bp in length
* 76189 76288: gap of 100 bp
* 76289 83580: contig of 7292 bp in length
* 83581 83680: gap of 100 bp
* 83681 90511: contig of 6831 bp in length
* 90512 90511: gap of 100 bp
* 90612 95493: contig of 4882 bp in length
* 95494 95593: gap of 100 bp
* 95594 102262: contig of 6669 bp in length
* 102263 102362: gap of 100 bp
* 102363 105866: contig of 3504 bp in length
* 105867 105866: gap of 100 bp
* 105967 111142: contig of 5176 bp in length
* 111143 111242: gap of 100 bp
* 111243 115923: contig of 4681 bp in length
* 115243 116023: gap of 100 bp
* 116024 121747: contig of 5724 bp in length
* 121748 121847: gap of 100 bp
* 121848 125532: contig of 3685 bp in length
* 125533 125632: gap of 100 bp
* 125633 127927: contig of 2295 bp in length

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Db      59095 CTACGACCATAGACTCTGCCAGAACTGAGAGGCC 59060
|||||
AB097521 3296 bp mRNA linear PRI 06-DEC-2002
Macaca fascicularis brain cDNA clone: QmoA-13657, full insert
sequence.
AB097521
ACCESSION GI:26449236
VERSION
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Macaca fascicularis (crab-eating macaque)
ORGANISM Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
1
REFERENCE
AUTHORS Oeada, N., Hida, M., Kusuda, J., Tanuma, R., Iseki, K., Hirata, M.,
Suto, Y., Hirai, M., Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K.
TITLE Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
chromosomes
JOURNAL Gene 275 (1), 31-37 (2001)
MEDLINE 21458551
PUBMED 11574149
REFERENCE
2 (bases 1 to 3296)
HASHIMOTO, K., Oeada, N., Hida, M., Kusuda, J. and Sugano, S.
Direct Submission
Submitted (05-DEC-2002) Katsuyuki Hashimoto, National Institute of
Infectious Diseases, Division of Genetic Resources, 23-1, Toyama
1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
[E-mail: khash@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/,
Tel: 81-3-5285-1111 (ex.2120), Fax: 81-3-5285-1181]
Lab host: TOP10
Vector: pME18S-FL3 (Acc.No. AB009864)
R. Site1: DraIII (CACTGTGTG)
R. Site2: DraIII (CACCATGTG)
Description: 1st strand cDNA was primed with an oligo(dT) primer
[ATGCGCGTTTATTTTATTTT]; double-stranded cDNA was synthesized
using specific 5' and 3' primers and amplified by PCR. The PCR
product was digested with SfiI and size selection was performed to
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned
into distinct DraIII sites of pME18S-FL3. XhoI sites just outside
the DraIII sites can be used to isolate the cDNA insert. Libraries
were constructed by oligo-capping method. Custom primers used for
sequencing ( 5' end primer [CTTCTGCTCTAAAGGCTGG];
3' end primer [CGACCTGCAGCTCGAGCACA] ).
FEATURES
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/clone="QmoA-13657"
/sex="male"
/tissue_type="medulla oblongata"
/clone_lib="macaque brain cDNA library QmoA"
/dev_stage="adult"
6..653
/codon_start=1
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/db_xref="GI:26449237"
/translation="WPAFNRFLPPLVSLVLIYNASVCFVVCVVPSETEAQNPKMLR
CISCKMREVEATVVEYRFGKGLFLIYRNHQVEFSPFQGRQWNGSKDLQD
VSTLVNLVNSGLYTCNVSREFEFAHRPFVKTRLPLRTEAGEDFTSVVSEI
MMYILLVFLTLMLLIEMIYCRKSKAEAAQENASDYLAIPSENKENSAPVVE"
ORIGIN
Query Match 85.5%; Score 203.6; DB 9; Length 3296;
Best Local Similarity 94.5%; Pred. No. 4e-49;
Matches 223; Conservative 0; Mismatches 9; Indels 4; Gaps 1;
QY 1 AACAGGAGCAGTGTGACATGAGTGGCTGGAACACCTGAGGGACTGGACATCCCATGTTTC 60
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654 AACAGGAGCAGTGTGACATGAGTGGCTGGAACACCTGAGGACTGGACATCCCATGTTTC 713
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61 AGCAATGTCAATGGCATCAGAGGGGGCCCCAAGGGCCCCCATCGCTTCCCTTCATGCATC 120
|||||
714 AGCAATGTCAATGGCATCAGAGGGGGCCCCAAGGGTCCCATTCATCCCTTCATGCATC 773
|||||
121 CATTGTTCTGTTCAATTCATTCATCCATCATCCACTGCCTCTGAGCTTTACCTCTGAC 180
|||||
774 CATCCTTCT- - -ATTCAATTCATCCATCATCCACTGCCTCTGAGCTTTACCTCTGAC 829
|||||
181 TCCCTAACTCCATCAGACCTCTACCCACCATAGACTCTGCCAGAACTCAGAGGCC 236
|||||
830 TTCCTAACTCCATCAGACCTCTACCTAGTACCAAGACTCTGCCAGAACTCAGAGGCC 885
|||||
RESULT 13
AC145484 174285 bp DNA linear HTG 17-JUL-2003
LOCUS Lemur catta clone LB2-244B5, WORKING DRAFT SEQUENCE, 3 ordered
DEFINITION pieces.
ACCESSION AC145484
VERSION AC145484.1 GI:32880237
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE Lemur catta (ring-tailed lemur)
ORGANISM Lemur catta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Lemur.
1 (bases 1 to 174285)
AUTHORS Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
Peng, Z., Malinov, I. and Rubin, E.M.
Direct Submission
Unpublished
2 (bases 1 to 174285)
AUTHORS Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
Peng, Z., Malinov, I. and Rubin, E.M.
Direct Submission
Submitted (17-JUL-2003) Genome Sciences, Lawrence Berkeley National
Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
Sequence Produced by Berkeley PGA
Web site: http://pga.lbl.gov
Center Code: PGABERK
Center Project Name: L133
Bac Clone Name: LB2-244B5
This sequence has been compared to sequences of other species
using Vista (http://www-gsd.lbl.gov/VISTA). The results can be
viewed at:
http://pga.lbl.gov/cgi-bin/search_cvcgd?type=nvalue=ZNF202
The order-orientation of the draft sequence was accomplished by
using:
Avid (http://baboon.math.berkeley.edu/mavid),
Lagan (http://lagan.stanford.edu/) and paired end information.
Funding agent: Programs for Genomic Applications (NHLBI)
If the Bac Library Name is LB1 to LB4, please see website
for the description: http://www-gsd.lbl.gov/cheng/BAC.html
These libraries are available through the BACPAC Resources Center:
http://www.chori.org/bacpac/libraryres.htm as LBNU-1 to LBNU-4.
Summary Statistics:
Sequencing vector: plasmid; pUC18
Chemistry: Dye-terminator Big Dye
Assembly program: Phrap version 0.990329.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.

```


* 20971 21671: contig of 701 bp in length
* 21672 21771: gap of 100 bp
* 21772 22480: contig of 709 bp in length
* 22481 22580: gap of 100 bp
* 22581 23293: contig of 713 bp in length
* 23294 23393: gap of 100 bp
* 23394 24095: contig of 702 bp in length
* 24096 24195: gap of 100 bp
* 24196 24917: contig of 721 bp in length
* 24917 25017: gap of 100 bp
* 25017 25727: contig of 710 bp in length
* 25727 25826: gap of 100 bp
* 25827 26534: contig of 708 bp in length
* 26535 26634: gap of 100 bp
* 26635 27333: contig of 699 bp in length
* 27334 27433: gap of 100 bp
* 27434 28131: contig of 698 bp in length
* 28132 28231: gap of 100 bp
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* 32184 32284: gap of 100 bp
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* 32982 33081: gap of 100 bp
* 33082 33798: contig of 717 bp in length
* 33799 33898: gap of 100 bp
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* 35434 35533: gap of 100 bp
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* 36354 37079: contig of 726 bp in length
* 37080 37179: gap of 100 bp
* 37180 37893: contig of 714 bp in length
* 37894 37993: gap of 100 bp
* 37994 38700: contig of 707 bp in length
* 38701 38800: gap of 100 bp
* 38801 39505: contig of 705 bp in length
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* 39606 40316: contig of 711 bp in length
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* 41940 42039: gap of 100 bp
* 42040 42748: contig of 709 bp in length
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* 50062 50751: contig of 690 bp in length

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* 50852 51567: contig of 716 bp in length
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* 52401 52500: gap of 100 bp
* 52501 53225: contig of 725 bp in length
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* 53326 53974: contig of 649 bp in length
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* 56427 56526: gap of 100 bp
* 56527 57244: contig of 718 bp in length
* 57245 57344: gap of 100 bp
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* 58152 58860: contig of 709 bp in length

Query Match 45.4%; Score 108; DB 2; Length 66980;
Best Local Similarity 96.7%; Pred. No. 4.9e-21;
Matches 119; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 114 ATGCATCCATTGTTCTGTTTCATTTCATTCATCATCATCCACCTGCTGAGCTTTTCAC 173
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QY 174 CTCTGACTCCCTTAACCTCCATCAGACCTCTAGCACCATAAGACTCTGCAGAACTGAGAA 233
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Db 53166 CTTGACTCCCTTAACCTCCATCAGACCTTAGCACCATAAGACTCTGCAGAACTGAGAA 53107
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QY 234 GCC 236
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Db 53106 GCC 53104

RESULT 15
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LOCUS
DEFINITION Rattus norvegicus clone CH230-287P8, *** SEQUENCING IN PROGRESS
AC114854 linear HTG 15-NOV-2002
Rattus norvegicus
AC114854
AC114854.4 GI:25007034
VERSION HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 189486)
Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Ayodeji, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
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Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
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Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W.,
Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M.,
Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,

Karpthy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulsged, H., Lozano, R.J., Lu, X., Ma, J., Maheshwari, M., Mahndartine, M., Mahmood, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Minor, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokemele, O., Okwunonu, G., Olarunpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajda, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiser, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstein, G. and Gibbs, R.A.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

ORIGIN

Query Match 19.9%; Score 47.4; DB 2; Length 189486;
 Best Local Similarity 63.7%; Pred. No. 0.0034;
 Matches 72; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 99 CCATCGCTTCCCTTCATGCATCCATTCCTGTTCTGTTTCATTCATCCATCCACCTG 158
 Db 125370 CCACATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 125429

QY 159 CCTCTGAGCTTTTCACCTTCGACTCCCTTAAGTCCATCCATCCATCCATCCATCC 211
 Db 125430 ACTCATCCATTTCACTGTTTCATCTCTATCCATAAATCATCCACTTACTAT 125482

Search completed: April 7, 2005, 12:50:07
 Job time : 1140.27 secs

FEATURES

source

1. 189486

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/db_xref="taxon:10116"

/clone="CH230-287P8"

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/notes="clone boundary"

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site:

end sequence:RXAHT88TV"

7765..9270

/notes="wgs contig"

21532..23046

/notes="wgs contig"

94040..94123

/notes="clone boundary"

clone_end:T7

end sequence:BZ135992"

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: GSNV

Center clone name: CH230-287P8

Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 168507 bases at least Q40

Consensus quality: 171284 bases at least Q30

Consensus quality: 173231 bases at least Q20

Estimated insert size: 174384; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 1 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 189486: contig of 189486 bp in length.

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 06:13:29 ; Search time 172.885 Seconds
(without alignments)
8149.338 Million cell updates/sec

Title: US-09-977-579-4_COPY_1024_1261

Perfect score: 238

Sequence: 1 aacaggagcagtgtgacatg.....tgccagaactgagaagccgg 238

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
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9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	238	100.0	1261	3	AAC67837 Human bet
2	238	100.0	1261	10	ADB78651 Human ion
3	238	100.0	1261	10	ACF57870 Human SCN
4	236	99.2	1510	4	Aaf84146 Human nov
5	236	99.2	4052	6	ABA91727 Human sig
6	216	90.8	4625	4	AAL04971 Human rep
7	216	90.8	4625	4	ABL97864 Human tes
8	131.8	55.4	493	13	ADQ55080 Novel can
9	40.6	17.1	220756	12	ADG86300 Human SMR
10	40.6	17.1	233380	11	ACN44282 Human gen
11	38.6	16.2	11089	4	AAK79653 Human imm
12	38	16.0	26891	11	ADL27167 Mouse gen
13	38	16.0	27079	9	ADA03089 Mouse lfn
14	38	16.0	27079	9	ADA66373 Mouse lfn
15	38	16.0	27079	10	ADB72827 Mouse lfn
16	38	16.0	38360	6	Abq75124 Human pl5
17	37.8	15.9	3768	6	ABL69598 Prostate
18	37.8	15.9	3768	6	ABL63103 Breast ca
19	37.8	15.9	3768	6	ABL62894 Breast ca
20	37.8	15.9	3768	6	ABK64794 Human ben

c	21	37.8	15.9	3768	8	ACA64938	ACA64938 Human myo
c	22	37.8	15.9	3768	11	ADP65339	ADP65339 Human myo
c	23	37.8	15.9	8222	8	ACF62757	ACF62757 Human myo
c	24	37.8	15.9	8222	8	ACF62815	ACF62815 Colon can
c	25	37.8	15.9	8222	8	ACF62793	ACF62793 Colon can
c	26	37.8	15.9	11222	10	ADB54189	ADB54189 Pretreate
c	27	37.8	15.9	11222	10	ADB54001	ADB54001 MB genomi
c	28	37.8	15.9	11222	10	ADB54317	ADB54317 Pretreate
c	29	37.6	15.8	1367	3	AAA81673	AAA81673 N. mening
c	30	37.4	15.7	1576	4	AAK73497	AAK73497 Human imm
c	31	37.4	15.7	7954	4	AAK73498	AAK73498 Human imm
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c	33	37	15.5	2632	5	AAC90602	AAC90602 Rat sodiu
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c	39	36.6	15.4	4747	4	ABL98092	ABL98092 Human tes
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c	44	36.4	15.3	140152	12	ADP03002	ADP03002 Human hou
c	45	36.4	15.3	140152	13	ADS88500	ADS88500 Human hou

ALIGNMENTS

RESULT 1

AAC67837
ID AAC67837 standard; cDNA; 1261 BP.

XX AAC67837;

DT 15-FEB-2001 (first entry)

XX Human beta3 CDNA.

XX Human; beta sub-unit; beta3; analgesic; anticonvulsant;
KW cerebroprotective; vasotropic; cardiant; nootropic; cytostatic;
KW dermatological; gene therapy; voltage-gated sodium channel; pain;
KW epilepsy; stroke; ischaemia; heart disease; Jacobsen Syndrome;
KW familial nonchromaffin paraganglioma; phenylketonuria;
KW Charcot Marie Tooth disease; ss.

XX Homo sapiens.

XX WO200063367-A1.

XX 26-OCT-2000.

XX 24-FEB-2000; 2000WO-EP001783.

XX 15-APR-1999; 99US-0129473P.

XX (WARN) WARNER LAMBERT CO.

XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX Cox P, Dixon A, Jackson A, Morgan K;

XX WPI; 2000-665241/64.

XX P-PSDB; AAB36002.

XX Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium channel, and their corresponding polypeptides, useful for detecting and treating sodium channel-associated conditions, e.g. pain, epilepsy and stroke.

XX Claim 10; Page 70-71; 88pp; English.

XX The present sequence is given in the claims of a specification relating

CC to a novel family of beta sub-unit proteins from a voltage-gated sodium
CC channel. Human and rat beta sub-units, which have been collectively
CC identified as beta3, have been isolated. The polynucleotides and
CC polypeptides are useful for screening for agonists and antagonists of
CC sodium channels. The agonists, antagonists, proteins and nucleic acids
CC may be used diagnosing of treating diseases or conditions associated with
CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,
CC heart disease, Jacobson Syndrome, Familial Nonchromaffin Paraganglioma,
CC Phenylketonuria and Charcot Marie Tooth disease
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XX Sequence 1261 BP; 263 A; 366 C; 372 G; 260 T; 0 U; 0 Other;

Query Match 100.0%; Score 238; DB 3; Length 1261;
Best Local Similarity 100.0%; Pred. No. 6.4e-69;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACAGGAGCAGTGTGACATGAGTGGCTTGAACACCTGAGGAGCTGGACATCCCATGTTTC 60
DB 1024 AACAGGAGCAGTGTGACATGAGTGGCTTGAACACCTGAGGAGCTGGACATCCCATGTTTC 1083
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DB 1084 AGCAATGTCAATGGCATGAGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1143
QY 121 CATTGTTCTGTTTCATTTCATTCATCCATATCCACCTGGCTCTGAGCTTTACCTCTGAC 180
DB 1144 CATTGTTCTGTTTCATTTCATTCATCCATATCCACCTGGCTCTGAGCTTTACCTCTGAC 1203
QY 181 TCCTTAACCTCCATCAGACCTCTACGCACCATTAAGACTCTGCCAGAACTGAGAGCGGG 238
DB 1204 TCCTTAACCTCCATCAGACCTCTACGCACCATTAAGACTCTGCCAGAACTGAGAGCGGG 1261

RESULT 2
ADB78651
ID ADB78651 standard; cDNA; 1261 BP.
XX ADB78651;
XX ADB78651;
DT 04-DEC-2003 (first entry)
DE Human ion channel subunit cDNA mutant SCN1A exon 1 SEQ ID NO:22.
XX ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyrretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquilizer; analgesic;
KW nephrotoxic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX Synthetic.
OS Homo sapiens.
XX WO2003008574-A1.
XX 30-JAN-2003.
XX 08-JUL-2002; 2002WO-AU000910.
XX 18-JUL-2001; 2001AU-00006452.
XX 13-MAY-2002; 2002AU-00000910.
XX 13-MAY-2002; 2002AU-00002292.
XX (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX WPI; 2003-239332/23.
XX Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene

PT mutation events.
XX Claim 6; SEQ ID NO 22; 106pp; English.
XX The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyrretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquilizer, analgesic, nephrotoxic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant cDNA of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
XX Sequence 1261 BP; 263 A; 365 C; 372 G; 261 T; 0 U; 0 Other;

Query Match 100.0%; Score 238; DB 10; Length 1261;
Best Local Similarity 100.0%; Pred. No. 6.4e-69;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACAGGAGCAGTGTGACATGAGTGGCTTGAACACCTGAGGAGCTGGACATCCCATGTTTC 60
DB 1024 AACAGGAGCAGTGTGACATGAGTGGCTTGAACACCTGAGGAGCTGGACATCCCATGTTTC 1083
QY 61 AGCAATGTCAATGGCATGAGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 120
DB 1084 AGCAATGTCAATGGCATGAGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1143
QY 121 CATTGTTCTGTTTCATTTCATTCATCCATATCCACCTGGCTCTGAGCTTTACCTCTGAC 180
DB 1144 CATTGTTCTGTTTCATTTCATTCATCCATATCCACCTGGCTCTGAGCTTTACCTCTGAC 1203
QY 181 TCCTTAACCTCCATCAGACCTCTACGCACCATTAAGACTCTGCCAGAACTGAGAGCGGG 238
DB 1204 TCCTTAACCTCCATCAGACCTCTACGCACCATTAAGACTCTGCCAGAACTGAGAGCGGG 1261

RESULT 3
ACF57870
ID ACF57870 standard; cDNA; 1261 BP.
XX ACF57870;
XX ACF57870;
DT 15-JAN-2004 (first entry)
XX Human SCN3B protein encoding cDNA.
XX SCN3B; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
KW neuroprotective; anesthetic; cytotatic; cerebroprotective; cardiant;
KW hypertensive; gene therapy; SCN3B; human; gene; ss.
XX Homo sapiens.
XX Location/Qualifiers
FH Key 376..1023
FT CDS /*tag= a
FT /product= "SCN3B"

XX WO2003072751-A2.
 XX 04-SEP-2003.
 XX 25-FEB-2003; 2003WO-US006010.
 XX 25-FEB-2002; 2002US-0359382P.
 XX (UYVA-) UNIV VANDERBILT.
 XX George AL, Lossin C;
 XX WPI; 2003-712725/67.
 XX P-PSDB; ABR83183.
 XX Recombinantly expressed sodium channel type 1 alpha subunit, useful in
 XX screening for modulators, for treating e.g. epilepsy.
 XX Disclosure; Page 145-147; 176pp; English.
 XX The invention relates to a recombinantly expressed and isolated human
 XX SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
 XX incorporated into a cell, is used to screen for specific modulators,
 XX potentially useful as anticonvulsant, antiepileptic, neuroprotective,
 XX analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
 XX epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
 XX motor endplate diseases, hypertension, congestive heart failure and
 XX muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
 XX and metastatic cancer cell lines). These activities can also be provided
 XX by gene therapy vectors that express (I) or the modulators. The
 XX modulators, also antibodies directed against (I), are used to detect
 XX sodium channel polypeptides. The present sequence represents a human
 XX SCN3B protein encoding cDNA

SQ Sequence 1261 BP; 263 A; 366 C; 372 G; 260 T; 0 U; 0 Other;
 Query Match 100.0%; Score 238; DB 10; Length 1261;
 Best Local Similarity 100.0%; Pred. No. 6.4e-69;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACAGAGCAGTGTGACATGAGTGGCTGCTGAACACCTGAGGGACTGACATCCCATGTTTC 60
 DB 1024 AACAGAGCAGTGTGACATGAGTGGCTGCTGAACACCTGAGGGACTGACATCCCATGTTTC 1083

QY 61 AGCAATGTCATGTCATGAGGAGGGGCGCCCAAGGGCCCCATCGCTTCCCTTCATGCATC 120
 DB 1084 AGCAATGTCATGTCATGAGGAGGGGCGCCCAAGGGCCCCATCGCTTCCCTTCATGCATC 1143

QY 121 CATTGTTCTGTTCAATTCATTTCATCCATACATCCACCTGCGCTCTGAGCTTTTCACCTCTGAC 180
 DB 1144 CATTGTTCTGTTCAATTCATTTCATCCATACATCCACCTGCGCTCTGAGCTTTTCACCTCTGAC 1203

QY 181 TCCTTAACCTCAGACCTCTAGGACCATAGAGCTCTGCCAGAACTGAGAGCGCG 238
 DB 1204 TCCTTAACCTCAGACCTCTAGGACCATAGAGCTCTGCCAGAACTGAGAGCGCG 1261

RESULT 4
 AAF84146
 ID AAF84146 standard; cDNA; 1510 BP.
 XX
 AC AAF84146;
 XX
 DT 07-SEP-2001 (first entry)
 XX Human novel sodium channel betal-like subunit encoding cDNA.
 XX Sodium channel; sensory neurone specific channel; betal-like subunit;
 XX SNS; therapeutic; pain; analgesic; ss.
 XX Homo sapiens.
 OS
 XX

XX Key Location/Qualifiers
 CDS 213..860
 FT /*tag= a
 FT /product= "sodium channel betal-like subunit"
 XX
 XX WO200144293-A2.
 XX 21-JUN-2001.
 XX 14-DEC-2000; 2000WO-GB004802.
 XX 17-DEC-1999; 99GB-00029970.
 XX (GLAX) GLAXO GROUP LTD.
 XX Plumpton M, Powell AJ, Sanseau P;
 XX WPI; 2001-398139/42.
 XX P-PSDB; AAB85206.
 XX Novel sub-unit for voltage-gated sodium channel proteins for producing
 XX agents useful for treating pain.
 XX Claim 4; Page 29-30; 31pp; English.
 XX The invention provides a novel betal-like sub-unit for voltage-gated
 XX sodium ion channel polypeptide, specifically a sensory neurone specific
 XX channel (SNS) subunit. The novel betal-like subunit is useful for
 XX producing a therapeutic agent which is useful treating pain in a patient.
 XX The subunit can be expressed by standard recombinant methodology. The
 XX present sequence represents a human novel sodium channel betal-like
 XX subunit encoding cDNA

SQ Sequence 1510 BP; 350 A; 410 C; 414 G; 336 T; 0 U; 0 Other;
 Query Match 99.2%; Score 236; DB 4; Length 1510;
 Best Local Similarity 100.0%; Pred. No. 3.2e-68;
 Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACAGAGCAGTGTGACATGAGTGGCTGACACCTGAGGGAGTGGACATCCCATGTTTC 60
 DB 861 AACAGAGCAGTGTGACATGAGTGGCTGACACCTGAGGGAGTGGACATCCCATGTTTC 920

QY 61 AGCAATGTCATGTCATGAGGAGGGGCGCCCAAGGGCCCCATCGCTTCCCTTCATGCATC 120
 DB 921 AGCAATGTCATGTCATGAGGAGGGGCGCCCAAGGGCCCCATCGCTTCCCTTCATGCATC 980

QY 121 CATTGTTCTGTTCAATTCATTTCATCCATACATCCACCTGCGCTCTGAGCTTTTCACCTCTGAC 180
 DB 981 CATTGTTCTGTTCAATTCATTTCATCCATACATCCACCTGCGCTCTGAGCTTTTCACCTCTGAC 1040

QY 181 TCCTTAACCTCAGACCTCTAGGACCATAGAGCTCTGCCAGAACTGAGAGGCC 236
 DB 1041 TCCTTAACCTCAGACCTCTAGGACCATAGAGCTCTGCCAGAACTGAGAGGCC 1096

RESULT 5
 ABA93727
 ID ABA93727 standard; cDNA; 4052 BP.
 XX
 AC ABA93727;
 XX
 DT 30-APR-2002 (first entry)
 XX Human signal transduction cDNA clone amy2_2f18.
 XX Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
 XX gene therapy; ss.
 XX Homo sapiens.
 OS
 XX WO200198454-A2.
 XX

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PD 27-DEC-2001.
XX
XX 25-APR-2001; 2001WO-IB002050.
XX
XX 25-APR-2000; 2000US-0199380P.
XX
XX (GEHU-) GERMAN HUMAN GENOME PROJECT.
XX
XX WIEMANN S;
XX
XX WPI: 2002-055860/07.
XX P-PSDB; ABB05689.
XX
XX Human cDNA sequences and clones derived from human fetal brain, fetal
XX kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
XX screening and therapy.
XX
XX Claim 1; Page 174-175; 611pp; English.
XX
XX The present invention describes assemblages and computer readable media
XX comprising novel human cDNA sequences and clones derived from human
XX foetal brain, foetal kidney, melanoma, testis and amygdala cDNA
XX libraries. ABA93702 to ABA93766 represent human cDNA sequences from the
XX present invention which encode the proteins given in ABB05662 to
XX ABB05729. The human cDNA sequences and clones can be used in gene
XX therapy. The clones may be used in a variety of applications, for example
XX they may be used in profiling assays, for providing large arrays of human
XX genetic material for implementing large-scale screening strategies and
XX for treating diseases via gene therapy procedures
XX
XX Sequence 4052 BP; 994 A; 1033 C; 1036 G; 989 T; 0 U; 0 Other;
XX
Query Match 99.2%; Score 236; DB 6; Length 4052;
Best Local Similarity 100.0%; Pred. No. 4.8e-68;
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACAGGAGCAGTGTGACATGAGTGGCTTGACACCTGAGGAGCTGGACATCCCATGTC 60
DB 1452 AACAGGAGCAGTGTGACATGAGTGGCTTGACACCTGAGGAGCTGGACATCCCATGTC 1511
QY 61 AGCAATGTCAATGGCATCAGGAGGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGCATC 120
DB 1512 AGCAATGTCAATGGCATCAGGAGGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGCATC 1571
QY 121 CATTTGTTCTGTTCAATTCATTCATCCATATCCATATCCATCCATCCATCCATCCATC 180
DB 1572 CATTTGTTCTGTTCAATTCATTCATCCATATCCATATCCATCCATCCATCCATCCATC 1631
QY 181 TCCCTAACTCCATCAGACCTTACGACCATTAAGACTCTGCCAGAACTGAGAAGCC 236
DB 1632 TCCCTAACTCCATCAGACCTTACGACCATTAAGACTCTGCCAGAACTGAGAAGCC 1687

RESULT 6
AL04971
ID AAL04971 standard; DNA; 4625 BP.
XX
XX AAL04971;
XX
XX 21-NOV-2001 (first entry)
XX
XX Human reproductive system related antigen DNA SEQ ID NO: 7659.
XX
XX Human; reproductive system related antigen; reproductive system disorder;
XX cancer; gene therapy; ds.
XX
XX Homo sapiens.
XX
XX WO200155320-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001339.
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XX 31-JAN-2000; 2000US-0179065P.
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XX 04-FEB-2000; 2000US-0180628P.
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XX 24-FEB-2000; 2000US-0184664P.
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XX 02-MAR-2000; 2000US-0186350P.
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XX 16-MAR-2000; 2000US-0189874P.
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XX 17-MAR-2000; 2000US-0190076P.
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XX 18-APR-2000; 2000US-0198123P.
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XX 19-MAY-2000; 2000US-0205515P.
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XX 07-JUN-2000; 2000US-0209467P.
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XX 28-JUN-2000; 2000US-0214886P.
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XX 30-JUN-2000; 2000US-0215135P.
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XX 11-JUL-2000; 2000US-0217487P.
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XX 23-AUG-2000; 2000US-0227182P.
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XX 05-SEP-2000; 2000US-0229509P.
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XX 06-SEP-2000; 2000US-0230437P.
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XX 08-SEP-2000; 2000US-0231413P.
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XX 08-SEP-2000; 2000US-0232080P.
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XX 12-SEP-2000; 2000US-0231968P.
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XX 14-SEP-2000; 2000US-0232400P.
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XX 14-SEP-2000; 2000US-0233065P.
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XX 21-SEP-2000; 2000US-0234223P.
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XX 25-SEP-2000; 2000US-0234997P.
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XX 27-SEP-2000; 2000US-0235834P.
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XX 27-SEP-2000; 2000US-0235835P.
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XX 29-SEP-2000; 2000US-0236327P.
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XX 29-SEP-2000; 2000US-0236367P.
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PR	02-OCT-2000;	2000US-0236802P.
PR	02-OCT-2000;	2000US-0237037P.
PR	02-OCT-2000;	2000US-0237038P.
PR	02-OCT-2000;	2000US-0237039P.
PR	02-OCT-2000;	2000US-0237040P.
PR	13-OCT-2000;	2000US-0239353P.
PR	13-OCT-2000;	2000US-0239357P.
PR	20-OCT-2000;	2000US-0240360P.
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PR	20-OCT-2000;	2000US-0241785P.
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PR	17-NOV-2000;	2000US-0249244P.
PR	17-NOV-2000;	2000US-0249245P.
PR	17-NOV-2000;	2000US-0249264P.
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PR	17-NOV-2000;	2000US-0249267P.
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PR	17-NOV-2000;	2000US-0249300P.
PR	01-DEC-2000;	2000US-0250160P.
PR	03-DEC-2000;	2000US-0250391P.
PR	05-DEC-2000;	2000US-0250390P.
PR	05-DEC-2000;	2000US-0251988P.
PR	06-DEC-2000;	2000US-0256719P.
PR	06-DEC-2000;	2000US-0251479P.
PR	08-DEC-2000;	2000US-0251856P.
PR	08-DEC-2000;	2000US-0251868P.
PR	08-DEC-2000;	2000US-0251869P.
PR	08-DEC-2000;	2000US-0251989P.
PR	11-DEC-2000;	2000US-0251990P.
PR	05-JAN-2001;	2000US-0254097P.
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX	Rosen CA, Barash SC, Ruben SM;	
XX	WPI; 2001-465570/50.	
XX	Isolated nucleic acid molecule e	
PT	used in preventing, treating or	

XX	Disclosure; SEQ ID NO 7659; 1297pp + Sequence Listing; English.
XX	The present invention provides the protein and coding sequences of a
CC	number of human reproductive system related antigens. These can be used
CC	in the prevention and treatment of reproductive system disorders,
CC	including cancer. The present sequence is a genomic sequence encoding a
CC	protein of the invention
XX	
SQ	Sequence 4625 BP; 1222 A; 1130 C; 906 G; 1367 T; 0 U; 0 Other;
	Query Match 90.8%; Score 216; DB 4; Length 4625;
	Best Local Similarity 100.0%; Pred. No. 2.5e-61;
	Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	21 AGGTGGGCTCAACACACTTGAGGGAGTGCACATCCCATGTTTCAGCAATGTCATGGCATCAG 80
DB	33 AGGTGGGCTGAACACACTTGAGGGAGTGCACATCCCATGTTTCAGCAATGTCATGGCATCAG 92
QY	81 GAGGGGCCCCAAAGGGCCCCATCGCTTCCCCTTCATGCATCAATTGTTCTGTTTCATTCATT 140
DB	93 GAGGGGCCCCAAAGGGCCCCATCGCTTCCCCTTCATGCATCAATTGTTCTGTTTCATTCATT 152
QY	141 CATCCATACATCCACCTGCTGCTCTGAGCTTTTCACCTCTGACTCCCTAATCCATCAGACCT 200
DB	153 CATCCATACATCCACCTGCTGCTCTGAGCTTTTCACCTCTGACTCCCTAATCCATCAGACCT 212
QY	201 CTAGGCACCATAAGACTCTGCCAGAAGCTGAGAAGCC 236
DB	213 CTAGGCACCATAAGACTCTGCCAGAAGCTGAGAAGCC 248
RESULT 7	
ABL97864	
ID	ABL97864 standard; DNA; 4625 BP.
XX	
AC	ABL97864;
XX	
DT	21-JUN-2002 (first entry)
XX	
DE	Human testicular antigen encoding DNA fragment SEQ ID NO: 2516.
XX	
KW	Human; testicular antigen; testes; cancer; metastasis; immune disorder;
KW	reproductive system disorder; urinary system disorder; gene therapy;
KW	cardiovascular disorder; respiratory disorder; neurological disorder;
KW	gastrointestinal disease; infection; cytostatic; gene; ds.
XX	
OS	Homo sapiens.
XX	
FN	WO200155317-A2.
XX	
PD	02-AUG-2001.
XX	
PF	17-JAN-2001; 2001WO-US001329.
XX	
PR	31-JAN-2000; 2000US-0179065P.
PR	04-FEB-2000; 2000US-0180628P.
PR	24-FEB-2000; 2000US-0184664P.
PR	02-MAR-2000; 2000US-0186350P.
PR	16-MAR-2000; 2000US-0189874P.
PR	17-MAR-2000; 2000US-0190076P.
PR	18-APR-2000; 2000US-0198123P.
PR	19-MAY-2000; 2000US-0205515P.
PR	07-JUN-2000; 2000US-0209467P.
PR	28-JUN-2000; 2000US-0214886P.
PR	30-JUN-2000; 2000US-0215135P.
PR	07-JUL-2000; 2000US-0216647P.
PR	07-JUL-2000; 2000US-0216880P.
PR	11-JUL-2000; 2000US-0217487P.
PR	11-JUL-2000; 2000US-0217496P.
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PR	26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
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 PR 18-AUG-2000; 2000US-0226279P.
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 PR 22-AUG-2000; 2000US-0226686P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 06-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232337P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.

PR 08-NOV-2000; 2000US-0246477P.
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 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
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 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-483426/52.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 useful for preventing, diagnosing and/or treating cancers and metastasis.
 PS Disclosure; SEQ ID NO 34465; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 activity, and can be used in gene therapy and vaccine production. (I)
 proteins and polynucleotides may be used in the prevention, diagnosis and
 treatment of diseases associated with inappropriate (I) expression. For
 example, they may be used to treat disorders associated with decreased
 expression by rectifying mutations or deletions in a patient's genome
 that affect the activity of (I) by expressing inactive proteins or to
 supplement the patients own production of (I). Additionally, (I)
 polynucleotides may be used to produce the secreted (I), by inserting the
 nucleic acids into a host cell and culturing the cell to express the
 protein. (I) proteins and polynucleotides may be used to prevent,
 diagnose and treat immune/hematopoietic-related diseases, especially
 cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 to AAK87694 represent human immune/hematopoietic antigen genomic
 sequences from the present invention. AAK54942 to AAK54950 and AAM82169

Query Match 16.0%; Score 38; DB 9; Length 27079;
Best Local Similarity 57.6%; Pred. No. 0.17;
Matches 68; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 104 GCTTCCTTCATGCATCCATTTGCTTCATTCATTCATCCATCCATCCATCCCTCTCT 163
DB 3703 GCTTCCTTCATGCATCCATTTGCTTCATTCATTCATCCATCCATCCATCCATCCAT 3762

QY 164 GAGCTTTACCTCTGACTCCCTCACTCCATCAGACCTCTACGACCATAGACTCTGC 221
DB 3763 CCAACATCCCATCTGTCTCCCTCCACCCACCATCATCATCTCCATCCATCCATCCAT 3820

RESULT 14

ADA66373

ID ADA66373 standard; DNA; 27079 BP.

XX AC

XX AC ADA66373;

XX DT

XX DT 20-NOV-2003 (first entry)

XX DE

XX DE Mouse Lfng gene genomic DNA sequence.

XX carcinoma-associated gene; CA gene; Rorc gene; MCG15938 gene; BAT1 gene;
XX Igga1 gene; IQGAP1 gene; Zfp29 gene; hCG27579 gene; Kcnj9 gene;
XX Kcnj9 gene; Ppp3cc gene; Ppp3cc gene; MCG9110 gene; hCG27579 gene;
XX cancer cell; lymphatic cell; breast cell; prostate cell; epithelial cell;
XX carcinoma-associated protein; CAP; cytoskeletal; gene therapy; anticancer;
XX vaccine; carcinoma; lymphoma carcinoma; lymphatic cancer; breast cancer;
XX prostate cancer; DNA vaccine; animal model; mouse; murine; ds; Lfng.

XX OS

XX OS Mus sp.

XX PN

XX PN WO2003052224-A2.

XX PD

XX PD 03-JUL-2003.

XX PF

XX PF 20-DEC-2002; 2002WO-US041776.

XX PR

XX PR 20-DEC-2001; 2001US-00034650.

XX PA

XX PA (SAGR-) SAGRES DISCOVERY.

XX PI

XX PI Morris DW, Engelhard EK;

XX DR

XX DR WPI; 2003-569168/53.

XX Novel recombinant carcinoma-associated nucleic acid, useful for
XX evaluating the effect of a candidate carcinoma drug, and for diagnosing
XX carcinoma.

XX PS

XX PS Claim 1; Page 217-221; 229pp; English.

XX This invention relates to a novel recombinant carcinoma-associated (CA)
XX nucleic acid comprising a fully defined genomic, mRNA or coding sequences
XX of mouse Rorc gene or human RORC gene, mouse MCG15938 or human gene BAT1,
XX mouse Igga1 gene or human IQGAP1 gene, mouse Zfp29 gene or human
XX hCG27579 gene, mouse Kcnj9 gene or human KCNJ9 gene, mouse Ppp3cc gene or
XX human Ppp3cc gene, mouse MCG9110 gene or human hCG27579 gene, as given in
XX the specification. CA genes are genes which are preferably expressed in
XX cancer cells, preferably lymphatic, breast, prostate or epithelial cells.
XX A compound which modifies the expression of the CA genes or bind to
XX carcinoma-associated proteins (CAP) may have cytostatic activity and the
XX sequences of the invention may enable the use of gene therapy or a
XX development of an anticancer vaccine. Therefore the invention may be
XX useful for diagnosis and treatment of carcinomas, especially lymphoma
XX carcinoma, breast cancer and prostate cancer. The CA genes may also be
XX useful as DNA vaccines and for generating animal models of carcinomas.
XX The present sequence is that of the mouse Lfng gene genomic DNA sequence
XX of the invention.

XX SQ

XX SQ Sequence 27079 BP; 5965 A; 7344 C; 7585 G; 6185 T; 0 U; 0 Other;

Query Match 16.0%; Score 38; DB 9; Length 27079;
Best Local Similarity 57.6%; Pred. No. 0.17;
Matches 68; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 104 GCTTCCTTCATGCATCCATTTGCTTCATTCATTCATCCATCCATCCCTCTCT 163
DB 3703 GCTTCCTTCATGCATCCATTTGCTTCATTCATTCATCCATCCATCCATCCATCCAT 3762

QY 164 GAGCTTTACCTCTGACTCCCTCACTCCATCAGACCTCTACGACCATAGACTCTGC 221
DB 3763 CCAACATCCCATCTGTCTCCCTCCACCCACCATCATCATCTCCATCCATCCATCCAT 3820

RESULT 15

ADB72827

ID ADB72827 standard; DNA; 27079 BP.

XX AC

XX AC ADB72827;

XX DT

XX DT 04-DEC-2003 (first entry)

XX DE

XX DE Mouse Lfng gene.

XX mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
XX cancer; neoplasm; adenocarcinoma; sarcoma; gene.

XX OS

XX OS Mus sp.

XX PN

XX PN WO2003008583-A2.

XX PD

XX PD 30-JAN-2003.

XX PF

XX PF 26-DEC-2001; 2001WO-US051291.

XX PR

XX PR 02-MAR-2001; 2001US-00798586.

XX PR

XX PR 23-OCT-2001; 2001US-00004113.

XX PR

XX PR 08-NOV-2001; 2001US-00052482.

XX PR

XX PR 30-NOV-2001; 2001US-00997722.

XX PR

XX PR 20-DEC-2001; 2001US-00034650.

XX PA

XX PA (SAGR-) SAGRES DISCOVERY.

XX PI

XX PI Morris DW, Engelhard EK;

XX DR

XX DR WPI; 2003-239337/23.

XX PS

XX PS Claim 1; SEQ ID NO 655; 2304pp; English.

XX The invention relates to a novel recombinant nucleic acid comprising a
XX nucleotide sequence selected from any of the 660 sequences fully defined
XX in the specification. A polynucleotide of the invention has cytostatic
XX activity, and may have a use in gene therapy, or in a vaccine. The
XX recombinant nucleic acids and polypeptides are useful for treating
XX carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
XX sarcomas. The present sequence represents a mouse gene of the invention.

XX SQ

XX SQ Sequence 27079 BP; 5965 A; 7344 C; 7585 G; 6185 T; 0 U; 0 Other;

Query Match 16.0%; Score 38; DB 10; Length 27079;
Best Local Similarity 57.6%; Pred. No. 0.17;
Matches 68; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 104 GCTTCCTTCATGCATCCATTTGCTTCATTCATTCATCCATCCATCCCTCTCT 163
DB 3703 GCTTCCTTCATGCATCCATTTGCTTCATTCATTCATCCATCCATCCATCCATCCAT 3762

QY 164 GAGCTTTACCTCTGACTCCCTCACTCCATCAGACCTCTACGACCATAGACTCTGC 221
DB 3763 CCAACATCCCATCTGTCTCCCTCCACCCACCATCATCATCTCCATCCATCCATCCAT 3820

Search completed: April 7, 2005, 11:09:40
Job time : 177.885 secs


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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16765
; LENGTH: 14566
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16765

Query Match      15.9%; Score 37.8; DB 4; Length 14566;
Best Local Similarity 60.0%; Pred. No. 0.027;
Matches 63; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 105 CTTCCCTTCATCCATTCATTGTTCTGTTTCATTCATTCATCCATCCATCCACCTGCTCTG 164
Db 528 CATCCCTCCATCATCCATCCACCCATCCCTCATTCATCCATTCATTCCTCCATTC 469

QY 165 AGTTTCACTCTGACTCCCTCACTCACTCCATCCATCCAGACCTCTACGCACC 209
Db 468 ATCATCCCTCCCTCCATCCATCCATCCATCCATCCACCCACCATC 424

RESULT 3
US-09-949-016-13646
; Sequence 13646, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13646
; LENGTH: 23640
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(23640)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13646

Query Match      15.6%; Score 37.2; DB 4; Length 23640;
Best Local Similarity 65.9%; Pred. No. 0.056;
Matches 54; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 107 TCCTTCATCCATCCATTCATTGTTCTGTTTCATTCATTCATCCATCCACCTGCCTCTGAG 166
Db 7218 TCATCCATCCACCCATCCATCCATTCATCCATCCACCCATTCCTCCACCTATCCATCCA 7277

QY 167 CTTTCACCTCTGACTCCCTCAAC 189
Db 7278 CTTATACCTTCTACCTACCCATC 7299

RESULT 4
US-09-949-016-12147/c
; Sequence 12147, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12147
; LENGTH: 76767
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(76767)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12147

Query Match      15.5%; Score 37; DB 4; Length 76767;
Best Local Similarity 60.4%; Pred. No. 0.4;
Matches 61; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 109 CTTTCATCCATCCATTCATTGTTCTGTTTCATTCATTCATCCATCCACCTGCCTCTGAGCT 168
Db 542579 CTTTCCTCCATCCATCCATCCCTTCCATCCATCCACCCACATCCATCCATCCATCTTCT 542520

QY 169 TTCACCTCTGACTCCCTCACTCACTCCATCCATCCAGACCTCTACGCACC 209
Db 542519 TACATCCATCCACCCATCCATCCCTTCTTCATCCATCCATC 542479

RESULT 5
US-09-949-016-17361/c
; Sequence 17361, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17361
; LENGTH: 76767
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(76767)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361

Query Match      15.5%; Score 37; DB 4; Length 76767;
Best Local Similarity 60.4%; Pred. No. 0.4;
Matches 61; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 109 CTTTCATCCATCCATTCATTGTTCTGTTTCATTCATTCATCCATCCACCTGCCTCTGAGCT 168
Db 542579 CTTTCCTCCATCCATCCATCCCTTCCATCCATCCACCCACATCCATCCATCCATCTTCT 542520
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Qy 169 TTCACTCTGACTCCCTTAACATCCATCAGACTCTTACGCACC 209
Db 542519 TACATCCATCACCCATCCATCCTTCTTATCCATCCATC 542479

RESULT 6

US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHIEFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935.313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14

Query Match 15.2%; Score 36.2; DB 1; Length 7218;
Best Local Similarity 8.4%; Pred.No.0.068; 77; Indels 0; Gaps 0;
Matches 17; Conservative 109; Mismatches 77; Indels 0; Gaps 0;
Qy 20 GAGTGGCCTGAACACCTGAGGAGCTGACATCCATCCATGTTTCAGCAATGTCATGCGATCA 79
Db 1035 GAGCTTGCTGCAGTGCAGGAGCTTGCATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1094
Qy 80 GGAGGGCCCAAGGCCCATCGTTCCTTCATGATCCATGTTCTGTTCTGTTCTATTCAT 139
Db 1095 YY 1154
Qy 140 TCATCCATACATCCACCTGCTTTCAGCTTTCACCTGACTCCCTAATCCATCAGCACC 199
Db 1155 YY 1214
Qy 200 TCTACGCACCAATAGACTCTGCC 222

Db 1215 YYYYYYYYYYYYYYYYYYYYYY 1237

RESULT 7

US-09-949-016-15004
; Sequence 15004, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15004
; LENGTH: 60276
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(60276)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15004

Query Match 15.2%; Score 36.2; DB 4; Length 60276;
Best Local Similarity 57.5%; Pred.No.0.21; 48; Indels 0; Gaps 0;
Matches 65; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 111 TTCAATGATCCATGTTTCTGTTTCATTCATCCATCCATCCATCCATCCATCCATCCAT 170
Db 11773 TCCATGATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 11832
Qy 171 CACTCTGACTCCCTAACTCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 223
Db 11833 TCACCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 11885

RESULT 8

US-09-949-016-15694
; Sequence 15694, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15694
; LENGTH: 60338
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(60338)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15694

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Query Match      15.2%; Score 36.2; DB 4; Length 60338;
Best Local Similarity 57.5%; Pred. No. 0.21; Indels 0; Gaps 0;
Matches 65; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 111 TTTCATCATCCATTTGTTCTGTTTCATTCATTCATCCATACATCCATCGCTGCTGAGCTTT 170
    |||||
Db 11835 TCATCGATCCATCCATCCATCCATTCAGCCATCCATCCATCCATCCATCCATCCAT 11894
    |||||

QY 171 CACCTCTGACTCCCTAACTCCATCCATCAGACTCTTACGACCATTAAGACTCTGCCA 223
    |||||
Db 11895 TCACCCATCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 11947

RESULT 9
US-09-949-016-14139/c
; Sequence 14139, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14139
; LENGTH: 323820
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(323820)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14139

Query Match      15.1%; Score 36; DB 4; Length 323820;
Best Local Similarity 70.6%; Pred. No. 0.58; Indels 20; Gaps 0;
Matches 48; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 89 CCAAGGCGCCCATCGCTTCCCTTCATGCATCCATTCATTTCTGTTTCATTCATCCATCA 148
    |||||
Db 88457 CTCAGGCGCCCTGTTTCTCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 88398
    |||||

QY 149 CATCCACC 156
    |||||
Db 88397 CATCCAAC 88390

RESULT 10
US-09-949-016-11851/c
; Sequence 11851, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11851
; LENGTH: 71278
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(71278)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11851

Query Match      15.0%; Score 35.8; DB 4; Length 71278;
Best Local Similarity 56.3%; Pred. No. 0.31; Indels 52; Gaps 0;
Matches 67; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 105 CTTCCCTTCATGCATCCATTCATTTGTTTCATTCATTCATCCATCCATCCATCCATCC 164
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Db 40115 CATCCATCCATTCATCCATCCATCTCTGTCTATCTTCCATCCATCCATCCATCCATTC 40056
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QY 165 AGCTTTACCTCTGACTCCCTAACTCCATCCATCCATCCATCCATCCATCCATCCATCC 223
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Db 40055 ACCATCCACCCATCAATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCT 39997
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RESULT 11
US-09-949-016-17563/c
; Sequence 17563, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17563
; LENGTH: 71278
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(71278)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17563

Query Match      15.0%; Score 35.8; DB 4; Length 71278;
Best Local Similarity 56.3%; Pred. No. 0.31; Indels 52; Gaps 0;
Matches 67; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 105 CTTCCCTTCATGCATCCATTCATTTGTTTCATTCATTCATCCATCCATCCATCCATCC 164
    |||||
Db 40115 CATCCATCCATTCATCCATCCATCTCTGTCTATCTTCCATCCATCCATCCATCCATTC 40056
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QY 165 AGCTTTACCTCTGACTCCCTAACTCCATCCATCCATCCATCCATCCATCCATCCATCC 223
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RESULT 12
US-10-071-411A-63
; Sequence 63, Application US/10071411A
; Patent No. 6797475
; GENERAL INFORMATION:
; APPLICANT: Glenn Barnes
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APPLICANT: Joanne Meyer
; TITLE OF INVENTION: Detection of Polymorphisms in the Human
; FILE REFERENCE: MRI-021
; CURRENT APPLICATION NUMBER: US/10/071.411A
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/267,515
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/314,248
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 168174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(168174)
; OTHER INFORMATION: n = A,T,C or G
US-10-071-411A-63

Query Match 15.0%; Score 35.8; DB 4; Length 168174;
Best Local Similarity 56.3%; Pred. No. 0.48;
Matches 67; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 105 CTTCCCTTCATGCATCCATTTGTTCTTATTCATTCATCCATACATCCACCTGCTG 164
Db 12256 CATCCATCCATCATCCATCATCTCTGTTATATCTTCCATCCACCATCCATTC 12315
Qy 165 AGCTTTACCTCTGACTCCCTTAATCCATCAGACCTCTACGCACCATAGACTCTGCCA 223
Db 12316 ACCATCCACCATCAATCCATCCACCATCTATCCATCCATCTCACTAATCTGTCA 12374

RESULT 13

US-10-071-411A-2
; Sequence 2, Application US/10071411A
; Patent No. 6797475

GENERAL INFORMATION:

APPLICANT: Glenn Barnes
; APPLICANT: Joanne Meyer
; TITLE OF INVENTION: Detection of Polymorphisms in the Human
; FILE REFERENCE: MRI-021
; CURRENT APPLICATION NUMBER: US/10/071.411A
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/267,515
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/314,248
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2

LENGTH: 168273

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(168273)

OTHER INFORMATION: n = A,T,C or G

US-10-071-411A-2

Query Match 15.0%; Score 35.8; DB 4; Length 168273;
Best Local Similarity 56.3%; Pred. No. 0.48;
Matches 67; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 105 CTTCCCTTCATGCATCCATTTGTTCTTATTCATTCATCCATACATCCACCTGCTG 164
Db 12256 CATCCATCCATCATCCATCATCTCTGTTATATCTTCCATCCACCATCCATTC 12315
Qy 165 AGCTTTACCTCTGACTCCCTTAATCCATCAGACCTCTACGCACCATAGACTCTGCCA 223

Db 12316 ACCATCCACCATCAATCCATCCACCATCTATCCATCCATCTCACTAATCTGTCA 12374

RESULT 14

US-09-949-016-74297
; Sequence 74297, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74297

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-74297

Query Match 14.9%; Score 35.4; DB 4; Length 601;
Best Local Similarity 63.5%; Pred. No. 0.036;
Matches 54; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 105 CTTCCCTTCATGCATCCATTTGTTCTTATTCATTCATCCATACATCCACCTGCTG 164
Db 217 CATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAA 276

Qy 165 AGCTTTACCTCTGACTCCCTAACT 189

Db 277 AATTTTATTTCTCTCTCTCTCTCT 301

RESULT 15

US-09-949-016-74298
; Sequence 74298, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74298

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-74298

Query Match 14.9%; Score 35.4; DB 4; Length 601;
Best Local Similarity 63.5%; Pred. No. 0.036;
Matches 54; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 105 CTTCCCTTCATGCATCCATTTGTTCTTATTCATTCATCCATACATCCACCTGCTG 164
Db 158 CATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAA 217

Qy 165 AGCTTCACCTCTGACTCCCTAACT 189
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Db 218 AATTTTATTCTCTCTCTCTCT 242

Search completed: April 7, 2005, 15:00:38
Job time : 59.9231 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 10:54:05 ; Search time 213.086 Seconds
(without alignments)
6768.525 Million cell updates/sec

Title: US-09-977-579-4_COPY_1024_1261

Perfect score: 238

Sequence: 1 aacaggagcagtgatgacatg.....tgccagaactgagaagccgg 238

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- Published Applications NA:*
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 - 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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 - 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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 - 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
 - 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
 - 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
 - 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
 - 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
 - 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 - 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
 - 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 - 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	238	100.0	1261	11	US-09-977-579-4
2	216	90.8	4625	10	US-09-764-891-7659
3	40.6	17.1	221000	17	US-10-174-014-12
4	40.6	17.1	233380	13	US-10-087-192-652
5	38.4	16.1	228	18	US-10-674-124A-21325
6	38	16.0	27079	17	US-10-034-650-55
7	38	16.0	38360	10	US-09-999-121-14
8	37.8	15.9	109	18	US-10-674-124A-4659
9	37.8	15.9	195	18	US-10-674-124A-4658
10	37.8	15.9	1091	13	US-10-027-632-30772
11	37.8	15.9	1091	17	US-10-027-632-30772

12	37.8	15.9	1327	13	US-10-027-632-215913	Sequence 215913,
13	37.8	15.9	1327	17	US-10-027-632-215913	Sequence 215913,
14	37.8	15.9	3768	9	US-09-969-708-464	Sequence 464, App
15	37.8	15.9	3768	9	US-09-954-531-164	Sequence 164, App
16	37.8	15.9	3768	9	US-09-954-531-373	Sequence 373, App
17	37.8	15.9	3768	10	US-09-960-706-1041	Sequence 1041, App
18	37.8	15.9	3768	10	US-09-873-313-689	Sequence 689, App
19	37.8	15.9	3768	19	US-10-843-641A-1231	Sequence 1231, App
20	37.8	15.9	3768	19	US-10-843-641A-1440	Sequence 1440, App
21	37.8	15.9	3768	19	US-10-843-641A-7935	Sequence 7935, App
22	37.8	15.9	8222	19	US-10-486-319A-6	Sequence 6, Appli
23	37.8	15.9	8222	19	US-10-486-319A-42	Sequence 42, Appl
24	37.8	15.9	8222	19	US-10-486-319A-64	Sequence 64, Appl
25	37.6	15.8	339	18	US-10-674-124A-8325	Sequence 8325, App
26	37.6	15.8	1781	13	US-10-027-632-200093	Sequence 200093,
27	37.6	15.8	1781	17	US-10-027-632-200093	Sequence 200093,
28	37.2	15.6	775062	18	US-10-719-993-6844	Sequence 6844, App
29	37	15.5	2632	13	US-10-029-191-22	Sequence 22, Appl
30	37	15.5	3108	13	US-10-029-191-1	Sequence 1, Appli
31	37	15.5	6419	15	US-10-311-455-239	Sequence 239, App
32	36.8	15.5	434	18	US-10-674-124A-23074	Sequence 23074, A
33	36.6	15.4	148	18	US-10-674-124A-24954	Sequence 24954, A
34	36.6	15.4	494	13	US-10-027-632-320641	Sequence 320641,
35	36.6	15.4	494	17	US-10-027-632-320641	Sequence 320641,
36	36.6	15.4	642	13	US-10-027-632-61529	Sequence 61529, A
37	36.6	15.4	642	17	US-10-027-632-61529	Sequence 61529, A
38	36.6	15.4	4743	10	US-09-764-891-7898	Sequence 7898, App
39	36.6	15.4	4747	10	US-09-764-891-7897	Sequence 7897, App
40	36.4	15.3	29322	17	US-10-034-650-58	Sequence 58, Appl
41	36.4	15.3	140152	18	US-10-684-422-66	Sequence 66, Appl
42	36.2	15.2	615	13	US-10-027-632-278139	Sequence 278139,
43	36.2	15.2	615	17	US-10-027-632-278139	Sequence 278139,
44	36.2	15.2	626	13	US-10-027-632-278138	Sequence 278138,
45	36.2	15.2	626	17	US-10-027-632-278138	Sequence 278138,

ALIGNMENTS

RESULT 1

- US-09-977-579-4
- Sequence 4, Application US/09977579
- Publication No. US20040248240A1
- GENERAL INFORMATION:
- APPLICANT: Cambridge University Technical Services
- TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
- TITLE OF INVENTION: channel
- FILE OF INVENTION: nucleic
- FILE REFERENCE: 674558-2001
- CURRENT APPLICATION NUMBER: US/09/977,579
- CURRENT FILING DATE: 2001-10-15
- PRIOR APPLICATION NUMBER: PCT/EP00/01783
- PRIOR FILING DATE: 2000-02-24
- PRIOR APPLICATION NUMBER: 60,129,473
- PRIOR FILING DATE: 2000-02-24
- NUMBER OF SEQ ID NOS: 47
- SOFTWARE: Patentin version 3.1
- SEQ ID NO 4
- LENGTH: 1261
- TYPE: DNA
- ORGANISM: Homo sapiens
- US-09-977-579-4

Query Match	100.0%	Score 238;	DB 11;	Length 1261;
Best Local Similarity	100.0%;	Pred. No. 9.2e-69;		
Matches 238;	Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	AACAGGAGCAGTGTGACATGAGTGGCTGCAACACCTGAGGAGCTGGACATCCCATGTC	60	
Db	1024	AACAGGAGCAGTGTGACATGAGTGGCTGCAACACCTGAGGAGCTGGACATCCCATGTC	1083	
QY	61	AGCAATGTCAATGCATCAGGAGGCGGCCCAAGAGGCCCATCGCTTCCCTTCATCATC	120	

Db 1084 AGCAATGTCATGGCATCAGAGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGCATC 1143
QY 121 CATTGTTCTGTTCAATTCATTCATCCATCATCCACCTGCCTCTGAGCTTTCACCTCTGAC 180
Db 1144 CATTGTTCTGTTCAATTCATTCATCCATCATCCACCTGCCTCTGAGCTTTCACCTCTGAC 1203
QY 181 TCCCTTAACCTCCATCAGACCTCTACGACCATTAAGACTCTGCCAGAACTGAGAAGCGG 238
Db 1204 TCCCTTAACCTCCATCAGACCTCTACGACCATTAAGACTCTGCCAGAACTGAGAAGCGG 1261

RESULT 2

US-09-764-891-7659
; Sequence 7659, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7659
; LENGTH: 4625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7659

Query Match 90.8%; Score 216; DB 10; Length 4625;
Best Local Similarity 100.0%; Pred. No. 2.9e-61;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 AGTGTCCTGAACACCTGAGGGACTGGACATCCCATGTTTCAGCAATGTCAATGGCATCAG 80
Db 33 AGTGTCCTGAACACCTGAGGGACTGGACATCCCATGTTTCAGCAATGTCAATGGCATCAG 92
QY 81 GAGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGCATCCATTTGTTGTTCAATTCATT 140
Db 93 GAGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGCATCCATTTGTTGTTCAATTCATT 152
QY 141 CATCATACATCCATCCATCGCTCTGAGCTTTCACCTTGACTCCCTAACTCCATCAGACCT 200
Db 153 CATCATACATCCATCCATCGCTCTGAGCTTTCACCTTGACTCCCTAACTCCATCAGACCT 212
QY 201 CTACGCACCATTAAGACTCTGCCAGAACTGAGAAGCC 236
Db 213 CTACGCACCATTAAGACTCTGCCAGAACTGAGAAGCC 248

RESULT 3

US-10-174-014-12
; Sequence 12, Application US/10174014
; Publication No. US20040005292A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMRT EXPRESSION
; FILE REFERENCE: PTS-0012
; CURRENT APPLICATION NUMBER: US/10/174,014
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 12
; LENGTH: 221000
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 77967
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure

; NAME/KEY: unsure
; LOCATION: 77968
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 77969
; OTHER INFORMATION: unknown
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; NAME/KEY: unsure
; LOCATION: 77970
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; NAME/KEY: unsure
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; NAME/KEY: unsure
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; NAME/KEY: unsure
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; OTHER INFORMATION: unknown
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; NAME/KEY: unsure
; LOCATION: 77984
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 77985
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: unsure


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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(233380)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-652

Query Match      17.1%; Score 40.6; DB 13; Length 233380;
Best Local Similarity 57.5%; Pred. No. 0.027;
Matches 73; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 46 GGACATCCCATGTTACGACATTCATGCGATCAGGAGCGCCCAAGGGCCCATCCG 105
DB 55725 GGAGCTCCCATGCTGGGGAAGATTCATTCATTTGGGAGTCCCATCTGGGAGATCC 55784

QY 106 TTCCTTCATGCATCCATGTTCTGTTCATTCATCCATCATCATCCATCCATCTCTGA 165
DB 55785 ATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCTGGCAATA 55844

QY 166 GCTTCA 172
DB 55845 CTTATCA 55851

RESULT 5
US-10-674-124A-21325
; Sequence 21325, Application US/10674124A
; Publication No. US20040197797A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: TAMIYA, Gen
; TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
; FILE REFERENCE: GENETIC POLYMORPHISM MARKERS
; CURRENT APPLICATION NUMBER: US/10/674,124A
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/257,511
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/JP00/07621
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: JP2002-327516
; PRIOR FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: JP2002-383869
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 27110
; SEQ ID NO 21325
; LENGTH: 228
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: AC009700.4_30060
; OTHER INFORMATION: Located on chromosome 15
; FEATURE:
; OTHER INFORMATION: Distance between a terminus base of telomere on
; OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base
; OTHER INFORMATION: sequence : 41746864
; FEATURE:
; OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
; OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and
; OTHER INFORMATION: 5'-terminus of this base sequence : 51760
US-10-674-124A-21325

Query Match      16.1%; Score 38.4; DB 18; Length 228;
Best Local Similarity 62.5%; Pred. No. 0.018;
Matches 60; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 105 CTTCCCTTCATGCATCCATGTTCTGTTCATTCATCCATCCATCCATCCATCCGCTCG 164
DB 111 CATCCATCCATCCATCCATCCATCCATCCATTCATTCATTCATTCCTCCATA 170
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QY 165 AGCTTTACCTCTGACTCCCTAACTCCATCCATCAGACCT 200
DB 171 AACTAGCATCTCTTAGTTCTTAAGTCATTTGGGGCT 206

RESULT 6
US-10-034-650-55
; Sequence 55, Application US/10034650
; Publication No. US20030216558A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000128
; CURRENT APPLICATION NUMBER: US/10/034,650
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/474,377
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 27079
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-034-650-55

Query Match      16.0%; Score 38; DB 17; Length 27079;
Best Local Similarity 57.6%; Pred. No. 0.1;
Matches 68; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 104 GCTTCCTTCATGCATCCATGTTCTGTTCATTCATCCATCCATCCATCCGCTCT 163
DB 3703 GCTTCCTTCATGCATCCATGTTCTGTTCATTCATCCATCCATCCATCCATCCAT 3762

QY 164 GAGCTTTACCTCTGACTCCCTAACTCCATCCATCCATCCATCCATCCATCCATCC 221
DB 3763 CCAACATCCATCTGTCTCCCTCCACCCACATCATCTACACATCTCTCTCCCATG 3820

RESULT 7
US-09-999-121-14
; Sequence 14, Application US/09999121
; Publication No. US20030039982A1
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; TITLE OF INVENTION: ISOLATED GENOMIC NUCLEOTIDE FRAGMENTS FROM THE p15 REGION OF
; TITLE OF INVENTION: CHROMOSOME 11
; FILE REFERENCE: JR-10,001-US
; CURRENT APPLICATION NUMBER: US/09/999,121
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/244,705
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 38360
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-999-121-14

Query Match      16.0%; Score 38; DB 10; Length 38360;
Best Local Similarity 62.8%; Pred. No. 0.11;
Matches 59; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 97 CCGATCGCTTCCCTTCATGCATCCATGTTCTGTTCATTCATCCATCCATCCATCC 156
DB 25309 CCGCTTTCTTCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 25368

QY 157 TGCCTCTGAGCTTTTCCATCTCTGACTCCCTTAATC 190
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 08:50:34 ; Search time 1419.88 Seconds
(without alignments)
6380.306 Million cell updates/sec

Title: US-09-977-579-4_COPY_1024_1261

Perfect score: 238

Sequence: 1 aacaggagcagtgtgacatg.....tgccagaactgagaagccgg 238

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	236	99.2	975	5	BX452112	BX452112 BX452112
2	236	99.2	2555	3	CR609664	CR609664 full-length
3	236	99.2	4052	3	HS801563	AL136589 Homo sapi
4	214.4	90.1	443	7	D4825	D4825 HUMSUPV279
5	158.6	66.6	926	5	BX411288	BX411288 BX411288
6	101.2	42.5	484	6	CB441198	CB441198 691539 MA
7	95.6	40.2	1062	5	BX420015	BX420015 BX420015
8	46.4	19.5	637	9	CE517323	CE517323 tigr-gss-
9	42.2	17.7	4149	3	AK049286	AK049286 Mus muscu
10	42	17.6	322	4	EG001495	EG001495 MR3-GN022
11	41.8	17.6	601	6	CB442219	CB442219 692787 MA
12	40.8	17.1	941	9	CNS02DGR	AL192420 Tetraodon
13	40.2	16.9	844	9	CNS02UEH	AL124370 Tetraodon
14	40	16.8	611	8	BH308136	BH308136 CH230-193
15	39.4	16.6	702	9	CR196841	CR196841 Forward s
16	39.2	16.5	676	8	AQ835006	AQ835006 HS_3173 B
17	39	16.4	564	8	AZ627327	AZ627327 IM0469M04
18	39	16.4	637	9	CE447269	CE447269 tigr-gss-
19	38.8	16.3	712	5	BP380503	BP380503 BP380503
20	38.6	16.2	660	6	BY730622	BY730622 BY730622
21	38.6	16.2	675	9	CE070920	CE070920 tigr-gss-
22	38.6	16.2	1101	9	CNS0512Z	AL338372 Tetraodon
23	38.4	16.1	668	9	AG087943	AG087943 Pan trogl
24	38.4	16.1	750	8	BH356347	BH356347 CH230-82D

Query Match 99.2%; Score 236; DB 5; Length 975;

ALIGNMENTS

RESULT 1
BX452112
LOCUS BX452112 975 bp mRNA linear EST 05-MAY-2004
DEFINITION BX452112 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CS0DF023YA09 5-PRIME, mRNA sequence.
ACCESSION BX452112 GI:47054503
VERSION BX452112.2
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 975)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 22, 2003 this sequence version replaced gi:31024339.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 6147.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?8=CS0BAG018ZF03_CS01654_l&c=6147.r

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF023YA09"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

CE244764 tigr-gss-
AG432316 Mus muscu
AZ957360 2M0224011
AQ748173 HS_5536_A
AL564828 AL564828
CF979338 FAR008B2.
AL331549 Tetraodon
AL343609 Tetraodon
CE443630 tigr-gss-
AQ813992 HS_5253_B
AQ201281 RPC111-48
BE181389 CMO-HT063
BZ173993 CH230-505
CV396629 QV3-HT063
CE484391 tigr-gss-
CN315915 AGENCOURT
BZ258128 BX258128
BZ689975 M031F08 G
CO377943 Lr_CHRCF
CE805346 tigr-gss-
CR222933 Reverse s

25 38.2 16.1 694 9 CE244764
26 38.2 16.1 733 9 AG432316
27 38.2 16.1 751 8 AZ957360
28 38 16.0 835 8 AQ748173
29 38 16.0 1138 1 AL564828
30 37.8 15.9 537 7 CF979338
31 37.8 15.9 982 9 CNS05CTG
32 37.8 15.9 1045 9 CNS05M4G
33 37.6 15.8 221 9 CE443630
34 37.6 15.8 436 8 AQ813992
35 37.6 15.8 445 8 AQ201281
36 37.4 15.7 372 2 BE181389
37 37.4 15.7 542 8 BZ173993
38 37.4 15.7 543 7 CV396629
39 37.2 15.6 323 9 CE484391
40 37.2 15.6 443 7 CN315915
41 37.2 15.6 497 5 BX258128
42 37.2 15.6 530 8 BZ689975
43 37.2 15.6 686 7 CO377943
44 37.2 15.6 737 9 CE805346
45 37.2 15.6 743 9 CR222933

Best Local Similarity 100.0%; Pred. No. 1.1e-59; Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACAGGAGCAGTGTGACATGAGTGGCTGAAACACCTGAGGAGCTGGACATCCCATGTTTC 60
Db 117 AACAGGAGCAGTGTGACATGAGTGGCTGAAACACCTGAGGAGCTGGACATCCCATGTTTC 176
QY 61 AGCAATGTCAATGGCATCAGAGGGGCGCCCAAGAGGCCCATCGCTTCCCTTCATGCATC 120
Db 177 AGCAATGTCAATGGCATCAGAGGGGCGCCCAAGAGGCCCATCGCTTCCCTTCATGCATC 236
QY 121 CATTGTCTCTCATTTCATTCATCCATACATCCACCTGCTCTGAGCTTTCACCTCTGAC 180
Db 237 CATTGTCTCTCATTTCATTCATCCATACATCCACCTGCTCTGAGCTTTCACCTCTGAC 296
QY 181 TCCTTAACCTCCATCAGACCTCTACGACCATAGACTCTGCCAGAACTGAGAAGCC 236
Db 297 TCCTTAACCTCCATCAGACCTCTACGACCATAGACTCTGCCAGAACTGAGAAGCC 352

RESULT 2
CR609664
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK

CR609664 2555 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DF023YA09 of Fetal brain of Homo sapiens (human).
CR609664
CR609664.1 GI:50490471
HTC; CDSLT cDNA.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF023YA09"
/tissue_type="fetal brain"
/plasmid="pCMVSPORT_6"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.4e-59; Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACAGGAGCAGTGTGACATGAGTGGCTGAAACACCTGAGGAGCTGGACATCCCATGTTTC 60
Db 883 AACAGGAGCAGTGTGACATGAGTGGCTGAAACACCTGAGGAGCTGGACATCCCATGTTTC 942
QY 61 AGCAATGTCAATGGCATCAGAGGGGCGCCCAAGAGGCCCATCGCTTCCCTTCATGCATC 120
Db 943 AGCAATGTCAATGGCATCAGAGGGGCGCCCAAGAGGCCCATCGCTTCCCTTCATGCATC 1002
QY 121 CATTGTCTCTCATTTCATTCATCCATACATCCACCTGCTCTGAGCTTTCACCTCTGAC 180

Db 1003 CATTGTCTCTCATTTCATTCATCCATACATCCACCTGCTCTGAGCTTTCACCTCTGAC 1062
QY 181 TCCTTAACCTCCATCAGACCTCTACGACCATAGACTCTGCCAGAACTGAGAAGCC 236
Db 1063 TCCTTAACCTCCATCAGACCTCTACGACCATAGACTCTGCCAGAACTGAGAAGCC 1118

RESULT 3
HSM801563
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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TITLE
JOURNAL
COMMENT
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/db_xref="taxon:9606"
/clone="DKFZp761F182"
/tissue_type="amygdala"
/clone_lib="761 (synonym: hamy2). Vector pSport1; host DH10B; sites NotI + SalI"
/dev_stage="adult"
/note="voltage-gated sodium channel beta-3 subunit"
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/gene="DKFZp761F182"
804..1451
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/db_xref="GOA:Q9NY72"
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HSM801563 4052 bp mRNA linear HTC 22-SEP-2004
Homo sapiens mRNA; cDNA DKFZp761F182 (from clone DKFZp761F182).
AL136589
AL136589.1 GI:13276680
HTC.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4052)
Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Schaipp, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Direct Submission
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp761F182) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp761F182
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

ORIGIN
Query Match 99.2%; Score 236; DB 3; Length 4052;
Best Local Similarity 100.0%; Pred. No. 1.5e-59; Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACAGGAGCAGTGTGACATGAGTGGCTGAAACACCTGAGGAGCTGGACATCCCATGTTTC 60
Db 1452 AACAGGAGCAGTGTGACATGAGTGGCTGAAACACCTGAGGAGCTGGACATCCCATGTTTC 1511

LOCUS	EX4111288	926 bp	mRNA	linear	EST 03-MAY-2004
DEFINITION	EX4111288 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CS0DF023YA09 3-PRIME, mRNA sequence.				
ACCESSION	EX4111288				
VERSION	EX4111288.1	GI:30765121			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				

irms
 JOURNAL
 COMMENT
 full-length cDNA libraries and normalization
 unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Séquençage
 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized, library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 6147.r

For more information about this cluster see
http://www.ebi.ac.uk/Ensembl/Homo_sapiens/Gene/ViewLocation?g=ENSG00000103389&v=f-734323&c=chr3

FEATURES	source
Location/Qualifiers	
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/clone_lib="Homo sapiens FETAL BRAIN"	
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRI sites of the pCMVSPORT 6"	

ORIGIN

Query Match 66.6%; Score 158.6; DB: 5; Length 926;
Best Local Similarity 87.4%; Pred. No. 1.8e-36;
Matches 208; Conservative 0; Mismatches 25; Indels 5; Gaps 3;

[illegible]

CB441198	CB441198	484 bp	mRNA	linear	EST 25-MAR-2003
LOCUS	691539	MARC 6BOV	Bos taurus	cdna 5'	
DEFINITION	CB441198			mrna sequence.	
ACCESSION					

VERSION	CB441198.1	GI:29227980
KEYWORDS	EST.	
SOURCE	Bos taurus	
ORGANISM	Bos taurus	(cow)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 484)

Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Fax: 402 762 4366

Tel: 402 762 4390

Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329.

Plate: FOY8048 row: K column: 21

Seq primer: GTAATACGACTCATTATAGG.

Location/Qualifiers

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/organism="Bos taurus"

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/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARCB60V"

/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;

Library made with RNA pooled from multiple tissues

including liver, lung, hypothalamus, pituitary, and

placenta/endometrium."

ORIGIN

Query Match 42.5%; Score 101.2; DB 6; Length 484;
Best Local Similarity 78.5%; Pred. No. 2.6e-19;
Matches 135; Conservative 0; Mismatches 33; Indels 4; Gaps 1;

QY 65 ATGTCATGGCATCAGGAGGGGCCCAAGGGCCCATCGCTTCCCTTCATGATCATTT 124

Db 4 ATATCACTGTCATCAGGAGGGTCCCTAGGACCATCACTTCCCTTCGTGGTCCATC 63

QY 125 GTTCTGTTCAATTCATTCATCATACATCACTGCTGCTGAGCTTTCACCTCTGACTCC 184

Db 64 CT-----TTGAGTTCATCTTCATACATCACTCACTCTGAACCTTTCACCTCTGCTTGC 119

QY 185 TTAATCCATCAGACCTCTACGACCATTAAGACTTCCGCAAGACTGAGAGGCC 236

Db 120 TTAATCCACAGACCTCTACACACTCAAGACTTTGCCAGAACTGAGGAGCC 171

RESULT 7

BX420015

LOCUS

DEFINITION: BX420015 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone

CS0DF023YA09 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

On May 13, 2003 this sequence version replaced gi:30646738.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 6147.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DF023AA05QP1&c=6147.r.

FEATURES

source

1..1062

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DF023YA09"

/tissue_type="FETAL BRAIN"

/dev_stage="fetal"

/clone_lib="Homo sapiens FETAL BRAIN"

/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

ORIGIN

Query Match 40.2%; Score 95.6; DB 5; Length 1062;
Best Local Similarity 68.1%; Pred. No. 1.5e-17;
Matches 124; Conservative 14; Mismatches 43; Indels 1; Gaps 1;

QY 1 AACAGAGCAGTGTGACATGAGTGGCTGGAACACCTGAGGGAGCTGGACATCCCATGTTTC 60

Db 882 AACAGAGCAGTGTGACATGAGTGGCTGGAACACCTGAGGGAGCTGGACATCCCATGTTTC 941

QY 61 ACCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGCATC 120

Db 942 ACAAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGCATC 1000

QY 121 CATTTGTTCTGTTTCATTCATTCATCATCATCATCCATCGCTCTGAGCTTTCACCTCTGAC 180

Db 1001 ATTGTYTTTTCATTATTTATCMAAAATCAMCTKCTTKASGTTTACYTGTGTCYCTAAW 1060

QY 181 TC 182

Db 1061 TC 1062

RESULT 8

CE517323

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

The dog genome: survey sequencing and comparative analysis

Science 301 (5641), 1898-1903 (2003)

22875432

14512627

Contact: Kirkness EF

The Institute for Genomic Research

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,

Rockville, MD 20850, USA

Tel: 301-838-0200

Fax: 301-838-0208

Email: ekirknes@tigr.org

Class: shotgun.

Location/Qualifiers

1..637

source

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/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BtXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 19.5%; Score 46.4; DB 9; Length 637;
Best Local Similarity 58.8; Pred. No. 0.0076;
Matches 80; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 33 CACCTGAGGACTGGACATCCCATGTTTCAGCAATGTCATGCGATCAGGAGGGCGCCCCA 92
Db 24 CAAGCGAAGCTGAGACACCCCAAGATGCTCCCAACTGGGTTCTGAAAGGCTTCACA 83

Qy 93 AGGGCCCCATCGCTCCCTTCATGCAATCCATGTTCTGTTTCATTCATTCATCCATCATC 152
Db 84 AGTGCCTTCGTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 143

Qy 153 CACTGCGCTCGAGCT 168
Db 144 CACAAGCCCATTCCT 159

RESULT 9
LOCUS AK049286 4149 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus ES cells cDNA, RIKEN full-length enriched library,
clone:C330019I03 product:VOLTAGE-GATED SODIUM CHANNEL BETA-3
SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog [Rattus
norvegicus], full insert sequence.
ACCESSION AK049286
VERSION AK049286.1 GI:26093400
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20493374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kiteunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamanoto,K., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5

```

```

AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 4149)
AUTHORS Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,P., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akai,H.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gscc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
FEATURES             Location/Qualifiers
     source            1..4149
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                     /mol_type="mRNA"
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                     /db_xref="PANTOM.DB:C330019I03"
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                     /clone="C330019I03"
                     /cell_type="ES cells"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
     misc_feature       410..1058
                     /note="VOLTAGE-GATED SODIUM CHANNEL BETA-3 SUBUNIT (SODIUM
CHANNEL BETA 3 SUBUNIT) homolog [Rattus norvegicus]
(SPTR|Q9JUK0, evidence: FASTA, 99.5%ID, 100%length,
match=646)
putative"
     polyA_signal        4129..4134
                     /note="putative"
     polyA_site          4149
                     /note="putative"

ORIGIN
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Best Local Similarity 67.8%; Pred. No. 0.21;
Matches 59; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 36 CTGAGGAGCTGGACATCCCATGTTTCAGCAATGTCATGCGATCAGGAGGGCGCCCCAAG 95
Db 1310 CTGAGCAACTGGCTATCCCGAGTTCCAGCAATGCCCAATCAGGAAGTGCCCCCAGGT 1369

Qy 96 GCCCATCGCTTCCTTCATGCATCCA 122
Db 1370 GTCCCAACACATCATCTTTCTATTCA 1396

RESULT 10
LOCUS BG001495/c 322 bp mRNA linear EST 24-JAN-2001
DEFINITION MR3-GN0229-141100-003-f07 GN0229 Homo sapiens cDNA, mRNA sequence.

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ACCESSION      BG001495
VERSION         BG001495.1  GI:12439883
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE
AUTHORS        Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
               Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.
TITLE          Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
               Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
               Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
               Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
               O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
               Simpson, A.J.
               Shotgun sequencing of the human transcriptome with ORF expressed
               sequence tags
JOURNAL        Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE        20202663
PUBMED         10737800
COMMENT        Contact: Simpson A.J.G.
               Laboratory of Cancer Genetics
               Ludwig Institute for Cancer Research
               Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
               Brazil
               Tel: +55-11-2704922
               Fax: +55-11-2707001
               Email: asimpson@ludwig.org.br
               This sequence was derived from the FAPESP/LICR Human Cancer Genome
               Project. This entry can be seen in the following URL
               (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR3&t2=MR3-GN0229-
               141100-003-f07&t3=2000-11-14&t4=1)
               Seq primer: puc 18 forward
               High quality sequence start: 51
               High quality sequence stop: 161.
               Location/Qualifiers
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               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /dev_stage="Adult"
               /clone_lib="GN0229"
               /note="Organ: Placenta normal; Vector: puc18; Site 1:
               SmaI; Site 2: SmaI; A mini-library was made by cloning
               products derived from ORESTES PCR (U.S. Letters Patent
               application No. 196,716 - Ludwig Institute for Cancer
               Research) profiles into the pUC 18 vector. Reverse
               transcription of tissue mRNA and cDNA amplification were
               performed under low stringency conditions."
ORIGIN
Query Match      17.6%; Score 42; DB 4; Length 322;
Best Local Similarity 64.3%; Pred. No. 0.14;
Matches 63; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 98 CCCATCGCTTCCTTCATCCATCCATCTGTTGTTTCATTCATCCATCATCCATCCACT 157
Db 118 CCTATCCCATTCATCCATCCATCCATCTTACCTATCCATCCATCCATCCATCCACTT 59
QY 158 GCCTCTGAGCTTTCACCTCTGACTCCCTAACTCCATCA 195
Db 58 ACCTATCATTCATCCATCCATCCATCCATCCATCTCCATCA 21
RESULT 11
LOCUS           CB442219
DEFINITION      601 bp mRNA linear EST 25-MAR-2003
ACCESSION      CB442219
VERSION        CB442219.1  GI:29230022
KEYWORDS       Bos taurus (cow)
SOURCE         Bos taurus
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
               Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
               Tetraodontidae; Tetraodontidae; Tetraodon.
               Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
               Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
               Saurin, W. and Weissenbach, J.
               Estimate of human gene number provided by genome-wide analysis
               using Tetraodon nigroviridis DNA sequence
               Nat. Genet. 25 (2), 235-238 (2000)
               20296633
               10835645
REFERENCE
AUTHORS        Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,
               Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
               Saurin, W., Bernot, A. and Weissenbach, J.
               Characterization and repeat analysis of the compact genome of the
               freshwater pufferfish Tetraodon nigroviridis
               Genome Res. 10 (7), 939-949 (2000)
               20359837
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 601)
Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G.,
Wray, J.E. and Keelle, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: FOY8048 row: K column: 21
Seq primer: TAGAAGGCACACTCGAGG.
Location/Qualifiers
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Query Match      17.6%; Score 41.8; DB 6; Length 601;
Best Local Similarity 86.8%; Pred. No. 0.18;
Matches 46; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 184 CTAACCTCCATCAGACTCTACGACACATAGACTCTGCCAGAACTCAGAGGCC 236
Db 599 CTAACCTCCATCAGACTCTTACACACTTTCACAGAACTTTCAGAGAGGCC 547
RESULT 12
CNS02DGR/c
LOCUS          CNS02DGR
DEFINITION     Tetraodon nigroviridis genome survey sequence T7 end of clone
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               sequence.
ACCESSION      AL192420.1  GI:7830524
VERSION        AL192420.1
KEYWORDS       GSS; genome survey sequence.
SOURCE         Tetraodon nigroviridis
ORGANISM       Tetraodon nigroviridis
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
               Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
               Tetraodontidae; Tetraodontidae; Tetraodon.
               1
               Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
               Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
               Saurin, W. and Weissenbach, J.
               Estimate of human gene number provided by genome-wide analysis
               using Tetraodon nigroviridis DNA sequence
               Nat. Genet. 25 (2), 235-238 (2000)
               20296633
               10835645
REFERENCE
AUTHORS        Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,
               Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
               Saurin, W., Bernot, A. and Weissenbach, J.
               Characterization and repeat analysis of the compact genome of the
               freshwater pufferfish Tetraodon nigroviridis
               Genome Res. 10 (7), 939-949 (2000)
               20359837

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PUBLISHED 10899143
REFERENCE 3 (bases 1 to 941)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.
FEATURES
source
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Location/Qualifiers
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ORIGIN
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Best Local Similarity 51.4%; Pred. No. 0.39;
Matches 108; Conservative 5; Mismatches 92; Indels 5; Gaps 1;
QY 4 AGGAGCAGTGTGACATGAGTGGCTGAACACCTGAGGGACTGGACATCCCATCTTCAGC 63
Db 868 AGTGGCGCGGACAGAGTGTACAGACACCTGTGGAGGAAACASACAGGTGGGA 809
QY 64 AATGTCAATGGCATCAGGAGGGCGCCCAAGGGGCCCATCGCTTCCCTTCATGCATCAT 123
Db 808 CAGCAGGASGTGAGRGGGGGGCGACCGTCTCCATCCCTCCCTCCATCCATC--- 752
QY 124 TGTCTCTTCATTCATTCATCCATCAGTCCACCTGCTCTGAGCTTCACCTTCGATCC 183
Db 751 --ATCCCTCCATCCATCCCTCCATCCATCCCTCCATCCATCCATCCCTCCCTCC 694
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Db 693 ATCCCTCCATCCCTCCATCCCTCCATCCATCCATCCATCCATCCATCCATCCATCC 664
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LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION 167G23 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL214370
VERSION AL214370.1 GI:7873189
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE 1
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PUBLISHED 10835645
REFERENCE 2
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)

20359837
PUBLISHED 10899143
REFERENCE 3 (bases 1 to 844)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.
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Matches 60; Conservative 7; Mismatches 40; Indels 0; Gaps 0;
QY 105 CTTCCCTTCATGCATCCATTTGTTCTGTTTCATTCATCCATCCATCCACCTGCTG 164
Db 661 CATCTTCCATCCATCCATCCATTCATCCATCCATCCATCCATCCATCCATCTTT 602
QY 165 AGCTTTCACCTCTGACCTCCCTAACTCCATCCATCCATCCATCCATCCATCCAT 211
Db 601 ATCTTTCWYCATYCATCTTTCATCCATCCATCCATCCATCCATCCATCCATCC 555
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BH308136 611 bp DNA linear GSS 03-DEC-2001
LOCUS CH230-193A19, TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
DEFINITION CH230-193A19, genomic survey sequence.
ACCESSION BH308136
VERSION BH308136.1 GI:17233605
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 611)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Teagave,G., Geer,K., Shivartebeyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.
TITLE Rat BAC End sequences from Library CHORI-230 EcoRI segment
JOURNAL Unpublished (1999)
COMMENT Other GSSs: CH230-193A19.TV
Contact: Shaving Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/orering/information.htm>). BAC end plate: 193 row: A column: 19
Seq primer: SP6
Class: BAC ends.
FEATURES
source
1. .611
Location/Qualifiers

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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
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/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 1"
/notes="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong"
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ORIGIN

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Best Local Similarity 58.3%; Pred. No. 0.62;
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QY 105 CTTCCCTTCATGCATCCATGTTCTGTCATTCATCCATCCATCCACCTGCCTCTG 164
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
432 CATCCATCCATCCATCCATCCCTTCTGTCGTCATCCATCCGTCGTCGTCGTCGTC 491
QY 165 AGCTTTCACCTCTGACTCCCTTAACCTCCATCCAGACCTCTACGCACCAAGACTCTGCCAG 224
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
492 TGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 551
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RESULT 15

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CR196841
LOCUS 702 bp DNA linear GSS 06-JUL-2004
DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and
chromosome engineering clone MHPN375j17, genomic survey sequence.
ACCESSION CR196841
VERSION 1 GI:49975690
KEYWORDS GSS; genome survey sequence; MICR.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 702)
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
Rogers,J. and Bradley,A.
Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICR
FEATURES
source
1..702
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/clone_lib="MHPN"
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ORIGIN

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Best Local Similarity 65.2%; Pred. No. 0.97;
Matches 58; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 106 TTCCCTTCATGCATCCATGTTCTGTCATTCATCCATCCATCCACCTGCCTCTGA 165
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
567 TTCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 626
QY 166 GCCTTCACCTCTGACTCCCTTAACCTC 194
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
627 ATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 655
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Job time : 1426.88 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 07:44:40 ; Search time 1788.76 Seconds
(without alignments)

10158.276 Million cell updates/sec

Title: US-09-977-579-4_COPY_1_375

Perfect score: 375

Sequence: 1 cctcctctccgagctgagc.....gaagccgagcccccagaag 375

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	375	100.0	1261	6 AR359850	AR359850 Sequence
2	375	100.0	1261	6 AX039100	AX039100 Sequence
3	375	100.0	1261	9 HSA243396	AJ243396 Homo sapi
C 4	373	99.5	127347	2 AP000682	AP000682 Homo sapi
C 5	373	99.5	144833	2 AC063921	AC063921 Homo sapi
C 6	373	99.5	149800	2 AC021981	AC021981 Homo sapi
C 7	373	99.5	172546	2 AC024604	AC024604 Homo sapi
C 8	373	99.5	178169	9 AP002765	AP002765 Homo sapi
C 9	373	99.5	181471	9 AC069539	AC069539 Homo sapi
C 10	350	93.3	178431	2 AP002749	AP002749 Homo sapi
C 11	164	43.7	174285	2 AC145484	AC145484 Lemur cat
C 12	122	32.5	66980	2 AC013796	AC013796 Homo sapi
C 13	74	19.7	66980	2 AC013796	AC013796 Homo sapi
C 14	53	14.1	521	11 PM12B8G	AL684336 Penicilli
C 15	51	13.6	134226	2 AC148923	AC148923 Alligator
C 16	46.4	12.4	148643	2 AC011871	AC011871 Homo sapi
C 17	45.6	12.2	216449	2 AC051616	AC051616 Mus muscu
C 18	45.4	12.1	140307	2 AC135353	AC135353 Mus muscu
C 19	45.4	12.1	238861	2 AC148331	AC148331 Mus muscu

C	20	45.4	12.1	239130	2	AC079420	Mus muscu
C	21	44.8	11.9	11608	9	HSINT2	X14445 Human int-2
C	22	44.8	11.9	104202	9	AP006345	AP006345 Homo sapi
C	23	44.6	11.9	58293	8	AC096781	AC096781 Oryza sat
C	24	44.6	11.9	117157	8	AC034258	AC034258 Oryza sat
C	25	44.6	11.9	306161	8	AB017102	AB017102 Oryza sat
C	26	44.4	11.8	21481	2	CR847893	CR847893 Danio rer
C	27	44.4	11.8	59364	2	AC102347	AC102347 Mus muscu
C	28	44.2	11.8	3252	9	HSTAF113	Y11354 H. sapiens m
C	29	44.2	11.8	110000	2	BX255276_08	Continuation (9 of
C	30	44.2	11.8	146691	2	BX927196	BX927196 Danio rer
C	31	44	11.7	85434	2	AC066610	AC066610 Homo sapi
C	32	44	11.7	223971	2	AC115753	AC115753 Mus muscu
C	33	43.8	11.7	152347	2	AC021096	AC021096 Homo sapi
C	34	43.8	11.7	196950	2	CR589874	CR589874 Danio rer
C	35	43.6	11.6	972	11	PM12A12G	AL684288 Penicilli
C	36	43.6	11.6	1094	11	PM7G11B	AL685196 Penicilli
C	37	43.6	11.6	53897	2	AC101434	AC101434 Mus muscu
C	38	43.6	11.6	191983	9	AF274858	AF274858 Homo sapi
C	39	43.4	11.6	33676	1	SCARD1GN	X84374 Saccharothr
C	40	43.4	11.6	150399	2	AC013385	AC013385 Homo sapi
C	41	43.4	11.6	240411	2	AC105428	AC105428 Mus muscu
C	42	43.2	11.5	61967	2	AC100100	AC100100 Mus muscu
C	43	43.2	11.5	64970	2	AC099958	AC099958 Mus muscu
C	44	43.2	11.5	208238	2	CR385024	CR385024 Danio rer
C	45	43.2	11.5	239130	2	AC079420	AC079420 Mus muscu

ALIGNMENTS

RESULT 1	AR359850	AR359850	Sequence 4 from patent US 6593565.	1261 bp	DNA	linear	PAT 17-AUG-2003
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DEFINITION	AR359850	AR359850	Sequence 4 from patent US 6593565.	1261 bp	DNA	linear	PAT 17-AUG-2003
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KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 1261)						
AUTHORS	Heslin, P. and Lynam, N.R.						
TITLE	Vehicle interior rearview mirror assembly including an accessory-containing housing						
JOURNAL	Patent: US 6593565-A 4 15-JUL-2003;						
FEATURES	Location/Qualifiers						
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Best Local Similarity	100.0%;	Pred. No. 1.4e-70;		
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Qy	121	GGCGGCGCGAGCGGTGATTCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTGGCTTAG	180	
Db	121	GGCGGCGCGAGCGGTGATTCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTGGCTTAG	180	
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Db	181	GGCCCCAAGCCCCACCGGCTCCAAAGCTCCAGGGCTCCCGAGGACCGGTGCTCG	240	
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Db 361 CGCCAGCCCGCAGAAG 375

RESULT 2
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LOCUS Homo sapiens 1261 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 4 from Patent WO063367.
ACCESSION AX039100
VERSION AX039100.1 GI:11229276
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Morgan, K., Jackson, A., and Morgan, K.
TITLE A novel family of beta sub-unit proteins from a voltage-gated sodium channel, nucleic acids encoding them and therapeutic or diagnostic uses there of
JOURNAL PATENT: WO 063367-A 4 26-OCT-2000; WARNER-LAMBERT COMPANY (US); Cambridge University Technical Services Limited (GB)
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Best Local Similarity 100.0%; Pred. No. 1.4e-70;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTCCCTCCGAGTGTAGCTTACCTGGCGGAGCGGAGTGTCCGTGTGTGTGAGCGCGCGAGA 60
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Qy 241 GGCCTTCCTTCGGTCAGAAAGTCGCCCTCGGGGCGAGTTCGTCCCAAGGGTTTCCTCG 300
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Qy 301 AAAGAATCTGAGAGGGCGCAGTCTTTGACCGAGGGAATCTCTCTGTGTAGCCTTGAAGC 360
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Qy 361 CGCCAGCCCGCAGAAG 375
Db 361 CGCCAGCCCGCAGAAG 375

RESULT 3
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ACCESSION AJ243396
VERSION AJ243396.2 GI:7242612
KEYWORDS scn3b gene; voltage-gated sodium channel beta-3 subunit.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Morgan, K., Stevens, E.B., Shaw, B., Cox, P., Dixon, A.K., Lee, K., Pincock, R.D., Hughes, J., Richardson, P.J., Mizuguchi, K. and Jackson, A.P.
TITLE beta 3: an additional auxiliary subunit of the voltage-sensitive sodium channel that modulates channel gating with distinct kinetics
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (5), 2308-2313 (2000)
MEDLINE 20160948
PUBMED 10688874
REFERENCE 2
AUTHORS Morgan, K.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-1999) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
REMARK Revised by [4]
REFERENCE 3 (bases 1 to 1261)
AUTHORS Morgan, K.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2000) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
COMMENT On Mar 14, 2000 this sequence version replaced gi:7160974.
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Query Match 100.0%; Score 375; DB 9; Length 1261;
Best Local Similarity 100.0%; Pred. No. 1.4e-70;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTCCCTCCGAGTGTAGCTTACCTGGCGGCGAAACGAGCGAGCGCGCGAGTGG 60
Db 1 CCCTCCCTCCGAGTGTAGCTTACCTGGCGGCGAAACGAGCGAGCGCGCGAGTGG 60
Qy 61 AAGCTGGAGTTCGGGGTGGCGGGAGCGGAGTTCGCTGTGTGTGTGAGCGCGCGAGA 120
Db 61 AAGCTGGAGTTCGGGGTGGCGGGAGCGGAGTTCGCTGTGTGTGTGAGCGCGCGAGA 120
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Qy 361 CGCCAGCCCGCAGAAG 375
Db 361 CGCCAGCCCGCAGAAG 375
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83108	100196	contig of 17089 bp in length	
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121414	121043	contig of 8630 bp in length	
121144	125917	contig of 4774 bp in length	
126018	127347	contig of 1330 bp in length	
* NOTE: This is a 'working draft' sequence. It currently			
* consists of 8 contigs. The true order of the pieces			
* is not known and their order in this sequence record is			
* arbitrary. Gaps between the contigs are represented as			
* runs of N, but the exact sizes of the gaps are unknown.			
* This record will be updated with the finished sequence.			
* as soon as it is available and the accession number will			
* be preserved.			
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100297	112313	contig of 12017 bp in length	
112314	121043	gap of 100 bp	
121044	121043	contig of 8630 bp in length	
121144	121143	gap of 100 bp	
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Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Qy	123	GGCGCGGAGCGCGCTGATCGGCTCCCTCGAACTGGGGAGGTCACAGTGGGGTTCGCTTAGGG	182
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Db 28892 CTTCTCTCGGTGAGAAAGTCCGCTCCGCTGGGGAGTTCGTCCTCGAA 28833

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Qy 363 CCAGCCCCCAGAG 375

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RESULT 5

AC063921/c

LOCUS

DEFINITION Homo sapiens chromosome 3 clone RP11-142P10, WORKING DRAFT

ACCESSION AC063921

VERSION AC063921.18 GI:20335587

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 144833)

AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alebrooks,S.L., Amaratunge,H.C., Are,J.R., Ayale,M., Banks,T., Barbara,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouay,J., Bowls,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,D., Edwards,C.C., Elhaj,C., Escotto,M., Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Foster,P., Frantz,P., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Haviak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozadó,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okunolu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,I., Peters,L., Pockens,A., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vaquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G., and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 144833)

Worley,K.C.

Direct Submission

JOURNAL

REFERENCE

AUTHORS

TITLE

COMMENT

Submitted (22-Apr-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 144833)

Worley,K.C.

Direct Submission

Submitted (08-JAN-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Apr 28, 2002 this sequence version replaced gi:16117924.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: HAXY

Center clone name: RP11-142P10

----- Summary Statistics

Sequencing vector: M13;

Chemistry: Dye-Primer Bodipy: 14% of reads

Assembly: Dye-terminator Big Dye: 86% of reads

Assembly program: Phrap: version 0.990329

Consensus quality: 127260 bases at least Q40

Consensus quality: 132735 bases at least Q30

Consensus quality: 136183 bases at least Q20

Estimated insert size: 139078; sum-of-contigs estimation

Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence. as soon as it is available and the accession number will be preserved.

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2438 2537: gap of unknown length

2538 4812: contig of 2275 bp in length

4813 4912: gap of unknown length

4913 8488: contig of 3576 bp in length

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FEATURES

source

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Best Local Similarity 100.0%; Pred. No. 1.8e-70;
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 50293 GCTGGAGTTCGGGCTCGGGGAGGCGAGCTGTCGCTGTGCTGACGCCGCGGAGGC 50234

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Db 50233 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGCTCGCTTAGGG 50174

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QY 303 AGAATCTGAGAGCGCGCAGTCTTGACCGAGGGAATCTCTGTGTGACCTTGGAAAGCCG 362
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RESULT 6
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LOCUS Homo sapiens chromosome 11 clone RP11-11C15 map 11, WORKING DRAFT
DEFINITION SQUENCE, 29 unordered pieces.
ACCESSION AC021981
VERSION AC021981.2 GI:9280747
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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Homo sapiens chromosome 11, clone RP11-11C15
Unpublished
2 (bases 1 to 149800)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguelavkiy,L., Boukhalter,B., Brown,A., Burkett,G., Castle,A.,
Choepey,Y., Collange,M., Collins,S., Collymore,A., Cooke,P.,
DeArellano,K., Dewar,K., Domino,M., Doyle,M., Feneator,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrum,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivat,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo.A., Wu.X., Wyman,D., Ye.W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 19, 2000 this sequence version replaced gi:6731265.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR

Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information

Center project name: L1335
Center clone name: L1 C.15

----- Summary Statistics

Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 135317 bases at least Q40
Consensus quality: 141872 bases at least Q30
Consensus quality: 144404 bases at least Q20
Insert size: 121000; agarose-fp
Insert size: 147000; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; agarose-fp
Quality coverage: 3.5 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

1
1441: contig of 1441 bp in length
1442: gap of 100 bp
1542: contig of 1342 bp in length
2884: gap of 100 bp
2884: contig of 1666 bp in length
4749: gap of 100 bp
6112: contig of 1363 bp in length
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7413: contig of 1201 bp in length
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9050: contig of 1537 bp in length
9150: gap of 100 bp
10944: contig of 1794 bp in length
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13203: contig of 2159 bp in length
13204: gap of 100 bp
16118: contig of 2815 bp in length
16218: gap of 100 bp
18673: contig of 2455 bp in length
18773: gap of 100 bp
21180: contig of 2407 bp in length
21280: gap of 100 bp
23200: contig of 1920 bp in length
23300: gap of 100 bp
26526: contig of 3226 bp in length
26527: gap of 100 bp
29655: contig of 3029 bp in length
29755: gap of 100 bp
34738: contig of 4983 bp in length
34838: gap of 100 bp
39394: contig of 4556 bp in length
39394: gap of 100 bp
43669: contig of 4175 bp in length
43769: gap of 100 bp
49948: contig of 6179 bp in length
50048: gap of 100 bp
55578: contig of 5530 bp in length
55678: gap of 100 bp
60959: contig of 5281 bp in length
61059: gap of 100 bp
66394: contig of 5335 bp in length
66494: gap of 100 bp
72947: contig of 6453 bp in length
73047: gap of 100 bp

Contact: gtc-seqcenter@genomecorp.com
 ----- Project Information
 Center project name: hg202
 ----- Summary Statistics

Sequencing vector: N/A
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 990315
 Consensus quality: 152033 bases at least Q40
 Consensus quality: 163535 bases at least Q30
 Consensus quality: 165256 bases at least Q20
 Insert size: 170446; sum-of-contigs
 Quality coverage: 4.3x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 22 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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 * 1340 1439: gap of unknown length
 * 1440 2789: contig of 1350 bp in length
 * 2790 2889: gap of unknown length
 * 2890 4562: contig of 1673 bp in length
 * 4563 4662: gap of unknown length
 * 4663 6344: contig of 1682 bp in length
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 * 6445 9221: contig of 2777 bp in length
 * 9222 11997: contig of 2676 bp in length
 * 11998 12097: gap of unknown length
 * 12098 14867: contig of 2770 bp in length
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 * 14968 19919: contig of 4952 bp in length
 * 19920 20019: gap of unknown length
 * 20020 24125: contig of 4106 bp in length
 * 24126 24225: gap of unknown length
 * 24226 29444: contig of 5219 bp in length
 * 29445 29544: gap of unknown length
 * 29545 34568: contig of 5024 bp in length
 * 34569 34668: gap of unknown length
 * 34669 39414: contig of 4746 bp in length
 * 39415 39514: gap of unknown length
 * 39515 45885: contig of 6371 bp in length
 * 45886 45985: gap of unknown length
 * 45986 50997: contig of 5012 bp in length
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 * 51098 59143: contig of 8046 bp in length
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 * 76430 76529: gap of unknown length
 * 76530 86704: contig of 10175 bp in length
 * 86705 86804: gap of unknown length
 * 86805 103147: contig of 16343 bp in length
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 * 116344 116443: gap of unknown length
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FEATURES
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ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 1.8e-70;

Query Match 99.5%; Score 373; DB 2; Length 172546;
 Best Local Similarity 100.0%; Pred. No. 1.8e-70;
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 QY 63 GCTGGAGTTCCGGGGTGGCGGGAGGCGAGCTGCTCGTGTGTGAGCGCGCGCGAGAGC 122
 DB 122437 GCTGGAGTTCCGGGGTGGCGGGAGGCGAGCTGCTCGTGTGTGAGCGCGCGCGAGAGC 122496
 QY 123 GGGCGGGAGCGGCTGATCCGCTCCCTCGAATCGGGAGGTCCAGTGGGTTCGCTTAGGG 182
 DB 122497 GGGCGGGAGCGGCTGATCCGCTCCCTCGAATCGGGAGGTCCAGTGGGTTCGCTTAGGG 122556
 QY 183 CCCAAAGCCCCCACCACCGGCTCCAAAAGCTCCAGGCGCTCCCAAGGACCGGTGCTCGGC 242
 DB 122557 CCCAAAGCCCCCACCACCGGCTCCAAAAGCTCCCAAGGACCGGTGCTCGGC 122616
 QY 243 CCTTCTTCTGGTCCAGAAAGTCGCCCCCTGGGGGAGTTCGTCCCAAGGGTTTCTCTCGAA 302
 DB 122617 CCTTCTTCTGGTCCAGAAAGTCGCCCCCTGGGGGAGTTCGTCCCAAGGGTTTCTCTCGAA 122676
 QY 303 AGAATCTGAGAGGCGCGCAGTCTTGTACCGAGGAATCTCTCTGTGTAGCCCTTGAAGCCG 362
 DB 122677 AGAATCTGAGAGGCGCGCAGTCTTGTACCGAGGAATCTCTCTGTGTAGCCCTTGAAGCCG 122736
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RESULT 8
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 LOCUS

DEFINITION Homo sapiens genomic DNA, chromosome 11q clone:RP11-634B22,
 complete sequence.
 ACCESSION AP002765
 VERSION AP002765.3 GI:16751488
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 Homo sapiens genomic DNA
 Published Only in Database (2000)
 REFERENCE 2 (bases 1 to 178169)
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 Direct Submission
 Submitted (10-JUL-2000) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan
 1-7-22, Suehiro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 COMMENT On Nov 5, 2001 this sequence version replaced gi:12381934.

FEATURES
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 /clone="RP11-634B22"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 1.8e-70;

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Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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VERSION AC069539.5 GI:20270093
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 181471)
AUTHORS Smith,D.R.
TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 181471)
AUTHORS Smith,D.R.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
REFERENCE 3 (bases 1 to 181471)
AUTHORS Smith,D.R.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
REFERENCE 4 (bases 1 to 181471)
AUTHORS Smith,D.R.
TITLE Direct Submission
JOURNAL Submitted (23-APR-2002) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
COMMENT On Apr 23, 2002 this sequence version replaced gi:10881056.
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ORIGIN
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Query Match 99.5%; Score 373; DB 9; Length 181471;
Best Local Similarity 100.0%; Pred. No. 1.8e-70;
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 63 GCTGGAGTTCCGGGGTGGGCGGGGAGGCGACTGTCTCGTGGTGTGAGCCCGCGAGAGC 122
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QY 303 AGAATCTGAGAGGGCGCAGTCCCTTGACCGAGGGAATCTCTGTGTAGCTTTGGAGCGC 362
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QY 363 CCAGCCCCCAGAAG 375
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Homo sapiens chromosome 11 clone RP11-158J21 map 11q24, WORKING
DRAFT SEQUENCE, 41 unordered pieces.
AP002749
AP002749.1 GI:9188598
HTG; HTGS PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 178,431 genomic DNA of 11q24
Published Only in DataBase (2000)
2 (bases 1 to 178431)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (10-JUL-2000) Maehira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-42-778-9923, Fax:81-42-778-9924)
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDraft11
Center clone name: RP11-158J21
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 155982 bases at least Q40
Consensus quality: 165758 bases at least Q30
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Consensus quality: 170239 bases at least Q20
Insert size: 174431; sum-of-contigs
Quality coverage: 4.20x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 41 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

```

1 13012: contig of 13012 bp in length
13113: 24677: contig of 11565 bp in length
24778: 34640: contig of 8456 bp in length
34741: 43196: contig of 6830 bp in length
43297: 50126: contig of 7499 bp in length
50227: 57826: contig of 6287 bp in length
64713: 70999: contig of 6287 bp in length
71100: 76188: contig of 5089 bp in length
76289: 83581: contig of 7292 bp in length
83681: 90511: contig of 6831 bp in length
90512: 95493: contig of 4882 bp in length
95494: 102262: contig of 6669 bp in length
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125633: 127927: contig of 2295 bp in length
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131185: 131284: contig of 100 bp in length
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132726: 132825: contig of 100 bp in length
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149633: 152157: contig of 2526 bp in length
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167137: 169169: contig of 2033 bp in length
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177006: 178431: contig of 1426 bp in length.

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NOTE: This is a 'working draft' sequence. It currently consists of 41 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

```

1 13012: contig of 13012 bp in length
13113: 13112: gap of 100 bp
13113: 24677: contig of 11565 bp in length
24678: 24777: gap of 100 bp
24778: 34640: contig of 8456 bp in length
34641: 34740: gap of 100 bp
34741: 43196: contig of 6830 bp in length
43197: 43296: gap of 100 bp
43297: 50126: contig of 6830 bp in length
50127: 50226: gap of 100 bp
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FEATURES
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* 76289 83580: contig of 7292 bp in length
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* 83681 90511: contig of 6831 bp in length
* 90512 90511: gap of 100 bp
* 90512 95493: contig of 4882 bp in length
* 95494 95594: gap of 100 bp
* 95594 102262: contig of 6669 bp in length
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* 102363 105866: contig of 3504 bp in length
* 105867 105966: gap of 100 bp
* 105967 111142: contig of 5176 bp in length
* 111143 111242: gap of 100 bp
* 111243 115923: contig of 4681 bp in length
* 115924 121747: contig of 5724 bp in length
* 121748 121847: gap of 100 bp
* 121848 125532: contig of 3685 bp in length
* 125533 125632: gap of 100 bp
* 125633 127927: contig of 2295 bp in length
* 127928 128027: gap of 100 bp
* 128028 131184: contig of 3157 bp in length
* 131185 131284: gap of 100 bp
* 131285 132725: contig of 1441 bp in length
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* 164910 167036: contig of 2127 bp in length
* 167037 167136: gap of 100 bp
* 167137 169169: contig of 2033 bp in length
* 169170 169269: gap of 100 bp
* 169270 171052: contig of 1783 bp in length
* 171053 171152: gap of 100 bp
* 171153 172933: contig of 1781 bp in length
* 172934 173033: gap of 100 bp
* 173034 174180: contig of 1147 bp in length
* 174181 174280: gap of 100 bp
* 174281 175729: contig of 1449 bp in length
* 175730 175829: gap of 100 bp
* 175830 176905: contig of 1076 bp in length
* 176906 177006: contig of 1426 bp in length.
* 177006 178431: contig of 1426 bp in length.

```

```

/misc_feature 1. .13012
/misc_feature 13113. .24677
/misc_feature 24778. .34640
/misc_feature 34741. .43196
/misc_feature 43297. .50126
/misc_feature 50227. .57725
/misc_feature 57826. .64612

Query Match 93.3%; Score 350; DB 2; Length 178431;
Best Local Similarity 99.5%; Pred. No. 1.6e-65;
Matches 372; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 3 CTCCTTCCGAGCTGAGCTTACCTTGGCGCAACGAGCGAGCGCGGCGAGTGGAA 62
DB 111367 CTCCTTCCGAGCTGAGCTTACCTTGGCGCAACGAGCGAGCGCA-GGCGCGAGTGGAA 111425

QY 63 GCTGAGTTCGGGGTGGCGGAGGAGGAGTGTGCTGCTGAGCGCCGCGAGAGC 122
DB 111426 GCTGAGTTCGGGGTGGCGGAGGAGGAGTGTGCTGCTGAGCGCCGCGAGAGC 111485

QY 123 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCAGTGGGTCGCTTAGG 182
DB 111486 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCAGTGGGTCGCTTAGG 111545

QY 183 -CCCAAGCCCGGCTCCAAAGCTCCAGGCGCTCCCGAGCACCGGTCGTCGG 241
DB 111546 CCCAAAGCCCGGCTCCAAAGCTCCAGGCGCTCCCGAGCACCGGTCGTCGG 111605

QY 242 CCTTCTTCGCTGAGAAAGTGCCTTGGGGGCGAGTTCGTCGCAAGGGTTCTCGA 301
DB 111606 CCTTCTTCGCTGAGAAAGTGCCTTGGGGGCGAGTTCGTCGCAAGGGTTCTCGA 111665

QY 302 AAGATCTCAGAGGGCGGAGTCTTGACCGAGGAGTCTCTGTGTAGCTTGAAGCC 361
DB 111666 AAGATCTCAGAGGGCGGAGTCTTGACCGAGGAGTCTCTGTGTAGCTTGAAGCC 111725

QY 362 GCCAGCCCCAGAG 375
DB 111726 GCCAGCCCCAGAG 111739

RESULT 11
AC145484/c
LOCUS
DEFINITION Lemur catta clone LB2-244B5, WORKING DRAFT SEQUENCE, 3 ordered
pieces.
AC145484
VERSION AC145484.1 GI:32880237
KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT.
SOURCE Lemur catta (ring-tailed lemur)
ORGANISM Lemur catta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Lemur.
1 (bases 1 to 174285)
Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
Peng, Z., Malinov, I. and Rubin, E.M.
Direct Submission
Unpublished
2 (bases 1 to 174285)
Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
Peng, Z., Malinov, I. and Rubin, E.M.
Direct Submission
Submitted (17-JUL-2003) Genome Sciences, Lawrence Berkeley National
Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
```

COMMENT

Sequence Produced by Berkeley PGA
Web site: <http://pga.lbl.gov>
Center Code: PGABERK
Center Project Name: L133
Bac Clone Name: LB2-244B5

This sequence has been compared to sequences of other species
using Vista (<http://www-gsd.lbl.gov/VISTA>). The results can be
viewed at:
http://pga.lbl.gov/cgi-bin/search_cvcgd?type=nkvalue=ZNF202

The order-orientation of the draft sequence was accomplished by
using:
Avid (<http://baboon.math.berkeley.edu/mavid/>),
Lagan (<http://lagan.stanford.edu/>) and paired end information.

Funding agent: Programs for Genomic Applications (NHLBI)

If the Bac Library Name is LB1 to LB4, please see website
for the description: <http://www-gsd.lbl.gov/cheng/BAC.html>
These libraries are available through the BACPAC Resources Center:
<http://www.chori.org/bacpac/libraryres.htm> as LBNL-1 to LBNL-4.

Summary Statistics:

Sequencing vector: plasmid; pUC18

Chemistry: Dye-terminator Big Dye

Assembly program: Phrap version 0.990329.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 87364: contig of 87364 bp in length

* 87365 87464: gap of unknown length

* 87465 151123: contig of 63659 bp in length

* 151124 151223: gap of unknown length

* 151224 174285: contig of 23062 bp in length.

FEATURES

Location/Qualifiers
1..174285
/organism="Lemur catta"
/mol_type="genomic DNA"
/db_xref="taxon:9447"
/clone="LB2-244B5"

ORIGIN

Query Match 43.7%; Score 164; DB 2; Length 174285;
Best Local Similarity 75.8%; Pred. No. 1.5e-25;
Matches 288; Conservative 0; Mismatches 70; Indels 22; Gaps 6;
QY 12 GAGCTGAGCTTACCTTGGCGCAACGAGCGAGCGCGGCGGAGTGGAAAGCTGAGATT 71
DB 22530 GAGCCGAGCTTCCCGCGCGCAACGAGAAAGGC-CGGAGCAAGTGGGATTTGAAGTT 22472
QY 72 CCGGGGTGGGGGAGGCGAGCTGTCCGTGTGCTGAGC-----GCCGG 115
DB 22471 CC-GGGTGGGGGGAAGCCACTGTCTCTGTGTGCTGAGCGGATCCAGCAACCGGCTCC 22413
QY 116 CGAGAGCGGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCAGTGGGGTCG 175
DB 22412 GGGGAGAGCGGCGAGAGCGGCTGCTC-GCTCCCCCAATTTGGGGCGCTCTGCTGGGAAG 22354
QY 176 CTTAGGGCCCAAGCCCGCCCGGCTCCCAAGCTCCAGGGCTCCCGAGCACCGGCT 235
DB 22353 CTCGAG--CAGAGACCCCGCGCGCCAGCCCGGAGAGCTCCCGAGCGAGGA 22296
QY 236 GCTCGGCCCTTCTTCGTCAGAAAGTCGCCCGCTGGGGGCGAGTTCTGTCCTCCAAAGGTTT 295
DB 22295 GGCTGGTCTTCTTTCAATCGGAAAGTCGCCCGCTTGGGGCGAGTTCTGTCCTCCAGAGGTTT 22236

```

QY      296  CCTGAAGAATCTGAGAGGGCGCAGTCCTTGTACCGAGGAATCTCTGTGTAGCCCTTG 355
      |||||
Db      22235  CCTGAAGAATCTGAGAGGGCGCAGTCCTTGTACTGAGGGAATCTCTGTGTAGCC-GG 22177
      |||||

QY      356  GAGCGCCGCGCCGCCAGAG 375
      |||||
Db      22176  GAGCCCAACGCTGAAGAAG 22157
      |||||

RESULT 12
AC013796
LOCUS      Homo sapiens clone RP11-20H9, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC013796
VERSION    AC013796.4 GI:12583842
KEYWORDS   HTG; HTGS_PHASE0.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 66980)
            Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baldwin,J., Barna,N., Beckerly,R., Boguslavskiy,L., Boukhgalter,B.,
            Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
            Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
            Ferrelira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
            Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
            Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
            McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
            Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
            Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
            Direct Submission
            Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            On Jan 27, 2001 this sequence version replaced gi:7582586.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997).
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            ----- Genome Center
            Center: Whitehead Institute/ MIT Center for Genome Research
            Center code: WtBR
            Web site: http://www-seq.wi.mit.edu
            Contact: sequence_submissions@genome.wi.mit.edu
            ----- Project Information
            Center project name: L3904
            Center clone name: 20_H_9
            -----
            * NOTE: This record contains 83 individual
            * sequencing reads that have not been assembled into
            * contigs. Runs of N are used to separate the reads
            * and the order in which they appear is completely
            * arbitrary. Low-pass sequence sampling is useful for
            * identifying clones that may be gene-rich and allows
            * overlap relationships among clones to be deduced.
            * However, it should not be assumed that this clone
            * will be sequenced to completion. In the event that
            * the record is updated, the accession number will
            * be preserved.
            *
            * 1      683: contig of 683 bp in length
            *      684      783: gap of 100 bp
            *      784      1488: contig of 705 bp in length
            *      1489      1588: gap of 100 bp
            *      1589      2296: contig of 708 bp in length
            *      2297      2396: gap of 100 bp
            *
            * 2297      3101: contig of 705 bp in length
            *      3102      3916: contig of 715 bp in length
            *      3917      4016: gap of 100 bp
            *      4017      4737: contig of 721 bp in length
            *      4738      5557: contig of 720 bp in length
            *      5558      5657: gap of 100 bp
            *      5658      6372: contig of 715 bp in length
            *      6373      7155: contig of 683 bp in length
            *      7156      7255: gap of 100 bp
            *      7256      7958: contig of 702 bp in length
            *      7958      8057: gap of 100 bp
            *      8058      8773: contig of 716 bp in length
            *      8774      9577: gap of 100 bp
            *      9578      9577: contig of 704 bp in length
            *      9578      10392: contig of 715 bp in length
            *      10393      11179: contig of 687 bp in length
            *      11180      11279: gap of 100 bp
            *      11280      11984: contig of 705 bp in length
            *      11985      12084: gap of 100 bp
            *      12085      12791: contig of 707 bp in length
            *      12792      12891: gap of 100 bp
            *      12892      13600: contig of 709 bp in length
            *      13601      13700: gap of 100 bp
            *      13701      14409: contig of 709 bp in length
            *      14410      14509: gap of 100 bp
            *      14510      15221: contig of 712 bp in length
            *      15222      15321: gap of 100 bp
            *      15322      16025: contig of 704 bp in length
            *      16026      16125: gap of 100 bp
            *      16126      16822: contig of 697 bp in length
            *      16823      16922: gap of 100 bp
            *      16923      17621: contig of 699 bp in length
            *      17622      17721: gap of 100 bp
            *      17722      18423: contig of 702 bp in length
            *      18424      18523: gap of 100 bp
            *      18524      19241: contig of 718 bp in length
            *      19242      19341: gap of 100 bp
            *      19342      20056: contig of 715 bp in length
            *      20057      20156: gap of 100 bp
            *      20157      20870: contig of 714 bp in length
            *      20871      20970: gap of 100 bp
            *      20971      21671: contig of 701 bp in length
            *      21672      21771: gap of 100 bp
            *      21772      22480: contig of 709 bp in length
            *      22481      22580: gap of 100 bp
            *      22581      23293: contig of 713 bp in length
            *      23294      23394: gap of 100 bp
            *      23394      24095: contig of 702 bp in length
            *      24096      24195: gap of 100 bp
            *      24196      24916: contig of 721 bp in length
            *      24917      25016: gap of 100 bp
            *      25017      25726: contig of 710 bp in length
            *      25727      25826: gap of 100 bp
            *      25827      26534: contig of 708 bp in length
            *      26535      26634: gap of 100 bp
            *      26635      27333: contig of 699 bp in length
            *      27334      27434: gap of 100 bp
            *      27434      28131: contig of 698 bp in length
            *      28132      28231: gap of 100 bp
            *      28232      28926: contig of 695 bp in length
            *      28927      29026: gap of 100 bp
            *      29027      29758: contig of 732 bp in length
            *      29759      29858: gap of 100 bp
            *      29859      30566: contig of 708 bp in length
            *      30567      30666: gap of 100 bp
            *      30667      31368: contig of 702 bp in length
            *      31369      31468: gap of 100 bp
            *      31469      32183: contig of 715 bp in length
            *      32183: contig of 715 bp in length

```

```
*
* 32184 32283: gap of 100 bp
* 32284 32981: contig of 698 bp in length
* 32982 33081: gap of 100 bp
* 33082 33798: contig of 717 bp in length
* 33799 33898: gap of 100 bp
* 33899 34634: contig of 736 bp in length
* 34635 34734: gap of 100 bp
* 34735 35433: contig of 699 bp in length
* 35434 35533: gap of 100 bp
* 35534 36253: contig of 720 bp in length
* 36254 36353: gap of 100 bp
* 36354 37079: contig of 726 bp in length
* 37080 37179: gap of 100 bp
* 37180 37893: contig of 714 bp in length
* 37894 37993: gap of 100 bp
* 37994 38700: contig of 707 bp in length
* 38701 38800: gap of 100 bp
* 38801 39505: contig of 705 bp in length
* 39506 39605: gap of 100 bp
* 39606 40316: contig of 711 bp in length
* 40317 40416: gap of 100 bp
* 40418 41131: contig of 715 bp in length
* 41132 41231: gap of 100 bp
* 41232 41939: contig of 708 bp in length
* 41940 42039: gap of 100 bp
* 42040 42748: contig of 709 bp in length
* 42749 42848: gap of 100 bp
* 42849 43555: contig of 707 bp in length
* 43556 43655: gap of 100 bp
* 43656 44368: contig of 713 bp in length
* 44369 44468: gap of 100 bp
* 44469 45271: contig of 703 bp in length
* 45172 45271: gap of 100 bp
* 45272 45943: contig of 672 bp in length
* 45944 46043: gap of 100 bp
* 46044 46749: contig of 706 bp in length
* 46750 46849: gap of 100 bp
* 46850 47550: contig of 701 bp in length
* 47551 47650: gap of 100 bp
* 47651 48350: contig of 700 bp in length
* 48351 48450: gap of 100 bp
* 48451 49148: contig of 698 bp in length
* 49149 49248: gap of 100 bp
* 49249 49961: contig of 713 bp in length
* 49962 50061: gap of 100 bp
* 50062 50751: contig of 690 bp in length
* 50752 50851: gap of 100 bp
* 50852 51567: contig of 716 bp in length
* 51568 51667: gap of 100 bp
* 51668 52400: contig of 733 bp in length
* 52401 52500: gap of 100 bp
* 52501 53225: contig of 725 bp in length
* 53226 53325: gap of 100 bp
* 53326 53974: contig of 649 bp in length
* 53975 54074: gap of 100 bp
* 54075 54781: contig of 707 bp in length
* 54782 54881: gap of 100 bp
* 54882 55608: contig of 727 bp in length
* 55609 55708: gap of 100 bp
* 55709 56426: contig of 718 bp in length
* 56427 56526: gap of 100 bp
* 56527 57244: contig of 718 bp in length
* 57245 57344: gap of 100 bp
* 57345 58051: contig of 707 bp in length
* 58052 58151: gap of 100 bp
* 58152 58860: contig of 709 bp in length

Query Match
Best Local Similarity 32.5%; Score 122; DB 2; Length 66980;
Matches 133; Conservative 99.3%; Pred. No. 1.8e-16;
Mismatches 0; Gaps 1; Indels 1;

QY 242 CCCTTCCTCGTGCAGAAAGTCGCCCGGGGCGAGTTCGTCGACCGAGGTTCTCTGTTGGAAGCC 301
|||||
```

```
Db 63886 CCCTTCCTCGTGCAGAAAGTCGCCCGGGGCGAGTTCGTCGCC-AAGGTTTCTCGA 63944
QY 302 AAGAAATCTGAGAGCGCGCAGTCTTTGACCGAGGGAATCTCTGTTGAGCCTTGAAGCC 361
|||||
63945 AAGAAATCTGAGAGCGCGCAGTCTTTGACCGAGGGAATCTCTGTTGAGCCTTGAAGCC 64004
QY 362 GCCAGCCCCAGAG 375
|||||
64005 GCCAGCCCCAGAG 64018
Db

RESULT 13
AC013796/c
LOCUS AC013796 66980 bp DNA linear HTG 27-JAN-2001
DEFINITION Homo sapiens clone RP11-20H9, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC013796
VERSION AC013796.4 GI:12583842
KEYWORDS HTG; HTGS PHASE0
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 66980)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-20H9
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 66980)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearrellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Headford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tefaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Jan 27, 2001 this sequence version replaced gi:7582586.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L3904
Center clone name: 20_H_9
-----
* NOTE: This record contains 83 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1 683: contig of 683 bp in length
* 684 783: gap of 100 bp
* 784 1488: contig of 705 bp in length
* 1489 1588: gap of 100 bp
* 1589 2296: contig of 708 bp in length
```

* 2297 2396: gap of 100 bp
 * 2397 3101: contig of 705 bp in length
 * 3102 3201: gap of 100 bp
 * 3202 3916: contig of 715 bp in length
 * 3917 4016: gap of 100 bp
 * 4017 4737: contig of 721 bp in length
 * 4738 4837: gap of 100 bp
 * 4838 5557: contig of 720 bp in length
 * 5558 5657: gap of 100 bp
 * 5658 6372: contig of 715 bp in length
 * 6373 6472: gap of 100 bp
 * 6473 7155: contig of 683 bp in length
 * 7156 7255: gap of 100 bp
 * 7256 7957: contig of 702 bp in length
 * 7958 8057: gap of 100 bp
 * 8058 8773: contig of 716 bp in length
 * 8774 8873: gap of 100 bp
 * 8874 9577: contig of 704 bp in length
 * 9578 9677: gap of 100 bp
 * 9678 10392: contig of 715 bp in length
 * 10393 10492: gap of 100 bp
 * 10493 11176: contig of 687 bp in length
 * 11180 11279: gap of 100 bp
 * 11280 11984: contig of 705 bp in length
 * 11985 12084: gap of 100 bp
 * 12085 12791: contig of 707 bp in length
 * 12792 12891: gap of 100 bp
 * 12892 13600: contig of 709 bp in length
 * 13601 13700: gap of 100 bp
 * 13701 14409: contig of 709 bp in length
 * 14410 14509: gap of 100 bp
 * 14510 15221: contig of 712 bp in length
 * 15222 15321: gap of 100 bp
 * 15322 16025: contig of 704 bp in length
 * 16026 16125: gap of 100 bp
 * 16126 16822: contig of 697 bp in length
 * 16823 16922: gap of 100 bp
 * 16923 17621: contig of 699 bp in length
 * 17622 17721: gap of 100 bp
 * 17722 18423: contig of 702 bp in length
 * 18424 18523: gap of 100 bp
 * 18524 19241: contig of 718 bp in length
 * 19242 19341: gap of 100 bp
 * 19342 20056: contig of 715 bp in length
 * 20057 20156: gap of 100 bp
 * 20157 20870: contig of 714 bp in length
 * 20871 20970: gap of 100 bp
 * 20971 21671: contig of 701 bp in length
 * 21672 21771: gap of 100 bp
 * 21772 22480: contig of 709 bp in length
 * 22481 22580: gap of 100 bp
 * 22581 23293: contig of 713 bp in length
 * 23294 23393: gap of 100 bp
 * 23394 24095: contig of 702 bp in length
 * 24096 24195: gap of 100 bp
 * 24196 24916: contig of 721 bp in length
 * 24917 25016: gap of 100 bp
 * 25017 25726: contig of 710 bp in length
 * 25727 25826: gap of 100 bp
 * 25827 26534: contig of 708 bp in length
 * 26535 26634: gap of 100 bp
 * 26635 27333: contig of 699 bp in length
 * 27334 27433: gap of 100 bp
 * 27434 28131: contig of 698 bp in length
 * 28132 28231: gap of 100 bp
 * 28232 28926: contig of 695 bp in length
 * 28927 29026: gap of 100 bp
 * 29027 29758: contig of 732 bp in length
 * 29759 29858: gap of 100 bp
 * 29859 30566: contig of 708 bp in length
 * 30567 30666: gap of 100 bp
 * 30667 31368: contig of 702 bp in length
 * 31369 31468: gap of 100 bp

* 31469 32183: contig of 715 bp in length
 * 32184 32283: gap of 100 bp
 * 32284 32981: contig of 698 bp in length
 * 32982 33081: gap of 100 bp
 * 33082 33798: contig of 717 bp in length
 * 33799 33898: gap of 100 bp
 * 33899 34634: contig of 736 bp in length
 * 34635 34734: gap of 100 bp
 * 34735 35433: contig of 699 bp in length
 * 35434 35533: gap of 100 bp
 * 35534 36253: contig of 720 bp in length
 * 36254 36353: gap of 100 bp
 * 36354 37079: contig of 726 bp in length
 * 37080 37179: gap of 100 bp
 * 37180 37893: contig of 714 bp in length
 * 37894 37993: gap of 100 bp
 * 37994 38700: contig of 707 bp in length
 * 38701 38800: gap of 100 bp
 * 38801 39505: contig of 705 bp in length
 * 39506 39605: gap of 100 bp
 * 39606 40316: contig of 711 bp in length
 * 40317 40416: gap of 100 bp
 * 40418 41131: contig of 715 bp in length
 * 41132 41231: gap of 100 bp
 * 41232 41939: contig of 708 bp in length
 * 41940 42039: gap of 100 bp
 * 42040 42748: contig of 709 bp in length
 * 42749 42848: gap of 100 bp
 * 42849 43555: contig of 707 bp in length
 * 43556 43655: gap of 100 bp
 * 43656 44368: contig of 713 bp in length
 * 44369 44468: gap of 100 bp
 * 44469 45171: contig of 703 bp in length
 * 45172 45271: gap of 100 bp
 * 45272 45943: contig of 672 bp in length
 * 45944 46043: gap of 100 bp
 * 46044 46749: contig of 706 bp in length
 * 46750 46849: gap of 100 bp
 * 46850 47550: contig of 701 bp in length
 * 47551 47650: gap of 100 bp
 * 47651 48350: contig of 700 bp in length
 * 48351 48450: gap of 100 bp
 * 48451 49148: contig of 698 bp in length
 * 49149 49248: gap of 100 bp
 * 49249 49961: contig of 713 bp in length
 * 49962 50061: gap of 100 bp
 * 50062 50751: contig of 690 bp in length
 * 50752 50851: gap of 100 bp
 * 50852 51567: contig of 716 bp in length
 * 51568 51667: gap of 100 bp
 * 51668 52400: contig of 733 bp in length
 * 52401 52500: gap of 100 bp
 * 52501 53225: contig of 725 bp in length
 * 53226 53325: gap of 100 bp
 * 53326 53974: contig of 649 bp in length
 * 53975 54074: gap of 100 bp
 * 54075 54781: contig of 707 bp in length
 * 54782 54881: gap of 100 bp
 * 54882 55608: contig of 727 bp in length
 * 55609 55708: gap of 100 bp
 * 55709 56426: contig of 718 bp in length
 * 56427 56526: gap of 100 bp
 * 56527 57244: contig of 718 bp in length
 * 57245 57344: gap of 100 bp
 * 57345 58051: contig of 707 bp in length
 * 58052 58151: gap of 100 bp
 * 58152 58860: contig of 709 bp in length

Query Match 19.7% Score 74; DB 2; Length 66980;
 Best Local Similarity 100.0%; Pred. No. 3.7e-06;
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Db      48350 AAGAACTCAGAGGCGCAGTCTTACCGAGGAATCTCTGTGTAGCTTGGAGCC 48291
QY      362 GCCAGCCCGCAGAG 375
Db      48290 GCCAGCCCGCAGAG 48277

RESULT 14
LOCUS   PM12B8G/c
DEFINITION Penicillium marneffeii STS, clone pm12b8.g, sequence tagged site.
ACCESSION AL684326
VERSION   AL684326.1 GI:19337430
KEYWORDS STS.
SOURCE   Penicillium marneffeii
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
          Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
REFERENCE 1
AUTHORS  Yuen,K.Y., Pascal,G., Wong,S.S., Glaser,P., Woo,P.C., Kunst,F.,
          Cai,J.J., Cheung,B.Y., Medigue,C. and Danchin,A.
TITLE    Exploring the Penicillium marneffeii genome
JOURNAL  Arch. Microbiol. 179 (5), 339-353 (2003)
MEDLINE  22595073
PUBMED   12640520
REFERENCE 2 (bases 1 to 521)
AUTHORS  Danchin,A. and Pascal,G.
TITLE    Direct Submission
JOURNAL  Submitted (08-MAR-2002) Danchin A., HKU-Pasteur Research Centre,
          Dexter HC Man Building 8, Sassoon Road, Pokfulam, Hong Kong
FEATURES
    source
        1..521
            /organism="Penicillium marneffeii"
            /mol_type="genomic DNA"
            /db_xref="taxon:37727"
            /clone="pm12b8.g"

ORIGIN
Query Match      14.1%; Score 53; DB 11; Length 521;
Best Local Similarity 51.0%; Pred. No. 0.26;
Matches 122; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
QY      48 GGGGCGCGAGTGAAGCTGGAGTTCCGGGTGGCGGGAGGCGGACTGTCCGTGTGCTG 107
Db      317 GGGCGCGCGGGGGCGGGGGGGTGGCGGGCGCGCGCGCGCGCGCGCGCGCGCGG 258
QY      108 AGCGCGCGGAGAGCGGCGCGGCGGCTGATCGGCTCCCTCGAACTCGGGAGGTCCAG 167
Db      257 GCGCGGGGGGGGGCGGGCGGGGGGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 198
QY      168 TGGGGTGTCTAGGGCCCAAGCCCGCCACCGGCTCCAAAGCTCCAGGGCTCCCCAG 227
Db      197 GGGGGGGGGGGGGGGGGGGGGCGGGCGCGCGCGCGCGCGCGCGCGCGGGG 138
QY      228 GCACCGGTGTGCGCCCTTCTTCGTGTGAGAAAGTCCGCCCGCGGGGGGAGTTCGTCCC 286
Db      137 GCGCGCGCGGGGGGGGGCGCGCGCGGGGGGGGGCGCGCGCGGGGGGGGGCGGGCC 79

RESULT 15
AC148923/c
LOCUS   AC148923
DEFINITION Alligator mississippiensis clone VMRC8-211A13, WORKING DRAFT
SEQUENCE, 10 unordered pieces.
ACCESSION AC148923
VERSION   AC148923.2 GI:48427699
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT;
SOURCE   Alligator mississippiensis (American alligator)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Archosauria; Crocodylidae; Alligatorinae; Alligator.
REFERENCE 1 (bases 1 to 134226)

```

AUTHORS

Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W.,
 Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,B.,
 Coleman,H., Daki,N., Engle,J., Guan,X., Gupta,J., Haghighi,P.,
 Han,J., Hansen,N., Ho,S.-L., Hu,P., Hurle,B., Idol,J.R., Jones,C.,
 Karlins,E., Kim,H., Kwong,P., Laric,P., Larson,S., Lee-Lin,S.-O.,
 Legaspi,R., Madden,M., Maduro,Q.L., Maduro,V.B., Margulies,E.H.,
 Mastaglio,C., Maskeri,B., McDowell,J., Mullikin,J.C., Faguirigan,C.,
 Park,M., Portnoy,M.E., Prasad,A., Puri,O., Reddix-Dugue,N.,
 Shandler,K., Schueier,M.G., Shah,K., Sison,C., Stantripoop,S.,
 Thomas,J.W., Thomas,P.J., Tsipouri,V., Vogt,J.L., Wetherby,K.D.,
 Young,A. and Green,E.D.

NISC Comparative Sequencing Initiative

Unpublished

2 (bases 1 to 134226)

Green,E.D.

Direct Submission

Submitted (24-APR-2004) NIH Intramural Sequencing Center, 8717
 Grovemont Circle, Gaithersburg, MD 20877, USA

3 (bases 1 to 134226)

Green,E.D.

Direct Submission

Submitted (08-JUN-2004) NIH Intramural Sequencing Center, 8717
 Grovemont Circle, Gaithersburg, MD 20877, USA

On Jun 8, 2004 this sequence version replaced gi:46559454.

COMMENT

----- Genome Center

Center: NIH Intramural Sequencing Center

Center code: NISC

Web site: http://www.nisc.nih.gov

Contact: nisc_zoo@nhgri.nih.gov

----- Project Information

Center project name: gng

Center clone name: 211A13

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 130266 bases at least Q40

Consensus quality: 131160 bases at least Q30

Consensus quality: 132052 bases at least Q20

Insert size: 137000; agarose-fp

Insert size: 133326; sum-of-contigs

Quality coverage: 12.67x in Q20 bases; agarose-fp

Quality coverage: 13.02x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 10 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 2413: contig of 2413 bp in length

* 2414 2513: gap of unknown length

* 2514 5428: contig of 2915 bp in length

* 5429 5528: gap of unknown length

* 5529 8416: contig of 2887 bp in length

* 8416 8515: gap of unknown length

* 8515 11298: contig of 2783 bp in length

* 11299 11398: gap of unknown length

* 11399 13851: contig of 2453 bp in length

* 13852 13951: gap of unknown length

* 13952 20601: contig of 6649 bp in length

* 20601 20701: gap of unknown length

* 20701 30256: contig of 9556 bp in length

* 30257 30356: gap of unknown length

* 30357 46982: contig of 16625 bp in length

* 46982 47081: gap of unknown length

* 47082 84167: contig of 37086 bp in length

* 84168 84267: gap of unknown length

* 84268 134226: contig of 49959 bp in length.

* Location/Qualifiers

1. .134226

source

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 06:13:29 ; Search time 272.403 Seconds
(without alignments)
8149.338 Million cell updates/sec

Title: US-09-977-579-4_COPY_1_375

Perfect score: 375

Sequence: 1 cctcccttcgagctgagc.....gaagccgagcccccagaag 375

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	375	100.0	1261	3 AAC67837	AAC67837 Human bet
2	375	100.0	1261	10 ADB78651	ADB78651 Human ion
3	375	100.0	1261	10 ACF57870	ACF57870 Human SCN
4	369.8	98.6	4052	6 ABA93727	ABA93727 Human sig
5	288.4	76.9	953	13 ADS10151	ADS10151 Human the
6	288.4	76.9	978	4 AAH98320	AAH98320 Human EST
7	288.4	76.9	978	13 ADS11487	ADS11487 Human the
8	286.8	76.5	1045	4 AAK52345	AAK52345 Human pol
9	44.8	11.9	29340	13 ABD33482	ABD33482 Human can
10	42.6	11.4	4650	10 ADC32422	ADC32422 Human nov
11	41.2	11.0	922	10 ADC86708	ADC86708 Human GPC
12	41.2	11.0	4542	10 ADC30607	ADC30607 Human nov
13	40.2	10.7	766	12 ADJ39052	ADJ39052 Plant cDN
14	40.2	10.7	1678	12 ADE28355	ADE28355 Human KPP
15	40.2	10.7	2304	13 ACN43300	ACN43300 Human dia
16	40.2	10.7	2377	13 ACN43299	ACN43299 Human dia
17	40.2	10.7	2387	13 ACN43298	ACN43298 Human dia
18	40.2	10.7	2603	13 ACN43295	ACN43295 Human dia
19	40.2	10.7	2806	2 AAZ40538	AAZ40538 Full leng
20	40.2	10.7	2811	5 AAS83495	AAS83495 DNA encod

ALIGNMENTS

RESULT 1

AAC67837
ID AAC67837 standard; CDNA; 1261 BP.

AC AAC67837;

DT 15-FEB-2001 (first entry)

XX Human beta3 CDNA.

XX Human; beta sub-unit; beta3; analgesic; anticonvulsant;
KW cerebroprotective; vasotropic; cardiac; nootropic; cytostatic;
KW dermatological; gene therapy; voltage-gated sodium channel; pain;
KW epilepsy; stroke; ischaemia; heart disease; Jacobsen Syndrome;
KW familial nonchromaffin paraganglioma; phenylketonuria;
KW Charcot Marie tooth disease; ss.

OS Homo sapiens.

XX WO200063367-A1.

PN 26-OCT-2000.

PD 24-FEB-2000; 2000WO-EF001783.

XX 15-APR-1999; 99US-0129473P.

XX (WARN) WARNER LAMBERT CO.

PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX Cox P, Dixon A, Jackson A, Morgan K;

XX WPI; 2000-665241/64.

DR P-PSDB; AAB36002.

XX Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium channel, and their corresponding polypeptides, useful for detecting and treating sodium channel-associated conditions, e.g. pain, epilepsy and stroke.

PS Claim 10; Page 70-71; 88pp; English.

XX The present sequence is given in the claims of a specification relating

Adh23361 Human PAK
Acn40564 Tumour-as
Adc37306 Nuclear f
Adl22600 Human dis
Ade62339 Human gen
Ade60439 Human gen
Adq85762 Human tum
Adq84045 Human tum
Adq84295 Human tum
Adq83621 Human tum
Adq86840 Human tum
Adj19056 Human ins
Adl10418 Full leng
Abx37073 Bovine ES
Abk83742 Human cDN
Adq21323 Human sof
Adq25196 Human sof
Ade57070 Human gen
Ade57074 Human gen
Adj39230 Plant cDN
Ad89110 Human ONE
Ach89785 Human gen
ABK73545 Bacillus
AB199475 Mouse isc
Adp65862 Mouse EST

21 40.2 10.7 2838 12 ADH23361
22 40.2 10.7 2838 13 ACN40564
23 40.2 10.7 3025 10 ADC37306
C 24 40.2 10.7 4813 11 ADL22600
C 25 40.2 10.7 4881 10 ADE62339
C 26 40.2 10.7 4881 10 ADE60439
27 40.2 10.7 6231 12 ADQ85762
28 40.2 10.7 6231 13 ADQ84045
29 40.2 10.7 6231 13 ADQ84295
30 40.2 10.7 6231 13 ADQ83621
31 40.2 10.7 6231 13 ADQ86840
C 32 40.2 10.7 20000 12 ADJ19056
C 33 40 10.7 4147 13 ADR10418
34 39.8 10.6 392 8 ABX37073
35 39.6 10.6 2685 6 ABK83742
C 36 39.6 10.6 4233 12 ADQ21323
C 37 39.6 10.6 4244 12 ADQ25196
C 38 39.6 10.6 28564 10 ADE57070
C 39 39.6 10.6 28564 10 ADE57074
40 39.2 10.5 759 12 ADJ39230
C 41 39.2 10.5 6001 13 AD89110
C 42 39 10.4 587 12 ACH89785
43 39 10.4 936 6 ABK73545
44 39 10.4 3272 6 AB199475
45 38.8 10.3 1041 11 ADP65862


```
Db      361  GCGGAGCCCGAGAG 375
|||||
RESULT 3
ACF57870
ID      ACF57870 standard; cDNA; 1261 BP.
XX
AC      ACF57870;
XX
DT      15-JAN-2004 (first entry)
XX
DE      Human SCN3B protein encoding cDNA.
XX
KW      SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
KW      neuroprotective; anesthetic; cytotatic; cerebroprotective; cardiant;
KW      hypotensive; gene therapy; SCN3B; human; gene; ss.
XX
OS      Homo sapiens.
XX
FH      Key
CD      376..1023
FT      /*tag= a
FT      /product= "SCN3B"
XX
PN      WO2003072751-A2.
XX
PD      04-SEP-2003.
XX
PF      25-FEB-2003; 2003WO-US006010.
XX
PR      25-FEB-2002; 2002US-0359382P.
XX
PA      (UYVA-) UNIV VANDERBILT.
XX
PI      George AL, Lossin C;
XX
DR      WPI; 2003-712725/67.
DR      P-PSDB; ABR83183.
XX
PT      Recombinantly expressed sodium channel type 1 alpha subunit, useful in
PT      screening for modulators, for treating e.g. epilepsy.
XX
PS      Disclosure; Page 145-147; 176pp; English.
XX
CC      The invention relates to a recombinantly expressed and isolated human
CC      SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
CC      incorporated into a cell, is used to screen for specific modulators,
CC      potentially useful as anticonvulsant, antiepileptic, neuroprotective,
CC      analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
CC      epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
CC      motor endplate diseases, hypertension, congestive heart failure and
CC      muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
CC      and metastatic cancer cell lines). These activities can also be provided
CC      by gene therapy vectors that express (I) or the modulators. The
CC      modulators, also antibodies directed against (I), are used to detect
CC      sodium channel polypeptides. The present sequence represents a human
CC      SCN3B protein encoding cDNA
XX
SQ      Sequence 1261 BP; 263 A; 366 C; 372 G; 260 T; 0 U; 0 Other;
Query Match      100.0%; Score 375; DB 10; Length 1261;
Best Local Similarity 100.0%; Pred. No. 8e-83;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1  CCCTCCCTTCGAGCTTACCTCGGGCGCAACGAGCGAGCGAGGCGCGAGTGG 60
Db      1  CCCTCCCTTCGAGCTTACCTCGGGCGCAACGAGCGAGCGAGGCGCGAGTGG 60
Qy      61  AAGCTGAGTTCGGGGTGGGGGAGGCGACTGTCGTTGCTGAGCGCCGCGAGA 120
Db      61  AAGCTGAGTTCGGGGTGGGGGAGGCGACTGTCGTTGCTGAGCGCCGCGAGA 120

Qy      121  GCGGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGTGCTTAG 180
Db      121  GCGGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGTGCTTAG 180
Qy      181  GGCCCAAAGCCCCCAGCGGCTCCAAAAGTCCAGGGCTCCCGAGGACACCGGTGCTCG 240
Db      181  GGCCCAAAGCCCCCAGCGGCTCCAAAAGTCCAGGGCTCCCGAGGACACCGGTGCTCG 240
Qy      241  GCCCTTCCTTCGGTCCAGAAAGTCCGCCCTGGGGGAGTTCGTCCTCCAAAGGTTTCCTCG 300
Db      241  GCCCTTCCTTCGGTCCAGAAAGTCCGCCCTGGGGGAGTTCGTCCTCCAAAGGTTTCCTCG 300
Qy      301  AAAGAATCTGAGAGGGCGCAGTCTTGACCGAGGGAATCTCTGTGTAGCTTTGGAAGC 360
Db      301  AAAGAATCTGAGAGGGCGCAGTCTTGACCGAGGGAATCTCTGTGTAGCTTTGGAAGC 360
Qy      361  CGCCAGCCCCAGAAAG 375
Db      361  CGCCAGCCCCAGAAAG 375

RESULT 4
ABA93727
ID      ABA93727 standard; cDNA; 4052 BP.
XX
AC      ABA93727;
XX
DT      30-APR-2002 (first entry)
XX
DE      Human signal transduction cDNA clone amy2_2f18.
XX
KW      Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
KW      gene therapy; ss.
XX
OS      Homo sapiens.
XX
PN      WO200198454-A2.
XX
PD      27-DEC-2001.
XX
PF      25-APR-2001; 2001WO-IB002050.
XX
PR      25-APR-2000; 2000US-0199380P.
XX
PA      (GEHU-) GERMAN HUMAN GENOME PROJECT.
XX
PI      Wiemann S;
XX
DR      WPI; 2002-055860/07.
DR      P-PSDB; ABB05689.
XX
PT      Human cDNA sequences and clones derived from human fetal brain, fetal
PT      kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
PT      screening and therapy.
XX
PS      Claim 1; Page 174-175; 611pp; English.
XX
CC      The present invention describes assemblages and computer readable media
CC      comprising novel human cDNA sequences and clones derived from human
CC      foetal brain, foetal kidney, melanoma, testis and amygdala cDNA
CC      libraries. ABA93702 to ABA93766 represent human cDNA sequences from the
CC      present invention which encode the proteins given in ABB05662 to
CC      ABB05729. The human cDNA sequences and clones can be used in gene
CC      therapy. The clones may be used in a variety of applications, for example
CC      they may be used in profiling assays, for providing large arrays of human
CC      genetic material for implementing large-scale screening strategies and
CC      for treating diseases via gene therapy procedures
XX
SQ      Sequence 4052 BP; 994 A; 1033 C; 1036 G; 989 T; 0 U; 0 Other;
Query Match      98.6%; Score 369.8; DB 6; Length 4052;
Best Local Similarity 99.5%; Pred. No. 1.8e-81;
Matches 371; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 3 CTCCTTCCGAGCTGAGCTTACCTCTGGGCGCAAAACGAGCGAGGCGGCGAGTGGAA 62
DB 431 CTCCTTCCGAGCTGAGCTTACCTCTGGGCGCAAAACGAGCGAGGCGGCGAGTGGAA 490
QY 63 GCTGGAGTTCCGGGCTGGGCGGAGCGGAGCTGCTCGTGGTCTGAGCGCGGCGAGGC 122
DB 491 GCTGGAGTTCCGGGCTGGGCGGAGCGGAGCTGCTCGTGGTCTGAGCGCGGCGAGGC 550
QY 123 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCAGTGGGCTCGCTTAGGG 182
DB 551 GGGCGGAGCGGCTGATCAGCTCCCTCGAACTGGGAGGTCAGTGGGCTCGCTTAGGG 610
QY 183 CCCAAGCCCCCACCAGGCTCCAAAGCTCCAGGGGCTCCCGAGGACCGGTCGTCGGC 242
DB 611 CCCAAGCCCCCAGGCTCCAAAGCTCCAGGGGCTCCCGAGGACCGGTCGTCGGC 670
QY 243 CCTTCCTTCGGTCAGAAAGTCGCGCCCTCGGGGAGTTCGTCCTCCAAAGGTTTCCTCGAA 302
DB 671 CCTTCCTTCGGTCAGAAAGTCGCGCCCTCGGGGAGTTCGTCCTCCAAAGGTTTCCTCGAA 730
QY 303 AGAATCTGAGAGGCGCAGTCCCTTGACCGAGGGAATCTCTCTGTGTAGCTTTGGAAAGCCG 362
DB 731 AGAATCTGAGAGGCGCAGTCCCTTGACCGAGGGAATCTCTCTGTGTAGCTTTGGAAAGCCG 790
QY 363 CAGCCCCCAGAAG 375
DB 791 CCAGCCCCAGAAG 803
RESULT 5
ID ADS10151 standard; DNA; 953 BP.
XX
AC ADS10151;
DT 16-DEC-2004 (first entry)
XX
DE Human therapeutic DNA - SEQ ID 388.
XX
KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
OS Homo sapiens.
XX
PN WO2004080148-A2.
XX
PD 23-SEP-2004.
XX
PF 30-SEP-2003; 2003WO-US030720.
XX
PR 02-OCT-2002; 2002US-0416186P.
XX
PA (NUVE-) NUVELO INC.
XX
PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
DR WPI: 2004-668857/65.
DR P-PSDB; ADS10835.
XX
PT New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.
XX
PS Claim 1; SEQ ID NO 388; 718pp; English.
XX
CC The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell

CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic DNA of
CC the invention. The current sequence is not shown explicitly within the
CC specification but can be accessed from the WIPO web-site.

XX
SQ Sequence 953 BP; 180 A; 279 C; 290 G; 204 T; 0 U; 0 Other;
Query Match 76.9%; Score 288.4; DB 13; Length 953;
Best Local Similarity 99.7%; Pred. No. 1.7e-61;
Matches 289; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 86 GAGGCGACTGTCCTGGTCTGAGCGCGCGGAGAGCGGCGGAGCGGCTGATCGGCT 145
DB 37 GTGGCGACTGTCCTGGTCTGAGCGCGCGGAGAGCGGCGGAGCGGCTGATCGGCT 96
QY 146 CCCTCGAACTGGGGAGGTCAGTGGGTCGCTTAGGGCCCAAAGCCCCACCCGGTCCA 205
DB 97 CCCTCGAACTGGGGAGGTCAGTGGGTCGCTTAGGGCCCAAAGCCCCACCCGGTCCA 156
QY 206 AAAGCTCCAGGGCTCCCGAGGACCGGTGTCGGCCCTTCTTCGGTCAAGAAATCGC 265
DB 157 AAAGCTCCAGGGCTCCCGAGGACCGGTGTCGGCCCTTCTTCGGTCAAGAAATCGC 216
QY 266 CCCCTGGGGCAGTTCGTCCTCCAAAGGTTTCCTCGAAAGAAATCTGAGAGGCGCAGTCCT 325
DB 217 CCCCTGGGGCAGTTCGTCCTCCAAAGGTTTCCTCGAAAGAAATCTGAGAGGCGCAGTCCT 276
QY 326 TGACCGAGGGAATCTCTGTGTAGCTTGGAAAGCGCCAGCCCGCCAGAAAG 375
DB 277 TGACCGAGGGAATCTCTGTGTAGCTTGGAAAGCGCCAGCCCGCCAGAAAG 326

RESULT 6
AAH98320
ID AAH98320 standard; cDNA; 978 BP.
XX
AC AAH98320;
DT 12-OCT-2001 (first entry)
XX
DE Human EST-derived coding sequence SEQ ID NO: 177.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002687.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
XX
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI: 2001-476164/51.
DR P-PSDB; AAM23661.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
PS Claim 1; Page 299-300; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention
XX
SQ Sequence 978 BP; 193 A; 283 C; 293 G; 209 T; 0 U; 0 Other;

Query Match 76.9%; Score 288.4; DB 4; Length 978;
Best Local Similarity 99.7%; Pred. No. 1.7e-61;
Matches 289; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 86 GAGCGCACTGTCCTGGTGTGCTGAGCGCGCGGAGCGGCGGCGGCGGCGGCTGATCGGCT 145
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
5 GTGCGCACTGTCCTGGTGTGCTGAGCGCGCGGAGCGGCGGCGGCGGCGGCTGATCGGCT 64
QY 146 CCCTCGAACTGGGAGGTCCAGTGGGTGCTTGGGCGCCAAAGCCCCCGGCTCCA 205
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
65 CCCTCGAACTGGGAGGTCCAGTGGGTGCTTGGGCGCCAAAGCCCCCGGCTCCA 124
QY 206 AAAGCTCCAGGGCTCCCGAGGACCGGTGCTCGGCGCCCTTCTCGGTGAGAAAGTCGC 265
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
125 AAAGCTCCAGGGCTCCCGAGGACCGGTGCTCGGCGCCCTTCTCGGTGAGAAAGTCGC 184
QY 266 CCCTCGGAGGACCTCTCTGTAGCCTTGGAGCGCGCCAGCCCGCAGAAG 375
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
245 TGACCGAGGAATCTCTGTGTAGCCTTGGAGCGCGCCAGCCCGCAGAAG 294

RESULT 7
ADSL1487
ID ADSL1487 standard; DNA; 978 BP.
XX AC ADSL1487;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human therapeutic contig DNA - SEQ ID 1724.
XX
KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
XX
OS Homo sapiens.
XX
PN WO2004080148-A2.
XX
PD 23-SEP-2004.
XX
PF 30-SEP-2003; 2003WO-US030720.
XX
PR 02-OCT-2002; 2002US-0416186P.
XX
PA (NUVE-) NUVELO INC.
XX
PI Tang YT, Asundi V, Ren F, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AU, Weng G, Zhou P;
PI WPI; 2004-668857/65.
DR P-PSDB; ADS12085.
XX
PT New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.
XX

PS Example 2; SEQ ID NO 1724; 718pp; English.
XX
CC The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic contig
CC DNA of the invention. The current sequence is not shown explicitly within
CC the specification but can be accessed from the WIPO web-site.
XX
SQ Sequence 978 BP; 193 A; 283 C; 293 G; 209 T; 0 U; 0 Other;

Query Match 76.9%; Score 288.4; DB 13; Length 978;
Best Local Similarity 99.7%; Pred. No. 1.7e-61;
Matches 289; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 86 GAGCGCACTGTCCTGGTGTGCTGAGCGCGCGGAGCGGCGGCGGCGGCTGATCGGCT 145
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
5 GTGCGCACTGTCCTGGTGTGCTGAGCGCGCGGAGCGGCGGCGGCGGCGGCTGATCGGCT 64
QY 146 CCCTCGAACTGGGAGGTCCAGTGGGTGCTTGGGCGCCAAAGCCCCCGGCTCCA 205
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
65 CCCTCGAACTGGGAGGTCCAGTGGGTGCTTGGGCGCCAAAGCCCCCGGCTCCA 124
QY 206 AAAGCTCCAGGGCTCCCGAGGACCGGTGCTCGGCGCCCTTCTCGGTGAGAAAGTCGC 265
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
125 AAAGCTCCAGGGCTCCCGAGGACCGGTGCTCGGCGCCCTTCTCGGTGAGAAAGTCGC 184
QY 266 CCCTCGGAGGACCTCTCTGTAGCCTTGGAGCGCGCCAGCCCGCAGAAG 375
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
185 CCCTCGGAGGACCTCTCTGTAGCCTTGGAGCGCGCCAGCCCGCAGAAG 294
QY 326 TGACCGAGGAATCTCTGTGTAGCCTTGGAGCGCGCCAGCCCGCAGAAG 375
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
245 TGACCGAGGAATCTCTGTGTAGCCTTGGAGCGCGCCAGCCCGCAGAAG 294

RESULT 8
AAKS2345
ID AAKS2345 standard; cDNA; 1045 BP.
XX AC AAKS2345;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 890.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI: 2001-476283/51.
 DR P-PSDB; AAM79212.
 XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 in diagnosis and gene therapy.
 PT Claim 1; Page 2934-2935; 6221pp; English.
 PS The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3656 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 SQ Sequence 1045 BP; 222 A; 289 C; 314 G; 220 T; 0 U; 0 Other;
 Query Match 76.5%; Score 286.8; DB 4; Length 1045;
 Best Local Similarity 99.3%; Pred. No. 4.2e-51;
 Matches 288; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 86 GAGGCGACTGTCTCGTGGTCTGAGCGCCGCGGAGAGCGGGCGGAGCGGCTGATCGGCT 145
 Db 12 GTGGCGACTGTCTCGTGGTCTGAGCGCCGCGGAGAGCTGGCGGAGCGGCTGATCGGCT 71
 QY 146 CCCTCGAATCGGGAGGTTCAGTGGGGTGGCTTAGGGCCCAAGCCCCACCGGCTCA.205
 Db 72 CCCTCGAATCGGGAGGTTCAGTGGGGTGGCTTAGGGCCCAAGCCCCACCGGCTCA 131
 QY 206 AAAGCTCCAGGGCCCTCCCGAGCCGCTGCTCGGCCCTTCTTCGTCAGAAAGTCGC 265
 Db 132 AAAGCTCCAGGGCCCTCCCGAGCCGCTGCTCGGCCCTTCTTCGTCAGAAAGTCGC 191
 QY 266 CCCTCGGGGCGAGTTCGTCCTCCAAAGGGTTTCCTCGAAAGAAATCTGAGAGGGCGCAGTCTCT 325
 Db 192 CCCTCGGGGCGAGTTCGTCCTCCAAAGGGTTTCCTCGAAAGAAATCTGAGAGGGCGCAGTCTCT 251
 QY 326 TGACCGAGGGAATCTCTGTGTAGCTTGGAAAGCCGCCAGCCCAAGAAG 375
 Db 252 TGACCGAGGGAATCTCTGTGTAGCTTGGAAAGCCGCCAGCCCAAGAAG 301
 RESULT 9
 ABD33482
 ID ABD33482 standard; DNA; 29340 BP.
 XX
 AC ABD33482;
 AC
 XX 18-NOV-2004 (first entry)
 DT
 XX Human cancer-associated (CA) gene HD07-093.
 DE
 XX Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
 XX Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
 KW ds; cancer; cytostatic.
 KW
 XX Homo sapiens.
 OS
 XX WO2004058146-A2.
 PN
 XX 15-JUL-2004.
 PD
 XX

PF 15-DEC-2003; 2003WO-US040081.
 XX
 PR 17-DEC-2002; 2002US-00322281.
 XX
 PA (SAGR-) SAGRES DISCOVERY INC.
 XX
 PI Morris DW, Malandro MS;
 XX
 DR WPI: 2004-499109/47.
 XX
 PT Novel human cancer associated protein encoded within open reading frame
 of cancer associated gene, useful as targets for diagnosing cancer.
 PT
 XX Claim 16; SEQ ID NO 642; 182pp; English.
 PS The invention relates to cancer-associated proteins (CAP) and the cancer-
 CC associated (CA) nucleic acids encoding them. The invention also relates
 CC to a method for treating cancers involving administering to a patient an
 CC inhibitor of CAP, and a method of screening for anticancer activity in a
 CC potential drug involving providing a cell that expresses a CA gene,
 CC contacting a tissue sample derived from a cancer cell with an anticancer
 CC drug candidate and monitoring the effect of the anticancer drug candidate
 CC on expression of the CA gene. The CAP proteins are useful for detecting
 CC cancer associated with expression of a CAP protein in a test cell sample
 CC and for screening for a bioactive agent capable of modulating the
 CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
 CC cancer, involving determining the expression of a CA nucleic acid in a
 CC tissue. This sequence represents a human CA gene of the invention. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 SQ Sequence 29340 BP; 6351 A; 8588 C; 8017 G; 5384 T; 0 U; 0 Other;
 Query Match 11.9%; Score 44.8; DB 13; Length 29340;
 Best Local Similarity 56.7%; Pred. No. 0.28;
 Matches 102; Conservative 0; Mismatches 77; Indels 1; Gaps 1;
 QY 74 GGGGTGGGGGGGAGGCGACTGTCTCGTGGTGTAGCCCGGCGAGAGCGGGCGGAGC 133
 Db 9834 GGGAGGGGGGGGTAGGGGACCTTTTCAGAGCCAGGAGGGGTTTCGGGGGGCGTGGGGGGCGC 9893
 QY 134 GCCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTCG-CTTAGGGCCCCCAAGCCC 192
 Db 9894 TCGGAGCGGAGCCCGGGCTCGACGGCGTGGCTGGCGCGAGTGTATGACAGCGCGC 9953
 QY 193 CCACCGGGCTCCAAAGCTCCAGGGCTCCCGAGGCAACCGGTGTCTGGCCCTTCCTTCG 252
 Db 9954 CCGGCCCGAAACCCGAGCCCGGGGCTCCCAACCCGCGGCTCCCGCCCTCCCGCGC 10013
 RESULT 10
 ADC32422
 ID ADC32422 standard; cDNA; 4650 BP.
 XX
 AC ADC32422;
 AC
 XX 18-DEC-2003 (first entry)
 DT
 XX Human novel cDNA contig sequence, SEQ ID NO:2504.
 DE
 XX Human; diagnostic; drug screening; forensics; gene mapping;
 KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;
 KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
 KW ulcers; osteoporosis; autoimmune disease; cancer;
 KW molecular weight marker; food supplement; antiparkinsonian; nootropic;
 KW neuroprotective; antianemic; anticoagulant; thrombolytic; vulnerary;
 KW antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
 KW gene therapy; chromosome 20; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO2003029271-A2.
 PN


```
XX PD 10-APR-2003.
XX XX
XX PF 24-SEP-2002; 2002WO-US030474.
XX XX
XX PR 24-SEP-2001; 2001US-0324631P.
XX XX
XX PA (HYSE-) HYSEQ INC.
XX XX
XX PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
XX PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
XX PI Haley-Vicente D, Drmanac RT;
XX XX
XX DR WPI; 2003-371981/35.
XX DR P-PSDB; ADC33189.
XX XX
XX PT New polynucleotide and polypeptide useful for diagnosing, preventing or
XX PT treating conditions such as neurodegenerative diseases, anemias, platelet
XX PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
XX PT cancer.
XX XX
XX PS Example 2; SEQ ID NO 2504; 1185pp; English.
XX XX
XX CC The invention relates to 971 novel human cDNA sequences (ADC29919-
XX CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
XX CC invention also relates to nucleic acid sequences over 99% identical with
XX CC the novel human cDNAs. The invention additionally encompasses expression
XX CC vectors and host cells comprising a nucleic acid of the invention; the
XX CC recombinant production of a polypeptide of the invention; an antibody
XX CC against a polypeptide of the invention; a method of detecting
XX CC polynucleotides or polypeptides of the invention; and methods of
XX CC identifying a compound which binds to a polypeptide of the invention. The
XX CC invention further discloses methods of preventing, treating or
XX CC ameliorating a medical condition; kits comprising polynucleotide probes
XX CC and/or monoclonal antibodies for carrying out the methods of the
XX CC invention; methods for the identification of compounds that modulate the
XX CC expression or activity of the polynucleotide and/or polypeptide; and 767
XX CC contig sequences corresponding to the cDNA sequences of the invention
XX CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
XX CC -ADC33394). The nucleic acids and polypeptides of the invention are
XX CC useful in diagnostics, drug screening, forensics, gene mapping, in the
XX CC identification of mutations responsible for genetic disorders or other
XX CC traits, for assessing biodiversity, and in producing many other types of
XX CC data and products dependent on DNA and amino acid sequences. They are
XX CC also used for treating diseases such as Parkinson's disease, Alzheimer's
XX CC disease and other neurodegenerative diseases, anaemia, platelet
XX CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
XX CC cancer. The nucleic acids may also be used as hybridisation probes or
XX CC primers, and in the recombinant production of a protein. The polypeptides
XX CC are also useful in generating antibodies, as molecular weight markers,
XX CC and as food supplements. The present sequence represents a human contig
XX CC sequence used in an example of the invention. Note: The sequence data for
XX CC this patent did not form part of the printed specification, but was
XX CC obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX XX
XX SQ Sequence 4650 BP; 911 A; 1214 C; 1469 G; 1056 T; 0 U; 0 Other;

Query Match 11.4%; Score 42.6; DB 10; Length 4650;
Best Local Similarity 54.9%; Pred. No. 0.77;
Matches 84; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 10 CCAGAGCTGAGCTTACCTGGCGCAACAGCGAGCGAGCGGGCGCGAGTGGAGCTGGAG 69
Db 3729 CGGCGCTGCCCCCGCTTCTGGCGCGCGCGCGCGCGCGACCGCGAGCGCGCGCTCGGG 3788
QY 70 TTCGGGGGTGGCGGGGAGCGAGCTGTCTCGTGTGTGTGAGCGCGCGGCGAGAGCGGGCGG 129
Db 3789 GTCCGGCGGGGTGGCCCGGGCGCGCGCGCGCGAGAGTGGCGGGCGCGCGGGGTGGCGGGGCG 3848
QY 130 GAGCGGCTGATCGGCTCCCTCGAACTCGGGAGG 162
Db 3849 GGGCGGCGGGGGCGGGCGCGCGCGGGCGGGCGG 3881

RESULT 11
ADC86708
ID ADC86708 standard; DNA; 922 BP.
XX AC
XX AC ADC86708;
XX DT
XX DT 01-JAN-2004 (first entry)
XX DE
XX DE Human GPCR gene SEQ ID NO:1161.
XX KW
XX KW ds; gene; human; GPCR;
XX KW guanosine triphosphate-binding protein coupled receptor; gene therapy.
XX OS
XX OS Homo sapiens.
XX PN
XX PN EP1270724-A2.
XX PD
XX PD 02-JAN-2003.
XX PF
XX PF 18-JUN-2002; 2002EP-00013517.
XX PR
XX PR 18-JUN-2001; 2001JP-00246789.
XX PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX PI
XX PI Suwa M, Asai K, Akiyama Y, Aburatani H;
XX DR
XX DR WPI; 2003-315783/31.
XX DR P-PSDB; ADC86709.
XX XX
XX PT New polynucleotide, useful for preparing a composition for treating a
XX PT patient in need of increased or suppressed activity or expression of the
XX PT guanosine triphosphate-binding protein coupled receptor.
XX PS
XX PS Claim 1; SEQ ID NO 1161; 28pp; English.
XX CC
XX CC The invention relates to a novel polynucleotide encoding a guanosine
XX CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
XX CC the invention may have a use in gene therapy. The polynucleotide and
XX CC polypeptide are useful for preparing a composition for treating a patient
XX CC in need of increased or suppressed activity or expression of the
XX CC guanosine triphosphate-binding protein coupled receptor. The
XX CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
XX CC invention.
XX SQ
XX SQ Sequence 922 BP; 118 A; 82 C; 356 G; 106 T; 0 U; 260 Other;

Query Match 11.0%; Score 41.2; DB 10; Length 922;
Best Local Similarity 40.9%; Pred. No. 1.4;
Matches 70; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 12 GAGCTGAGCTTACCTGGCGCAACCGAGCGAGCGGGCGCGAGTGGAGCTGGAGTT 71
Db 363 GGNNGNNNNNNNNNNNNNGGNGGNNNGGNGGNGGNGGNGGNGGNGGNGGNGGNGG 422
QY 72 CCGGGGTGGCGGGGAGGCGACTGTCCGTGTGTGTGAGCGCCCGCGAGAGCGGGCGCGGA 131
Db 423 GGGGGGGGGGGGGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGG 482
QY 132 GCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTGCCTTAGGG 182
Db 483 GGGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGG 533

RESULT 12
ADC30607/c
ID ADC30607 standard; cDNA; 4542 BP.
XX AC
XX AC ADC30607;
XX XX
```

DT 18-DEC-2003 (first entry)
 XX Human novel cDNA sequence, SEQ ID NO: 689.
 DE Human; diagnostic; drug screening; forensics; gene mapping;
 XX biodefensibility assessment; Parkinson's disease; Alzheimer's disease;
 KW neurodegenerative diseases; anemia; platelet disorder; wound; burns;
 KW ulcers; osteoporosis; autoimmune disease; cancer;
 KW molecular weight marker; food supplement; antiparkinsonian; nootropic;
 KW neuroprotective; antianemic; anticoagulant; thrombolytic; vulnerary;
 KW antitumor; osteoplastic; immunosuppressive; antiinflammatory; cytostatic;
 KW gene therapy; chromosome 20; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO2003029271-A2.
 PN
 XX 10-APR-2003.
 PD
 XX 24-SEP-2002; 2002WO-US030474.
 PF
 XX 24-SEP-2001; 2001US-0324631P.
 PR
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
 PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
 PI Haley-Vicente D, Drmanac RT;
 XX
 XX WPI: 2003-371981/35.
 DR P-PSDB; ADC31578.
 DR
 XX New polynucleotide and polypeptide useful for diagnosing, preventing or
 PT treating conditions such as neurodegenerative diseases, anemias, platelet
 PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
 PT cancer.
 PT
 XX Claim 1; SEQ ID NO 689; 1185pp; English.
 PS
 XX The invention relates to 971 novel human cDNA sequences (ADC29919-
 CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
 CC invention also relates to nucleic acid sequences over 99% identical with
 CC the novel human cDNAs. The invention additionally encompasses expression
 CC vectors and host cells comprising a nucleic acid of the invention; the
 CC recombinant production of a polypeptide of the invention; an antibody
 CC against a polypeptide of the invention; a method of detecting
 CC polynucleotides or polypeptides of the invention; and methods of
 CC identifying a compound which binds to a polypeptide of the invention. The
 CC invention further discloses methods of preventing, treating or
 CC ameliorating a medical condition; kits comprising polynucleotide probes
 CC and/or monoclonal antibodies for carrying out the methods of the
 CC invention; methods for the identification of compounds that modulate the
 CC expression or activity of the polynucleotide and/or polypeptide; and 767
 CC contig sequences corresponding to the cDNA sequences of the invention
 CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
 CC -ADC33394). The nucleic acids and polypeptides of the invention are
 CC useful in diagnostics, drug screening, forensics, gene mapping, in the
 CC identification of mutations responsible for genetic disorders or other
 CC traits, for assessing biodiversity, and in producing many other types of
 CC data and products dependent on DNA and amino acid sequences. They are
 CC also used for treating diseases such as Parkinson's disease, Alzheimer's
 CC disease and other neurodegenerative diseases, anemia, platelet
 CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
 CC cancer. The nucleic acids may also be used as hybridisation probes or
 CC primers, and in the recombinant production of a protein. The polypeptides
 CC are also useful in generating antibodies, as molecular weight markers,
 CC and as food supplements. The present sequence represents a specifically
 CC claimed human cDNA sequence of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 4542 BP; 1049 A; 1409 C; 1182 G; 902 T; 0 U; 0 Other;

Query Match 11.0%; Score 41.2; DB 10; Length 4542;
 Best Local Similarity 56.7%; Pred. No. 1.7;
 Matches 76; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
 QY 10 CCGAGCTGAGCTTACCTGGGCGCAACGAGCGAGCGAGGGCGGAGTGGAGCTGGAG 69
 DB 826 CGGCGCTGCCCCCGTTCGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 767
 QY 70 TTCCCGGGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 129
 DB 766 GTCCCGGGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 707
 QY 130 GAGCGGCTGATCGG 143
 DB 706 GGGCGGCGGCGGCGG 693
 RESULT 13
 ADJ39052/c
 ID ADJ39052 standard; cDNA; 766 BP.
 XX
 AC ADJ39052;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Plant cDNA #52.
 XX
 KW plant; gene; ss; transcription; plant genome augmentation; cereal;
 KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
 KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
 KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
 KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
 KW antifungal.
 XX
 OS Eukaryota.
 XX
 XX US2004016025-A1.
 PN
 XX 22-JAN-2004.
 PD
 XX 26-SEP-2002; 2002US-00260238.
 PF
 XX 26-SEP-2001; 2001US-0325277P.
 PR 26-SEP-2001; 2001US-0325448P.
 PR 04-APR-2002; 2002US-0370620P.
 XX
 XX (BUDW/) BUDWORTH P.
 PA (MOUG/) MOUGHAMER T.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZEBROOK J.
 PA (GOLF/) GOLF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (PROV/) PROVANT N.
 PA (RICK/) RICK D.
 PA (ZHUT/) ZHU T.
 XX
 XX Budworth P, Moughamer T, Briggs SP, Provant N, Ricke D, Zhu T;
 PI Goff SA, Katagiri F, Kreps J, Provant N, Ricke D, Zhu T;
 XX WPI; 2004-190374/18.
 DR
 XX New rice phenotypic characteristics, e.g. produce large quantities of oil
 PT improve phenotypic characteristics, e.g. produce large quantities of oil
 PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
 PT or high nutritional value.
 XX
 PS Claim 68; SEQ ID NO 52; 230pp; English.
 CC The invention relates to plant nucleotide sequences that direct seed-,
 CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential

or constitutive transcription of an operatively linked nucleic acid segment. The invention also relates to a method for augmenting a plant genome and a method of identifying a gene, where its expression is altered in the seed, leaf, stem, panicle, pollen, root or is constitutive in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley, sorghum, rice or wheat. The polynucleotides and the polypeptides they encode are useful for manipulating crop plants to alter or improve phenotypic characteristics, to produce large quantities of oil or proteins, to incur resistance to insecticides, viruses or fungi, and to incur stress tolerance (e.g. salt, cold or drought) to ensure the plants have a high nutritional value with reduced apical dominance or dwarfism, early flowering or altered metabolic pathways. This sequence represents a nucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 766 BP; 89 A; 343 C; 192 G; 141 T; 0 U; 1 Other;

Query Match 10.7%; Score 40.2; DB 12; Length 766;
Best Local Similarity 57.6%; Pred. No. 2.4;
Matches 72; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 12 GAGCTGAGTTCACCTCGGCGCGCAACGAGCGAGCGCGGCGAGTGGAGTGGAGTT 71
DB 686 GAGCGCGCGCGCGCGTTCGCGGAGCGAGTGTAGCGGCGAGCGCGAGTGGCGGCT 627
QY 72 CCGGGTGGCGCGGAGCGAGTCTCGTGTGTGTAGCGCGCGGCGAGCGCGCGGA 131
DB 626 CGGTGCGGAGCGAGCGCGGCGAGTGTGTGTAGCGCGGAGCGAGCGCGCGGA 567
QY 132 GCGGC 136
DB 566 TGACC 562

RESULT 14

ADE28355
ID ADE28355 standard; cDNA; 1678 BP.

XX ADE28355;

XX 29-JAN-2004 (first entry)

XX Human KPP cDNA - SEQ ID 66.

XX kinase, phosphatase; KPP; hepatotropic; antiarteriosclerotic;
KW antipsoriatic; cytostatic; haemostatic; muscular; cerebroprotective;
KW nontropic; ophthalmological; anticonvulsant; vasotropic; neuroprotective;
KW antiparkinsonian; antiasthmatic; antianaemic; antiarthritic;
KW antidiabetic; antiinflammatory; osteopathic; antiarthritic;
KW antirheumatic; dermatological; virucide; antibacterial; fungicide;
KW antiparasitic; protozoacide; antihelminthic; antigout; cardiovascular;
KW antiarteriosclerotic; immunosuppressive; cell proliferative; cirrhosis;
KW hepatitis; arteriosclerosis; psoriasis; primary thrombocytopenia; cancer;
KW developmental; renal tubular acidosis; Becker's muscular dystrophy;
KW gonadal dysgenesis; hypothyroidism; seizure; neurological;
KW Pick's disease; cataract; epilepsy; ischaemic cerebrovascular; stroke;
KW Alzheimer's; Parkinson's; dementia; autoimmune; inflammatory; AIDS;
KW allergy; anaemia; asthma; diabetes mellitus; bronchitis; osteoporosis;
KW osteoarthritis; rheumatoid arthritis; contact dermatitis; gout;
KW lipid disorder; cholestasis; Gaucher's; diabetes; atherosclerosis; liver;
KW viral; bacterial; fungal; parasitic; protozoan; helminthic infection;
KW trauma; gene therapy; human; ss; gene.

XX Homo sapiens.

XX OS 2020030805-A2.

XX PN 02-OCT-2003.

XX 18-MAR-2003; 2003WO-US008715.

XX

PR 19-MAR-2002; 2002US-0366088P.
PR 29-MAR-2002; 2002US-0369248P.
XX (INCY-) INCYTE CORP.

XX Chien D, Jin P, Hawkins PR, Baughn MR, Becha SD, Chang H;
PI Ding L, Elliott VS, Emerling BM, Gandhi AR, Gietzen KJ, Griffin JA;
PI Gururajan R, Hafalia AJA, Ison CH, Kahle AE, Khare R, Lee SY;
PI Lee EA, Lu Y, Marquis JP, Lehr-Mason PM, Ramkumar J, Richardson TW;
PI Swarnakar A, Tran UK, Chawla NK, Yao MG, Yue H, Bhatia U;
PI Burrill JD, Lee S, Blake JU, Ho A, Zheng W;

XX WPI; 2004-011523/01.

XX P-PSDB; ADE28303.

XX New human kinases and phosphatases, and polynucleotides encoding them,
PT useful for treating, preventing or diagnosing e.g. cell proliferative
PT disorders, inflammatory, autoimmune, viral, bacterial, parasitic or
PT fungal diseases.

XX Claim 5; SEQ ID NO 66; 340pp; English.

XX The invention relates to a novel isolated kinase and phosphatase (KPP)
CC polypeptide. The polypeptide of the invention demonstrates hepatotropic,
CC antiarteriosclerotic, antipsoriatic, cytostatic, haemostatic, muscular,
CC cerebroprotective, nontropic, ophthalmological, anticonvulsant,
CC vasotropic, neuroprotective, antiparkinsonian, antiasthmatic,
CC antianaemic, antiasthmatic, antidiabetic, antiinflammatory, osteopathic,
CC antirheumatic, dermatological, virucide, antihelminthic, antigout,
CC fungicide, antiparasitic, protozoacide, antihelminthic, antitubercular,
CC cardiovascular, antiarteriosclerotic and immunosuppressive activities.
CC The KPP polypeptides may be useful for diagnosing, treating or preventing
CC cell proliferative disorders including cirrhosis, hepatitis,
CC arteriosclerosis, psoriasis, primary thrombocytopenia and cancer,
CC developmental disorders such as renal tubular acidosis, Becker's muscular
CC dystrophy, gonadal dysgenesis, hypothyroidism or seizures, neurological
CC disorders e.g. Pick's disease, cataract, epilepsy, ischaemic
CC cerebrovascular disease, stroke, Alzheimer's disease, Parkinson's disease
CC or dementia, autoimmune or inflammatory disorders including AIDS,
CC allergies, anaemia, asthma, diabetes mellitus, bronchitis, osteoporosis,
CC osteoarthritis, rheumatoid arthritis, contact dermatitis or gout and
CC lipid disorders such as cholestasis, Gaucher's disease, diabetes,
CC atherosclerosis or liver disease, as well as viral, bacterial, fungal,
CC parasitic, protozoan or helminthic infections and trauma. Furthermore,
CC the polypeptide may be utilised during gene therapy procedures. The
CC current sequence is that of the human KPP cDNA of the invention.

XX Sequence 1678 BP; 316 A; 553 C; 527 G; 282 T; 0 U; 0 Other;

Query Match 10.7%; Score 40.2; DB 12; Length 1678;
Best Local Similarity 49.8%; Pred. No. 2.7;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 23 ACCCTGGGCGCAACGAGCGAGCGCGGCGCGAGTGGAGTTCGGGGTGGCG 82
DB 593 ACCACGCGCAGAGGGGGCGCCAGGAGGCGAGCGCGCGGTTCGCGGTACAGC 652
QY 83 GGGGAGCGGACTGTCGTCGTGTGTAGCGCGCGGAGCGGGCGGCGGCTGATCG 142
DB 653 GAGGCGGGTGGCGGACAGTGTGTACAGCGCGACGCGGGGGCCAGAGAGGCCCAAGTCT 712
QY 143 GCTCCCTCGAAGTGGGGAGTTCAGTGGGTTCGTTAGGCGCCCAAGCCCCCGCGCT 202
DB 713 TCAGGGAGGGGTTCAGGGGTTCCTCCAGGAGTCTCCCGGAGCAACGCCCCCTCTCCGGG 772
QY 203 CCAAGAGCTCCAGGGCGCTCCCGAG 227
DB 773 CTTGATGTCGGCACCCCCCAGCGCTG 797

RESULT 15

ACN43300

ID ACN43300 standard; cDNA; 2304 BP.

XX AC ACN43300;
 XX DT 18-NOV-2004 (first entry)
 XX DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2175.
 XX DE es; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
 XX DE dithp.
 XX OS Homo sapiens.
 XX PN WO2004023973-A2.
 XX PD 25-MAR-2004.
 XX PF 12-SEP-2003; 2003WO-US028227.
 XX PR 12-SEP-2002; 2002US-0410259P.
 XX PR 12-SEP-2002; 2002US-0410260P.
 XX PA (INCY-) INCYTE CORP.
 XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Harthorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;
 PI Mooney EM, Deleane AM, Pansar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patury S, Shi X, Suarez CJ;
 XX DR WPI; 2004-329368/30.
 XX DR P-PSDB; ABM84648.
 XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX PS Claim 1; Page; 190pp; English.
 XX CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp polynucleotide of
 CC the invention. Note: The sequence data for this patent is not represented
 CC in the printed specification, but was obtained in electronic format
 CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX SQ Sequence 2304 BP; 427 A; 796 C; 747 G; 334 T; 0 U; 0 Other;
 Query Match 10.7%; Score 40.2; DB 13; Length 2304;
 Best Local Similarity 49.8%; Pred. No. 2.8;
 Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
 QY 23 ACCCTGGGGGCAAAACGAGCGAGCGGCGCGAGTGGAGCTGAGTTCCGGGGTGGGC 82
 DB 552 ACCACGGCCAGAGGGGGCCACAGGAGGCGAGCGAGCGGTCGCCGGTCACAGC 611
 QY 83 GGGGAGGGCGACTGTTCGTGGTGTGAGCGCCCGGAGAGCGGGCGCGGCTGATCG 142
 DB 612 GAGGGCGGGTGGCGCAGTGGTGCAGCGCGAGCGGGCGGCGAGAGAGGCCCAAGTCT 671

QY 143 GCTCCCTCGAACTGGGGAGGTCCAGTGGGTGCTTTAGGGCCCAAGCCCAACCCGGCT 202
 DB 672 TCCAGGGAGGGCTCAGGGGGTCCCCCAGGAGTCTTCCCGGGACAACAGCCCCCTCTCCGGG 731
 QY 203 CCAAAAGCTCCAGGGGCTCCCGCAG 227
 DB 732 CCTGATGTGGGCACCCCCCAGCCTG 756
 Search completed: April 7, 2005, 11:09:30
 Job time : 277.403 secs

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OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 08:55:04 ; Search time 86.5385 Seconds
(without alignments)
7090.532 Million cell updates/sec

Title: US-09-977-579-4_COPY_1_375

Perfect score: 375

Sequence: 1 cctcccttcgagcgagc.....gaagccgagccagccagagaag 375

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44.8	11.9	11558	5	PCT-US93-06251-23
2	42	11.2	9622	4	US-09-949-016-15003
3	40.4	10.8	6651	4	US-09-902-540-4944
4	40.4	10.8	30780	4	US-09-902-540-1243
5	40.2	10.7	2802	4	US-09-949-016-1335
6	40.2	10.7	2806	4	US-09-688-188B-102
7	40.2	10.7	2806	4	US-09-231-117D-102
8	40.2	10.7	2838	4	US-09-949-016-794
9	40.2	10.7	57559	4	US-09-949-016-13077
10	40.2	10.7	57560	4	US-09-949-016-12536
11	40	10.7	21295	4	US-09-902-540-1194
12	39.2	10.5	601	4	US-09-949-016-124631
13	39.2	10.5	8374	4	US-09-949-016-15257
14	39.2	10.5	45225	4	US-09-949-016-12428
15	39.2	10.5	45226	4	US-09-949-016-12428
16	39	10.4	30635	4	US-09-949-016-16501
17	39	10.4	43414	4	US-09-949-016-12839
18	39	10.4	43415	4	US-09-949-016-16491
19	38.8	10.3	1941	4	US-09-902-540-4762
20	38.8	10.3	26492	4	US-09-902-540-1234
21	38.6	10.3	1940	4	US-09-718-032-1
22	38.6	10.3	1941	3	US-09-082-737-1
23	38.6	10.3	2310	4	US-09-774-528-142
24	38.6	10.3	32495	4	US-09-949-016-14952
25	38.4	10.2	505	4	US-09-621-976-15639
26	37.8	10.1	4286	4	US-09-899-634C-1
27	37.8	10.1	8033	4	US-09-574-779B-134

c	28	37.8	10.1	24942	4	US-09-949-016-13318	Sequence 13318, A
c	29	37.8	10.1	40237	4	US-09-949-016-16461	Sequence 16461, A
c	30	37.4	10.0	22712	4	US-09-949-016-16759	Sequence 16759, A
c	31	37.4	10.0	22712	4	US-09-949-016-16760	Sequence 16760, A
c	32	37.4	10.0	22712	4	US-09-949-016-16761	Sequence 16761, A
c	33	37.4	10.0	22712	4	US-09-949-016-16762	Sequence 16762, A
c	34	37.2	9.9	152331	3	US-09-128-155-16	Sequence 16, Appl
c	35	37	9.9	2694	4	US-09-902-540-4257	Sequence 4257, Ap
c	36	37	9.9	24791	4	US-09-902-540-1211	Sequence 1211, Ap
c	37	36.8	9.8	10029	4	US-09-949-016-11846	Sequence 11846, A
c	38	36.8	9.8	10029	4	US-09-949-016-16140	Sequence 16140, A
c	39	36.6	9.8	624	4	US-09-902-540-3091	Sequence 3091, Ap
c	40	36.6	9.8	15789	4	US-09-902-540-1139	Sequence 1139, Ap
c	41	36.6	9.8	31199	4	US-09-949-016-16516	Sequence 16516, A
c	42	36.4	9.7	187595	4	US-09-949-016-15546	Sequence 15546, A
c	43	36.2	9.7	2608	4	US-09-904-615-16	Sequence 16, Appl
c	44	36.2	9.7	18112	4	US-09-949-016-13648	Sequence 13648, A
c	45	36.2	9.7	25419	4	US-09-949-016-15476	Sequence 15476, A

ALIGNMENTS

RESULT 1

PCT-US93-06251-23

; Sequence 23, Application PC/TUS9306251

; GENERAL INFORMATION:

; APPLICANT: Wickstrom, Eric and Rife, Jason P.

; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing Stereospecific Alkylphosphonates and Arylphosphonates

; NUMBER OF SEQUENCES: 93

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: NY

; COUNTRY: USA

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/06251

; FILING DATE: 19930630

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Digiglio, Frank S.

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 8586

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 516-742-4343

; TELEFAX: 516-742-4366

; TELEX: 230 901 SANS UR

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11558 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

PCT-US93-06251-23

Query Match	11.9%;	Score	44.8;	DB	5;	Length	11558;
Best Local Similarity	56.7%;	Pred. No.	0.025;				
Matches	102;	Conservative					
		Mismatches	77;	Indels	1;	Gaps	1;
QY	74	GGGCGTGGGGGAGCGGACTGTCCTGTGTCTGAGCGCGGAGAGCGGCGCGGAGC	133				
Db	428	GGGAGGGGGGGTGGGGGACCTTCAGACGACGAGGCGCTTCGGGGGCGCGCGCGC	487				
QY	134	GGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTCG-CTTAGGGCCCAAGCCC	192				

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; ORGANISM: Myxococcus xanthus
US-09-902-540-4944

Query Match      10.8%; Score 40.4; DB 4; Length 6651;
Best Local Similarity 51.3%; Pred. No. 0.32;
Matches 120; Conservative 0; Mismatches 111; Indels 3; Gaps 1;

QY 39 AGCGAGGAGGCGCGGAGTGAAGCTGAGTTCGCGGGTGGCGGGGAGGCGACTGTGTC 98
Db 4498 ATCGAGGAGGCGCGCTCGAGCCCGGTGTGTCGGGACACGCGCATGAAGACACGCGGCC 4557
QY 99 GTGGTCTGAGCGCGCGGAGAGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGG 158
Db 4558 CTGGAGCTG---CTCTTCTGACCCCGCTCGCGGTATGAGCGCTGTCTGTGGCGAG 4614
QY 159 GAGGTCCAGTGGGGTCTGCTTAGGGGCCAAAGCCCAAGCCCGCTCCAAAGCTCCAGGG 218
Db 4615 GTGGAGCTGGTGAGTCTGTGCAATTGCGCTGTGGGCCCGCGGTGCTGATCCAAATG 4674
QY 219 CTCCCCAGGACACCGGTGCTCGGCCCTTCTCTTGGTTCAGAAAGTGCCTCCCTGG 272
Db 4675 TCGGGACTGTTTCGCGGGATGCTCAAGTCCATCGCGGCGGAAAGTGCCTGCCCGG 4728

RESULT 4
US-09-902-540-1243
; Sequence 1243, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1243
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(30780)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1243

Query Match      10.8%; Score 40.4; DB 4; Length 30780;
Best Local Similarity 51.3%; Pred. No. 0.43;
Matches 120; Conservative 0; Mismatches 111; Indels 3; Gaps 1;

QY 39 AGCGAGGAGGCGCGGAGTGAAGCTGAGTTCGCGGGTGGCGGGGAGGCGACTGTGTC 98
Db 28499 ATCGAGGAGGCGCGCTCGAGCCCGGTGTGTCGGGACACGCGCATGAAGACACGCGGCC 28558
QY 99 GTGGTCTGAGCGCGCGGAGAGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGG 158
Db 28559 CTGGAGCTG---CTCTTCTGACCCCGCTCGCGGTATGAGCGCTGTCTGTGGCGAG 28615
QY 159 GAGGTCCAGTGGGGTCTTAGGGGCCAAAGCCCAAGCCCGCTCCAAAGCTCCAGGG 218
Db 28616 GTGGAGCTGGTGAGTCTGTGCAATTGCGCTGTGGGCCCAAGCGCGGTGCTGATCCAAATG 28675
QY 219 CTCCCCAGGACACCGGTGCTCGGCCCTTCTCTTGGTTCAGAAAGTGCCTCCCTGG 272
Db 28676 TCGGGACTGTTTCGCGGGATGCTCAAGTCCATCGCGGCGGAAAGTGCCTGCCCGG 28729

RESULT 5
US-09-949-016-1335

; ORGANISM: Myxococcus xanthus
US-09-902-540-4944

Query Match      11.2%; Score 42; DB 4; Length 9622;
Best Local Similarity 49.5%; Pred. No. 0.13;
Matches 108; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 38 GAGCGAGGAGGCGCGGAGTGAAGCTGAGTTCGCGGGTGGCGGGGAGGCGACTGTGTC 97
Db 7138 GCGTGAAGGCGCTGCTGGAAGGGGTGCTGCTGCGGTAGGGGCTCTTCCATGGCCACGA 7079
QY 98 CGTGTGCTGAGCGCGCGGAGAGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGG 157
Db 7078 TCTGCTGCTGTGTGGGGGAGCGGCGGTAGGAGCCATCATGCTTCATGCGGCTGG 7019
QY 158 GGAGGTCCAGTGGGTGCTTGGGCCCCAAAGCCCCACCCGCTCCAAAGCTCCAGG 217
Db 7018 ACAGGACCTCTGGGGGACAGTGAGCCTTCAACCCCTGGCTGCTCCAGCCTCCAGC 6959
QY 218 GCTTCCCGAGGACCGGTGCTCGGCCCTTCTCTTGGTC 255
Db 6958 TACACCCGAGCAGCTCCCTTCTGTGATCTCTTGGGAC 6921

RESULT 3
US-09-902-540-4944
; Sequence 4944, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4944
; LENGTH: 6651
; TYPE: DNA
```

```
; Sequence 1335, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1335
; LENGTH: 2802
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1335

Query Match          10.7%; Score 40.2; DB 4; Length 2802;
Best Local Similarity 49.8%; Pred. No. 0.31;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 23 ACCCTGGGCGCAACGAGCGAGCGGGCGCGAGCTGGAGCTGGAGTTCGGGGTGGGC 82
DB 569 ACCAGCGCCAGAGGGGCGCCAGGAGGAGCGAGCGCGCGGGTTCGCGCGTCAAGTCT 628
QY 83 GGGGAGGCGCACTCTCCGTGTGTGTGAGCGCGCGAGAGCGGGCGCGGCGCTGATCG 142
DB 629 GAGCGGGTGGCGCAGTGTGTGACAGCGCGAGCGGGGCGCGAGAGGCCCAAGTCT 688
QY 143 GCTCCCTCGAACTGGGAGGTGCAGTGGGTTCGTTAGGCGCCCAAGCGCCCAAGTCT 202
DB 689 TCCAGGAGGCGCTCAGGGGTCCCGAGAGTCTCCCGGAGCAAGCGCCCTCTCCGGG 748
QY 203 CCAAAAGCTCCAGGGCGCTCCCGAG 227
DB 749 CCTGATGTGGCGACCCCGCCAGCCTG 773

RESULT 6
US-09-688-188B-102
; Sequence 102, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 2806
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-688-188B-102

Query Match          10.7%; Score 40.2; DB 4; Length 2806;
Best Local Similarity 49.8%; Pred. No. 0.31;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 23 ACCCTGGGCGCAACGAGCGAGCGGGCGCGAGTGGAGTTCGGGGTGGGC 82
DB 567 ACCAGCGCCAGAGGGGCGCCAGGAGGAGCGAGCGCGGGTTCGCGGTTCACAGC 626
QY 83 GGGGAGGCGCACTGTCTCGTGTGTGTGAGCGCGCGAGAGCGGGCGGAGCGGTGATCG 142
DB 627 GAGCGGGTGGCGGCGAGTGTGTGACAGCGCGAGCGGGCGCGAGAGGCCCAAGTCT 686
QY 143 GCTCCCTCGAACTGGGAGGTCCAGTGGGTTCGTTAGGCGCCCAAGCGCCCAAGTCT 202
DB 687 TCCAGGAGGCGTCCAGGGGTCCCGAGAGTCTCCCGGAGCAAGCGCCCTCTCCGGG 746
QY 203 CCAAAAGCTCCAGGGCGCTCCCGAG 227
DB 747 CCTGATGTGGCGACCCCGCCAGCCTG 771

RESULT 7
US-09-291-417D-102
; Sequence 102, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 2806
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-291-417D-102

Query Match          10.7%; Score 40.2; DB 4; Length 2806;
Best Local Similarity 49.8%; Pred. No. 0.31;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 23 ACCCTGGGCGCAACGAGCGAGCGGGCGCGAGTGGAGTTCGGGGTGGGC 82
DB 567 ACCAGCGCCAGAGGGGCGCCAGGAGGAGCGAGCGCGGGTTCGCGGTTCACAGC 626
QY 83 GGGGAGGCGCACTGTCTCGTGTGTGTGAGCGCGCGAGAGCGGGCGGAGCGGTGATCG 142
DB 627 GAGCGGGTGGCGGCGAGTGTGTGACAGCGCGAGCGGGCGCGAGAGGCCCAAGTCT 686
QY 143 GCTCCCTCGAACTGGGAGGTCCAGTGGGTTCGTTAGGCGCCCAAGCGCCCAAGTCT 202
DB 687 TCCAGGAGGCGTCCAGGGGTCCCGAGAGTCTCCCGGAGCAAGCGCCCTCTCCGGG 746
QY 203 CCAAAAGCTCCAGGGCGCTCCCGAG 227
DB 747 CCTGATGTGGCGACCCCGCCAGCCTG 771

RESULT 8
US-09-949-016-794
; Sequence 794, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 2806
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-016-794

Query Match          10.7%; Score 40.2; DB 4; Length 2806;
Best Local Similarity 49.8%; Pred. No. 0.31;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 23 ACCCTGGGCGCAACGAGCGAGCGGGCGCGAGTGGAGTTCGGGGTGGGC 82
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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 794
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-794

Query Match      10.7%; Score 40.2; DB 4; Length 2838;
Best Local Similarity 49.8%; Pred. No. 0.31; Indels 0; Gaps 0;
Matches 102; Conservative 0; Mismatches 103;

QY 23 ACCCTGGGCGCAACGAGCGAGCGAGGCGGCGAGTGGAGTTCGGGGTGGGC 82
DB 577 ACCACGGCCAGAGGGGCGCCAGGAGGCGAGCGAGCGGTTCCCGGTACAGC 636
QY 83 GGGGAGGCGACTGTCTCGTGTGTAGCCGCGGAGAGCGGCGCGGCGGTGATCG 142
DB 637 GAGGCGGTGGCGGCGAGTGTGACAGCGCGCGGCGGCGGCGGAGAGGCCAAGTCT 696
QY 143 GCTCCCTCAACTGGGAGGTCCAGTGGGGTCTTAGGCGCCAAAGCCCCCAGCGGCT 202
DB 697 TCAGGAGGGGCTCAGGGGGTCCCGAGGAGTCTTCCCGGGAACAAAGCCCCCTCTCCGGG 756
QY 203 CCAAAAGCTCCCGAGGCGCTCCCGAG 227
DB 757 CTGATGTCGGCACCCCGCAGCGTG 781

RESULT 9
US-09-949-016-13077
; Sequence 13077, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13077
; LENGTH: 57559
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13077

Query Match      10.7%; Score 40.2; DB 4; Length 57559;
Best Local Similarity 49.8%; Pred. No. 0.55; Indels 0; Gaps 0;
Matches 102; Conservative 0; Mismatches 103;

QY 23 ACCCTGGGCGCAACGAGCGAGCGAGGCGGCGAGTGGAGTTCGGGGTGGGC 82
DB 49236 ACCACGGCCAGAGGGGCGCCAGGAGGCGAGCGAGCGGTTCCCGGTACAGC 49295
QY 83 GGGGAGGCGACTGTCTCGTGTGTAGCCGCGGAGAGCGGCGCGGCGGTGATCG 142
DB 49296 GAGGCGGTGGCGGCGAGTGTGACAGCGCGGCGGCGGCGGCGGAGAGGCCAAGTCT 49355
QY 143 GCTCCCTCAACTGGGAGGTCCAGTGGGGTCTTAGGCGCCAAAGCCCCCAGCGGCT 202
DB 49356 TCAGGAGGGGCTCAGGGGGTCCCGAGGAGTCTTCCCGGGAACAAAGCCCCCTCTCCGGG 49415
QY 203 CCAAAAGCTCCCGAGGCGCTCCCGAG 227
DB 49416 CTGATGTCGGCACCCCGCAGCGTG 49440

RESULT 11
US-09-902-540-1194
; Sequence 1194, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1194
; LENGTH: 21295
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1194
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Query Match 10.7%; Score 40; DB 4; Length 21295;
 Best Local Similarity 47.9%; Pred. No. 0.51;
 Matches 115; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 45 GCAGGGCGGAGTGGAGCTGGAGTTCCGGGGTGGGGGGAGGCGACTGTCGGTGGTG 104
 DB 16255 GGAGGAGAGGCGGCTGGCAGCGCATCCAGAGCTGCTCGAGGGGGGGGGCGCGG 16314

QY 105 CTGAGCCCGCGAGAGCGGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGTGC 164
 DB 16315 CGCAGCGCGCCACGCGCGCGCGGAGCGCCCGCGAGCACCCCGGCTGGCGCGGG 16374

QY 165 CAGTGGGGTGGCTTAGGGGCCAAGACCCCGGCTCCAAAGCTCCCGAGGCGCTCCC 224
 DB 16375 CTGGCGGACGAGCTGCACGAGCGGCGCCCTTTCCGCAAGGCTCACGGTGGGAGCCT 16434

QY 225 CAGCACCAGTGTGCGGCCCTTCCTTGGTGCAGAAAGTCCGCCCTGGGGGCGAGTTCGTC 284
 DB 16435 CAGGGGACGCGCTGAGCTGATCCACGCGTCGAAGGTGGCGCGCTTTGTAGGCTCCGAC 16494

RESULT 12
 US-09-949-016-124631
 ; Sequence 124631, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 124631
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-124631

Query Match 10.5%; Score 39.2; DB 4; Length 601;
 Best Local Similarity 48.2%; Pred. No. 0.42;
 Matches 110; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 49 GGGCGGAGTGGAGCTGGAGTTCCGGGGTGGGGGGAGGCGACTGTCGGTGGTCTGA 108
 DB 84 GGGAGTGGTGCCCAAGGGGGTCTGGCGGGTGGAGAGCGTGTCTCCCTCGGACTCG 143

QY 109 GCGCCCGCAGAGCGGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGT 168
 DB 144 GGGCGCCCGACGCTGGCGGCTCCCGCTGAGCGGCTGCGGCTGCCCGGACCACTGCT 203

QY 169 GGGGTGCTTAGGGCCCAAGCCCGGCTCCAAAGTCCCGAGGCGCTCCCGCAGG 228
 DB 204 CACCTCCCGGGGGCTGCGCAGGCGGCGCTTGGGTGCGCGGCTGCGCGGCTGCCCAGG 263

QY 229 CACCGGTGCTCGGCCCTTCCTTCGCTCAGAAAGTTCGCCCTCGGGGC 276
 DB 264 GAGCGGAGTGGGTTTCCAGCGGGCCCGTGGCGACKCCGCTGGGC 311

RESULT 13
 US-09-949-016-15257
 ; Sequence 15257, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15257
 ; LENGTH: 8374
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-15257

Query Match 10.5%; Score 39.2; DB 4; Length 8374;
 Best Local Similarity 48.2%; Pred. No. 0.7;
 Matches 110; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 49 GGGCGGAGTGGAGCTGGAGTTCCGGGGTGGGGGGAGGCGACTGTCGGTGGTCTGA 108
 DB 5933 GGGAGTGGTGCCCAAGGGGGTCTGGCGGGTGGAGAGCGTGTCTCCCTCGGACTCG 5992

QY 109 GCGCCCGCAGAGCGGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGT 168
 DB 5993 GGGCGCCCGACGCTGCGGGTCCCGCTGAGCGGCTGCGCGGCTGCCCGGACCACTGCT 6052

QY 169 GGGGTGCTTAGGGCCCAAGCCCGGCTCCAAAGTCCCGAGGCGCTCCCGCAGG 228
 DB 6053 CACCTCCCGGGGGCTGCGCAGGCGGCGCTTCCAGCGGGGTGCGCGGCTGCCCAGG 6112

QY 229 CACCGGTGCTCGGCCCTTCCTTCGCTCAGAAAGTTCGCCCTCGGGGC 276
 DB 6113 GAGCGGAGTGGGTTTCCAGCGGGCCCGTGGCGACTCCGGCTGGGC 6160

RESULT 14
 US-09-949-016-12428/c
 ; Sequence 12428, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12428
 ; LENGTH: 45225
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-12428

Query Match 10.5%; Score 39.2; DB 4; Length 45225;
 Best Local Similarity 53.2%; Pred. No. 0.97;
 Matches 83; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 28 GGGCGCAAGCAGCAGGAGGCGGCGGAGTGGAACTGGAGTTCGGGGTGGGGCGGA 87
 DB 1994 GGGCGCGGGCGGCGGCGGCAAGCGCGTGGCGGGCTCGGCTGCGGAGTGGGGCGGG 1935

QY 88 GCGACTGTCCTGTGCTGAGCGCGGAGAGCGGGCGGAGCGGCTGATCGGCTCC 147
 Db 1934 CGCGGAGTGAGTGGAGAGAGTGCGCGGTGTCGCGCCCGGCTGCGGGCGGGCT 1875
 QY 148 CTCGAACCTGGGAGTCCAGTGGGTGCGCTTAGGGC 183
 Db 1874 CGCCCGGGTGGGGCGGGGTGGGGCGGACGGGGC 1839

RESULT 15
 US-09-949-016-13654/c
 ; Sequence 13654, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13654
 ; LENGTH: 45226
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-13654

Query Match 10.5%; Score 39.2; DB 4; Length 45226;
 Best Local Similarity 53.2%; Pred. No. 0.97;
 Matches 83; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 QY 28 GCGCGCAACGAGCGGAGCGGCGGAGTGGAGTTCGCGGGTGGGGCGGA 87
 Db 1994 GCGCGCGGCGGGCGGCAAGCGCGTGGCGGGCTCGGCTGCGGGAGTGGGGCGGG 1935
 QY 88 GCGACTGTCCTGTGCTGAGCGCGGAGAGCGGGCGGAGCGGCTGATCGGCTCC 147
 Db 1934 CGCGGAGTGAGTGGAGAGAGTGCGCGGTGTCGCGCCCGGCTGCGGGCGGGCT 1875
 QY 148 CTCGAACCTGGGAGTCCAGTGGGTGCGCTTAGGGC 183
 Db 1874 CGCCCGGGTGGGGCGGGGTGGGGCGGACGGGGC 1839

Search completed: April 7, 2005, 15:00:31
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 10:54:05 ; Search time 335.745 Seconds
(without alignments)
6768.525 Million cell updates/sec

Title: US-09-977-579-4_COPY_1_375

Perfect score: 375

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Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	375	100.0	1261	11	US-09-977-579-4
2	45.2	12.1	497	17	US-10-424-599-133788
3	44.8	11.9	2930	18	US-10-322-281-642
4	43	11.5	396	18	US-10-437-963-98256
5	43	11.5	1021	18	US-10-767-701-11876
6	42.6	11.4	419	18	US-10-425-115-24179
7	42.2	11.3	1211	18	US-10-437-963-27585
8	41.4	11.0	696	18	US-10-437-963-90177
9	41.4	11.0	58038	19	US-10-741-600-17942
10	41.4	11.0	333811	19	US-10-741-600-17681
11	41.2	11.0	922	15	US-10-017-161-1435

12	41.2	11.0	922	17	US-10-292-798-1161	Sequence 1161, Ap
13	41	10.9	1097	9	US-09-771-161A-58	Sequence 58, Appl
14	41	10.9	3382	9	US-09-771-161A-59	Sequence 59, Appl
15	40.2	10.7	786	17	US-10-260-238-52	Sequence 52, Appl
16	40.2	10.7	791	18	US-10-437-963-84059	Sequence 84059, A
17	40.2	10.7	1071	18	US-10-437-963-84064	Sequence 84064, A
18	40.2	10.7	2806	18	US-09-291-417-102	Sequence 102, App
19	40.2	10.7	2806	18	US-10-725-329-102	Sequence 102, Appl
20	40.2	10.7	2838	16	US-10-134-102-3	Sequence 3, Appl
21	40.2	10.7	20000	17	US-10-188-777-11	Sequence 11, Appl
22	40	10.7	645	18	US-10-767-701-25929	Sequence 25929, A
23	40	10.7	940	18	US-10-437-963-40850	Sequence 40850, A
24	39.8	10.6	332	9	US-09-960-352-2238	Sequence 2238, Ap
25	39.8	10.6	863	18	US-10-437-963-71791	Sequence 71791, A
26	39.6	10.6	712	18	US-10-425-115-118813	Sequence 118813, A
27	39.6	10.6	735	18	US-10-437-963-84061	Sequence 84061, A
28	39.6	10.6	1092	18	US-10-767-701-9739	Sequence 9739, Ap
29	39.6	10.6	4233	18	US-10-723-860-4143	Sequence 4143, Ap
30	39.6	10.6	4244	18	US-10-723-860-8016	Sequence 8016, Ap
31	39.2	10.5	759	17	US-10-260-238-230	Sequence 230, App
32	39.2	10.5	972	18	US-10-425-115-17653	Sequence 17653, A
33	39.2	10.5	1294	18	US-10-437-963-73166	Sequence 73166, A
34	39.2	10.5	6888	18	US-10-602-494-20	Sequence 20, Appl
35	39	10.4	485	17	US-10-424-599-65670	Sequence 65670, A
36	39	10.4	587	16	US-10-029-386-22980	Sequence 22980, A
37	39	10.4	936	9	US-09-974-300-836	Sequence 836, App
38	39	10.4	1087	17	US-10-424-599-81404	Sequence 81404, A
39	39	10.4	88400	18	US-10-844-716-1	Sequence 1, Appl
40	38.8	10.3	985	18	US-10-739-930-4166	Sequence 4166, Ap
41	38.6	10.3	263	18	US-10-021-323-16665	Sequence 16665, A
42	38.6	10.3	550	16	US-10-029-386-24925	Sequence 24925, A
43	38.6	10.3	1647	18	US-10-437-963-37566	Sequence 37566, A
44	38.6	10.3	1940	17	US-10-693-367-1	Sequence 1, Appl
45	38.6	10.3	2310	17	US-10-120-988-142	Sequence 142, App

ALIGNMENTS

RESULT 1

US-09-977-579-4
; Sequence 4, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
; TITLE OF INVENTION: channel
; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977, 579
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-977-579-4

Query Match	100.0%;	Score 375;	DB 11;	Length 1261;
Best Local Similarity	100.0%;	Pred. No. 7e-98;		
Matches 375;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CCCTCCCTTCGAGCTGAGCTTACCTCGGCGGAAACGACGAGGCGGCGGCGAGTGG	60	
Db	1	CCCTCCCTTCGAGCTGAGCTTACCTCGGCGGAAACGACGAGGCGGCGGCGAGTGG	60	
Qy	61	AAGCTGAGTCCCGGGTGGCGGAGGCGAGCTGTCCGTGGTGTGAGCCGCCGAG	120	

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Db      61  AAGCTGGAGTTCCGGGGTGGCGGGGAGGCGAGCTGTCCTGGTGTGCTGAGCGCGCGGAG 120
QY      121  GCGGGCGCGAGGCGGTGATCGGCTCCCTCGAAGCTGGGAGGTCCAGTGGGGTTCGCTTAG 180
Db      121  GCGGGCGCGAGGCGGTGATCGGCTCCCTCGAAGCTGGGAGGTCCAGTGGGGTTCGCTTAG 180
QY      181  GCGCCAAAGCCCCACCGGCTCCAAAGCTCCCAAGGCTCCCAAGGCTCCCAAGGCTCCCAAGGCTCC 240
Db      181  GCGCCAAAGCCCCACCGGCTCCAAAGCTCCCAAGGCTCCCAAGGCTCCCAAGGCTCCCAAGGCTCC 240
QY      241  GCGCTTCCTTCGCTCAGAAAGTCCGCGGCTCCGCGGCTCCGCGGCTCCGCGGCTCCGCGGCTCC 300
Db      241  GCGCTTCCTTCGCTCAGAAAGTCCGCGGCTCCGCGGCTCCGCGGCTCCGCGGCTCCGCGGCTCC 300
QY      301  AAGAATCTGAGAGGCGGAGTCCCTTGACCGAGGGAATCTCTGTGTAGCTTGAAGC 360
Db      301  AAGAATCTGAGAGGCGGAGTCCCTTGACCGAGGGAATCTCTGTGTAGCTTGAAGC 360
QY      361  CGCCAGCGCCCAAG 375
Db      361  CGCCAGCGCCCAAG 375

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RESULT 2

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US-10-424-599-133788/c
; Sequence 133788, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 133788
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(497)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_91816C.1
US-10-424-599-133788

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Query Match      12.1%; Score 45.2; DB 17; Length 497;
Best Local Similarity 54.6%; Pred. No. 0.0024;
Matches 89; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY      38  GAGCGAGGCGGCGCGAGTGGAACTCGAGTTCGGGGTGGCGGGGAGCGGAGTGTGTC 97
Db      301  GGGGGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 242

QY      98  CTTGTGTCTGAGCGCGCGGAGCGGGCGCGGAGCGGCTGTGATCGGCTCCCTCGAAGTGG 157
Db      241  CGGGGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 182

QY      158  GGAGGTCCAGTGGGTGCTTAGGGCCCAAGGCCCCACCCGG 200
Db      181  GGGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 139

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RESULT 3

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US-10-322-281-642
; Sequence 642, Application US/1032281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris

```

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; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 642
; LENGTH: 29340
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-322-281-642

Query Match      11.9%; Score 44.8; DB 18; Length 29340;
Best Local Similarity 56.7%; Pred. No. 0.0026;
Matches 102; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY      74  GGGGTGGGGGGGAGCGGAGCTGTCGTGCTGAGCGCGGAGAGCGGCGGCGGAGC 133
Db      9834  GGGAGGGGGGTAGGGGACCTTTTCAGAGCCAGGAGGGCTTTTCGGGGGGGTGGGGCGGC 9893

QY      134  GGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGTGCG-CTTAGGGGCCAAAGCCC 192
Db      9894  TCGGAGCGGAGCGCGCGGCTCGACGCGTGGCTGGCGGCGAGTGTATGCACAGCGCGC 9953

QY      193  CCACCGGCTCCAAAAGCTCCAGGGCCCTCCCGAGGACCGGTGCTCGGCCCTTCCTTCG 252
Db      9954  CCGGCGCCGAACCCGAGCGCGGGGCTCCCGCACCGCGGCTCCCGCCCTCCCGCG 10013

RESULT 4
US-10-437-963-98256
; Sequence 98256, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrei A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 98256
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_9617C.1
US-10-437-963-98256

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Query Match      11.5%; Score 43; DB 18; Length 396;
Best Local Similarity 50.7%; Pred. No. 0.011;
Matches 103; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY      72  CCGGGGTGGGGGAGGCGGAGTGTCCGTGTGTGCTGAGCGCGGCGGAGAGCGGGCGCGA 131
Db      129  CGCGCGGCGGAGGAGCGCGGCTGTGGCGGGGGCGCGCGAGCGCGGGGCGAG 188

QY      132  GCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTTCGCTTAGGGGCCAAAGCC 191
Db      189  CCGGGGTGGCGTGTCCCGGGCGGTCCCGAGCAGGCTTGGCGGCGCTGTGTGCCCGGGAC 248

QY      192  CCCACCGGCTCCAAAAGTCCAGGGCTCCCGAGGACCGGTGCTCGGCCCTTCCTTC 251
Db      249  CGCGGCTGTGGCGGCGGCTGTGGCGGGGGCGGGCGCGCGCGCGGAGCGGCGGCGCGG 308

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APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 90177
LENGTH: 696
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_88871C.1
US-10-437-963-90177

Query Match 11.0%; Score 41.4; DB 18; Length 696;
Best Local Similarity 48.5%; Pred. No. 0.029;
Matches 114; Conservative 0; Mismatches 121; Indels 0; Gaps 0;
QY 10 CCGAGCTGAGCTTACCTCGGCGCAAAACGAGCGAGCGCGCGCGAGTGGAGCTGGAG 69
DB 594 CGCGCGCGCGACACGCGCGGGATCGGAGCGCGAGCGCGCGCGCGCGCGCG 535
QY 70 TTCGGGGTGGCGGAGCGAGTCTCGTGTGTGTGAGCGCGCGCGAGAGCGCGCG 129
DB 534 GGTGAGCGAGCG 475
QY 130 GAGCGCTGATCGCTTCCCTCGAACTGGGAGGTCCAGTGGGTGCTTTAGGGCCCAAAG 189
DB 474 GAGGCGCAACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 415
QY 190 CCCCACCGCGTCCAAAGTCCAGAGCGCTCCCGAGCACCGGTGTCTCGGCC 244
DB 414 TCCCTTCTCCAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCC 360

RESULT 9
US-10-741-600-17942
Sequence 17942, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17942
LENGTH: 58038
TYPE: DNA
ORGANISM: Homo sapiens
US-10-741-600-17942

Query Match 11.0%; Score 41.4; DB 19; Length 58038;
Best Local Similarity 49.8%; Pred. No. 0.023;
Matches 132; Conservative 1; Mismatches 127; Indels 5; Gaps 1;
QY 28 GGGCGCAACGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 87
DB 6432 GGACRACACGGGCGCTGGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6491
QY 88 GCGACTGTCCGTGTGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCC 147
DB 6492 GCGGGTGTCCCTTGGCGGGGCTCAGGGGTGGAGCGCGGTGGAGCGCTGTGTTCCG- 6550
QY 148 CTCGAACCTGGGAGGTCCAGTGGGTGCTTTAGGGCCCAAGCCCCCAGCCCGGCTCCAAA 207
DB 6551 ----ACCCCTCGCGCCCTCTGGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCG 6606

QY 208 AGCTCCCGGGCTCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 267
DB 6607 AGACTCAAAGGCTCGCGGGGCGACTCGCTCTCCGCCCTTCCCGGAATCAAACCTTCCCTC 6666
QY 268 CCTGGGGCGAGTTCTGTCCTCCAAAGGG 292
DB 6667 TGCAGCGCGCGCGCTTACGGAGGG 6691

RESULT 10
US-10-741-600-17681
Sequence 17681, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17681
LENGTH: 333811
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(333811)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-;
US-10-741-600-17681

Query Match 11.0%; Score 41.4; DB 19; Length 333811;
Best Local Similarity 49.8%; Pred. No. 0.021;
Matches 132; Conservative 1; Mismatches 127; Indels 5; Gaps 1;
QY 28 GGGCGCAACGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 87
DB 191325 GGACRACACGGGCGCTGGGCGACGCGCGCGCGCGCGCGCGCGCGCGCG 191384
QY 88 GCGACTGTCCGTGTGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCC 147
DB 191385 GCGGGTGTCCCTTCCCGGGGCTCAGGGGTGGAGCGGTGCGACGCGTCTGTTCCG- 191443
QY 148 CTCGAACCTGGGAGGTCCAGTGGGTGCTTTAGGGCCCAAGCCCCCAGCCCGGCTCCAAA 207
DB 191444 ----ACCCCTCGCGCCCTCTGGCCCCCGCGCGCGCGCGCGCGCGCGCG 191499
QY 208 AGCTCCCGGGCTCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCC 267
DB 191500 AGACTCAAAGGCTCGCGGGGCGACTCGCTCTCCGCCCTTCCCGGAATCAAACCTTCCCTC 191559
QY 268 CCTGGGGCGAGTTCTGTCCTCCAAAGGG 292
DB 191560 TGCAGCGCGCGCGCTTACGGAGGG 191584

RESULT 11
US-10-017-161-1435
Sequence 1435, Application US/10017161
Publication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430

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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1435
LENGTH: 922
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: source
LOCATION: (1)..(922)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(722)
FEATURE:
NAME/KEY: modified_base
LOCATION: (1)..(26)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (62)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (124)..(125)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (127)..(128)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (131)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (133)..(134)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (138)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (142)..(145)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
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LOCATION: (151)
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NAME/KEY: modified_base
LOCATION: (311)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (322)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (326)
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FEATURE:
NAME/KEY: modified_base
LOCATION: (345)..(349)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
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LOCATION: (351)..(361)
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LOCATION: (364)
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LOCATION: (366)..(368)
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LOCATION: (413)
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OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (422)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (438)..(439)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (441)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (443)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (445)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (465)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (469)..(471)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (487)..(488)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (490)..(491)
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; OTHER INFORMATION: a, t, c, g, unknown or other
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; NAME/KEY: modified_base
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; LOCATION: (497)..(498)
; OTHER INFORMATION: a, t, c, g, unknown or other
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; NAME/KEY: modified_base
; LOCATION: (501)..(505)
; OTHER INFORMATION: a, t, c, g, unknown or other
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; NAME/KEY: modified_base
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; NAME/KEY: modified_base
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; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (540)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (548)..(549)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (564)..(568)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
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; NAME/KEY: modified_base
; LOCATION: (573)
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Query Match 11.0%; Score 41.2; DB 15; Length 922;
Best Local Similarity 40.9%; Pred. No. 0.033;
Matches 70; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 12 GAGCTGAGCTTACCTGGCGCGCAACGACGAGCGAGCGCGCGAGTGGAACTGGAGTT 71
DB 363 GNGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 422

QY 72 CCGGGGTGGCGGGAGGCGACTGTCTCGTGTCTGAGCGCGCGAGCGCGCGGA 131
DB 423 GGGGGGGGGGGGGGGGGGNNNGNNGNNGGNGGGGGGGGGGGGGGGGGGGGGGGGG 482

QY 132 GCGGCTGATCGGCTCCCTCGAAGTGGGAGGTCCAGTGGGGGTGCTTAGGG 182
DB 483 GGGGNNNGGNNNGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 533
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RESULT 12
US-10-292-798-1161
; Sequence 1161, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
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; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1161
; LENGTH: 922
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; LOCATION: (1)..(922)
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; NAME/KEY: CDS
; LOCATION: (201)..(722)
; FEATURE:
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; NAME/KEY: modified_base
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; OTHER INFORMATION: a, t, c, g, unknown or other
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; NAME/KEY: modified_base
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; OTHER INFORMATION: a, t, c, g, unknown or other
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; NAME/KEY: modified_base
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; OTHER INFORMATION: a, t, c, g, unknown or other
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; LOCATION: (469)..(471)
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; NAME/KEY: modified base
; LOCATION: (487)..(488)
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; OTHER INFORMATION: a, t, c, g, unknown or other
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; NAME/KEY: modified base
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; NAME/KEY: modified base
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; OTHER INFORMATION: a, t, c, g, unknown or other
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; NAME/KEY: modified base
; LOCATION: (529)..(530)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (540)..(540)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (548)..(549)
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; NAME/KEY: modified base
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; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (571)..(571)
; OTHER INFORMATION: a, t, c, g, unknown or other
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Query Match 11.0%; Score 41.2; DB 17; Length 922;
Best Local Similarity 40.9%; Pred. No. 0.033;
Matches 70; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

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Qy 12 GAGCTGAGCTTACCTGGGGCGCAACGAGCGAGCGGGCGCGAGTGGAGTGGAGTT 71
Db 363 GNGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 422
Qy 72 CCGGGGTGGGGGAGGAGGACTGTCGTGCTGCTGAGCGCCGCGAGAGCGGGCGGA 131
Db 423 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 482
Qy 132 GCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCAGTGGGGTGGCTTAGGG 182
Db 483 GGGGNNNGGNGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 533
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RESULT 13
US-09-771-161A-58
; Sequence 58, Application US/09771161A
; Patent No. US2002011081A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15

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; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 58
; LENGTH: 1097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-161A-58

Query Match          10.9%; Score 41; DB 9; Length 1097;
Best Local Similarity 52.0%; Pred. No. 0.037;
Matches 92; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 1 CCTCTCCCTCCGAGCTGAGCTTACCTGGCGCGGAGGCGACTGTCCTGTGTGCTGAGCGCGCGGCGAGA 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 CCCCCGGCTCGGGGCTGTGAGCGGCTCGGGGCGGGGGTGGCGGGGTGCGCGCGGGCGG 82
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 AAGCTGGAGTTCCGGGGTGGCGGGGAGGCGACTGTCCTGTGTGCTGAGCGCGCGGCGAGA 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 CGACGCTCTCTTCGCGCGCGCGCGCGCGCGCCATGCTGGGGCGCGCGCTGGGGCG 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 121 GCGGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTCCGCT 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 GCGGGCGCGAGTTGCTCTCCGGGGCCCGGCTGAGGGCCCCCGCGCGCGCGCT 199
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-09-771-161A-59
; Sequence 59, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 59
; LENGTH: 3382
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: -
; LOCATION: (1)..(3382)
; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'
US-09-771-161A-59

Query Match          10.9%; Score 41; DB 9; Length 3382;
Best Local Similarity 52.0%; Pred. No. 0.035;
Matches 92; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 1 CCTCTCCCTCCGAGCTGAGCTTACCTGGCGCGGAGGCGACTGTCCTGTGTGCTGAGCGCGCGGCGGAGTG 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 CCCCCGGCTCGGGGCTGTGAGCGGCTCGGGGCGGGGGTGGCGGGGTGCGCGCGGGCGG 82
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 AAGCTGGAGTTCCGGGGTGGCGGGGAGGCGACTGTCCTGTGTGCTGAGCGCGCGGCGAGA 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 CGACGCTCTCTTCGCGCGCGCGCGCGCGCCATGCTGGGGCGCGCGCTGGGGCG 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 121 GCGGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTCCGCT 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 GCGGGCGCGAGTTGCTCTCCGGGGCCCGGCTGAGGGCCCCCGCGCGCGCGCT 199
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 15

```
US-10-260-238-52/c
; Sequence 52, Application US/10260238
; Publication NO. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Krep, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 52
; LENGTH: 766
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: N region
; LOCATION: (357)..(357)
; OTHER INFORMATION: n = any nucleotide
US-10-260-238-52

Query Match          10.7%; Score 40.2; DB 17; Length 766;
Best Local Similarity 57.6%; Pred. No. 0.065; 53; Indels 0; Gaps 0;
Matches 72; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 12 GAGCTGAGCTTACCTGGGCGCAACGAGCGAGGCGGCGGCGGAGTGGAACTGGAGTT 71
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 686 GAGCGGCGGCGCGGTCGCGGAGCGAGGTGAGCGGAGGCGCGGACGAGTGGCGCGGT 627
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 72 CCGGGGTGGCGGGGAGGCGACTGTCCTGTGTGCTGAGCGCGCGGCGAGAGCGGGCGCGGA 131
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 626 CGGTGCGGACGAGGCGGCGACTGCTGCTGAGGCGGAGGAGGCGGAGCGGCGCGGA 567
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 132 GCGGC 136
   |||
Db 566 TGAGC 562

Search completed: April 7, 2005, 15:19:32
Job time : 337.745 secs
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 08:50:34 ; Search time 2237.21 Seconds
(without alignments)
6380.306 Million cell updates/sec

Title: US-09-977-579-4_COPY_1_375

Perfect score: 375

Sequence: 1 cctcccttcgagctgagc.....gaagccgagccagccagag 375

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST.*

1: gb_est1.*

2: gb_est2.*

3: gb_hc.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	369.8	98.6	4052	3	HSM801563	AL136589 Homo sapi
2	346	92.3	1078	1	AL534136	AL534136 AL534136
3	279.4	74.5	582	5	BP202832	BP202832 BP202832
4	213.8	57.0	972	5	BQ066875	BQ066875 AGENCOURT
C 5	59	15.7	935	9	CNS006XX	AL066051 Drosophil
C 6	53.8	14.3	1101	9	CNS00397	AL063912 Drosophil
7	53.2	14.2	2243	9	AG381986	AG381986 Mus muscu
C 8	53	14.1	693	9	AG060136	AG060136 Pan trogl
C 9	51.8	13.8	935	9	CNS006XX	AL066051 Drosophil
C 10	51.6	13.8	925	9	CNS0091P	AL053013 Drosophil
11	50.6	13.5	925	9	CNS0091P	AL053013 Drosophil
12	50.4	13.4	890	9	CL493826	CL493826 SAIL_586
13	50	13.3	964	9	AG127812	AG127812 Pan trogl
14	49.8	13.3	888	4	BG809572	BG809572 mgct001xa
C 15	49.6	13.2	932	9	CNS0072Q	AL066742 Drosophil
16	49.4	13.2	1289	4	BM807701	BM807701 AGENCOURT
17	49.2	13.1	892	9	CL482374	CL482374 SAIL_35 F
C 18	49.2	13.1	922	9	CL513414	CL513414 SAIL_875
19	49.2	13.1	957	9	CL476240	CL476240 SAIL_251
20	48.8	13.0	863	9	AG132157	AG132157 Pan trogl
21	48.6	13.0	970	5	BUS38852	BUS38852 AGENCOURT
C 22	48.6	13.0	1009	9	CNS010EW	AL098882 Drosophil
C 23	48.4	12.9	977	9	CL488066	CL488066 SAIL_503
C 24	48.2	12.9	950	9	CL501906	CL501906 SAIL_705

25	48.2	12.9	956	5	BU501227	BU501227 AGENCOURT
26	48.2	12.9	966	5	BQ672441	BQ672441 AGENCOURT
27	48.2	12.9	1203	9	CNS015Y4	AL106054 Drosophil
C 28	48	12.8	762	9	AG527521	AG527521 Mus muscu
C 29	48	12.8	921	9	CL516158	CL516158 SAIL_913
30	48	12.8	1171	5	BM914930	BM914930 AGENCOURT
31	47.8	12.7	873	9	AG043471	AG043471 Pan trogl
32	47.8	12.7	897	9	CNS015LJ	AL105601 Drosophil
C 33	47.6	12.7	941	9	CL485264	CL485264 SAIL_1237
C 34	47.6	12.7	1350	9	CL461110	CL461110 SAIL_113
35	47.4	12.6	897	9	CL470675	CL470675 SAIL_146
C 36	47.4	12.6	907	6	CB898968	CB898968 trico16x1
C 37	47.4	12.6	907	7	CF868868	CF868868 trico16x1
C 38	47.4	12.6	2332	9	AG363333	AG363333 Mus muscu
C 39	47.2	12.6	377	4	BG361509	BG361509 gb50d11.y
C 40	47.2	12.6	732	8	AZ196033	AZ196033 SP_1031.A
C 41	46.8	12.5	936	4	BG852371	BG852371 1034034A0
C 42	46.8	12.5	1048	5	BQ073800	BQ073800 AGENCOURT
C 43	46.6	12.4	442	8	BH172722	BH172722 SALK_0060
C 44	46.6	12.4	860	9	CNS0226P	AL220570 Tetraodon
45	46.6	12.4	881	9	AG384979	AG384979 Mus muscu

ALIGNMENTS

RESULT 1	HSM801563	HSM801563	4052 bp	mrna	linear	HTC 22-SEP-2004
LOCUS	Homo sapiens mRNA; cDNA DKF2p761F182 (from clone DKF2p761F182).					
DEFINITION	AL136589					
ACCESSION	AL136589.1	GI:13276680				
VERSION	HTC					
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 4052)					
AUTHORS	Ortenwaelder B., Obermaier B., Deutschbauer S., Schapp, A., Mewes, H.W., Weil, B., Amid, C., Oanger, A., Fobo, G., Han, M. and Wiemann, S.					
CONSRMT	The German CDNA Consortium					
TITLE	Direct Submission					
JOURNAL	Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY					
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de; sequenced by Medigenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKF2p761F182) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKF2p761F182 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.					
FEATURES	Location/Qualifiers					
source	1. .4052					
	/organism="Homo sapiens"					
	/mol_type="mrna"					
	/db_xref="RZPD:DKF2p761F182"					
	/db_xref="taxon:9606"					
	/clone="DKF2p761F182"					
	/tissue type="amygdala"					
	/clone_lib="761 (synonym: hamy2). Vector pSport1; host DH10B; sites NotI + SalI"					
	/dev_stage="adult"					
	/note="voltage-gated sodium channel beta-3 subunit"					
gene	1. .4052					
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CDS	804. .1451					
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	/codon_start=1					
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/protein_id="CAB6524.1"
/db_xref="GI:13276681"
/db_xref="GOA:Q9NY72"
/db_xref="UniProt/Swiss-Prot:Q9NY72"
translation="MPAFNRLPLASLVLIVVSVCFVCEVPSETEAVQGNPMKLR
CISMKREVEATTVVEFYPREGKDLIVYVRNGHOEVESPFQGRLOWNGSKDLQD
VSITVINTLNDSGLYTCNVSREPFPAHRFPVKTRILPLRVTEAGEDFTSVVSEI
MYYILLVFLTLMLLEMIYKRVKSKAEAAQENASDYLAIPSENKENSAPVEE"

ORIGIN
Query Match      98.6%; Score 369.8; DB 3; Length 4052;
Best Local Similarity 99.5%; Pred. No. 6.1e-80;
Matches 371; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CTCCTTCCGAGCTGAGCTTACCTTGGCGCGCAAAACGAGCGAGGCGGGCGCGAGTGGAA 62
DB 431 CTCCTTCCGAGCTGAGCTTACCTTGGCGCGCAAAACGAGCGAGGCGGGCGCGAGTGGAA 490
QY 63 GCTGGAGTTCCGGGTGGCGGGGAGGCGACTGTCCGTGGTGTCTGAGCGCCCGCGAGGC 122
DB 491 GCTGGAGTTCCGGGTGGCGGGGAGGCGACTGTCCGTGGTGTCTGAGCGCCCGCGAGGC 550
QY 123 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCAGTGGGGTGCCTTAGGG 182
DB 551 GGGCGGAGCGGCTGATCAGTCCCTCGAACTGGGAGGTCAGTGGGGTGCCTTAGGG 610
QY 183 CCCAAGCCCCCAGCGGCTCCAAAGCTCCAGGGCCCTCCCGAGCGACCGGTGCTCGGC 242
DB 611 CCCAAGCCCCCAGCGGCTCCAAAGCTCCAGGGCCCTCCCGAGCGACCGGTGCTCGGC 670
QY 243 CTTCTCTTGGTTCAGAAAGTCCGCCCTGGGGGAGTTCGTCCTCAAGGGTTTCCTCGAA 302
DB 671 CTTCTCTTGGTTCAGAAAGTCCGCCCTGGGGGAGTTCGTCCTCAAGGGTTTCCTCGAA 730
QY 303 AGAATCTGAGAGGCGGCGAGTCTTGACCGAGGGAATCTCTGTGTAGCTTTGGAAGCG 362
DB 731 AGAATCTGAGAGGCGGCGAGTCTTGACCGAGGGAATCTCTGTGTAGCTTTGGAAGCG 790
QY 363 CCAGCCCCAGAG 375
DB 791 CCAGCCCCAGAG 803

RESULT 2
AL534136      1078 bp mRNA linear EST 24-MAR-2004
LOCUS      CS0DF005Y102 5-PRIME, mRNA sequence.
DEFINITION      AL534136
ACCESSION      AL534136
VERSION      EST.
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      1 (bases 1 to 1078)
JOURNAL      Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
COMMENT      Full-length cDNA libraries and normalization
              Unpublished (2001)
              On Feb 13, 2001 this sequence version replaced gi:30539643.
              Contact: Genoscope
              Genoscope - Centre National de Sequencage
              2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
              end enriched, double-strand cDNA was digested with Not I and cloned
              into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
              division of invitrogen.
              This sequence belongs to sequence cluster 6147.r
              For more information about this cluster, see
              http://www.genoscope.cns.fr/cdna?c=CS0DF005B01QP1&c=6147.r.
              Location/Qualifiers

FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF005Y102"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN
Query Match      92.3%; Score 346; DB 1; Length 1078;
Best Local Similarity 98.9%; Pred. No. 3.7e-74;
Matches 369; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

QY 3 CTCCTTCCGAGCTGAGCTTACCTTGGCGCGCAAAACGAGCGAGGCGGGCGCGAGTGGAA 62
DB 392 CTCCTTCCGAGCTGAGCTTACCTTGGCGCGCAAAACGAGCGAGGCGGGCGCGAGTGGAA 451
QY 63 GCTGGAGTTCCGGGTGGCGGGGAGGCGACTGTCCGTGGTGTCTGAGCGCCCGCGAGGC 122
DB 452 GCTGGAGTTCCGGGTGGCGGGGAGGCGACTGTCCGTGGTGTCTGAGCGCCCGCGAGGC 511
QY 123 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCAGTGGGGTGCCTTAGGG 182
DB 512 GGGCGCGNA--GGCTGATCGGCTCCCTCGAACTGGGAGGTCAGTGGGGTGCCTTAGGG 569
QY 183 CCCAAGCCCCCAGCGGCTCCAAAGCTCCAGGGCCCTCCCGAGCGACCGGTGCTCGGC 242
DB 570 CCCAAGCCCCCAGCGGCTCCAAAGCTCCAGGGCCCTCCCGAGCGACCGGTGCTCGGC 629
QY 243 CTTCTCTTGGTTCAGAAAGTCCGCCCTGGGGGAGTTCGTCCTCAAGGGTTTCCTCGAA 302
DB 630 CTTCTCTTGGTTCAGAAAGTCCGCCCTGGGGGAGTTCGTCCTCAAGGGTTTCCTCGAA 689
QY 303 AGAATCTGAGAGGCGGCGAGTCTTGACCGAGGGAATCTCTGTGTAGCTTTGGAAGCG 362
DB 690 AGAATCTGAGAGGCGGCGA--TCCTTGACCGAGGGAATCTCTGTGTAGCTTTGGAAGCG 748
QY 363 CCAGCCCCAGAG 375
DB 749 CCAGCCCCAGAG 761

RESULT 3
BP202832      582 bp mRNA linear EST 14-SEP-2004
LOCUS      BP202832 Sugano cDNA library, amygdala Homo sapiens cDNA clone
DEFINITION      AMR09622, mRNA sequence.
ACCESSION      BP202832
VERSION      BP202832.1 GI:52054220
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      1 (bases 1 to 582)
JOURNAL      Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
COMMENT      Mizushima-Sugano, J., Nakai, K. and Sugano, S.
              Sequence comparison of human and mouse genes reveals a homologous
              block structure in the promoter regions
              Genome Res. 14 (9), 1711-1718 (2004)
              Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: shuzuki@ims.u-tokyo.ac.jp.
              Location/Qualifiers

FEATURES
source
1..582
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/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="AMR09622"
 /tissue_type="amygdala"
 /clone_lib="Sugano cDNA library, amygdala"

Query Match 74.5%; Score 279.4; DB 5; Length 582;
 Best Local Similarity 99.6%; Pred. No. 7e-58; Indels 0; Gaps 0;
 Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 95 GTCCGTGGTCTGAGCGCGCGGAGAGCGGCGGAGCGGCTGATCGGCTCCCTCGAAC 154
 DB 1 GTCGTGGTCTGAGCGCGCGGAGAGCGGCGGAGCGGCTGATCGGCGGCTCGAAC 60
 QY 155 TGGGAGGTCAGTGGGTCGCTTAGGGCCCAAGCCCCCAGCCGGTCCAAAAGCTCCC 214
 DB 61 TGGGAGGTCAGTGGGTCGCTTAGGGCCCAAGCCCCCAGCCGGTCCAAAAGCTCCC 120
 QY 215 AGGCGCTCCCGAGCGCGGTCGCGCCCTTCTTCGGTTCAGAAAGTCCGCCCTGGGG 274
 DB 121 AGGCGCTCCCGAGCGCGGTCGCGCCCTTCTTCGGTTCAGAAAGTCCGCCCTGGGG 180
 QY 275 GCAGTTGGTCCCAAGAGTTTCTCGAAAGAAATCTGAGAGCGGCGCAGTCTTGACCGAGG 334
 DB 181 GCAGTTGGTCCCAAGAGTTTCTCGAAAGAAATCTGAGAGCGGCGCAGTCTTGACCGAGG 240
 QY 335 GAATCTCTGTAGCTTGGAGCGCGCCAGCCCGCAGAG 375
 DB 241 GAATCTCTGTAGCTTGGAGCGCGCCAGCCCGCAGAG 281

RESULT 4
 BQ066875
 LOCUS
 DEFINITION BQ066875 972 bp mRNA linear EST 02-APR-2002
 5', mRNA sequence.
 ACCESSION BQ066875
 VERSION BQ066875.1 GI:19895921
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 972)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@email.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LNL2813 row: b column: 17
 High quality sequence start: 28
 High quality sequence stop: 456.
 Location/Qualifiers
 1..972
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5762608"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC 114"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
 male brains, age range 23-27 yo. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed)

FEATURES
 source

upon cloning). Average insert size 1.5 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 019. Note:
 this is a NIH_MGC Library."

ORIGIN

Query Match 57.0%; Score 213.8; DB 5; Length 972;
 Best Local Similarity 90.7%; Pred. No. 8e-42;
 Matches 262; Conservative 0; Mismatches 22; Indels 5; Gaps 3;

QY 3 CTCCTTCGAGCTGAGCTTACCTCGGCGCAACAGCGAGCGAGGGCGCGAGTGGA 62
 DB 412 CTCCTTCGAGCTGAGCTTACCTCGGCGCAACAGCGAGCGAGGGCGCGAGTGGA 471
 QY 63 GCTGGAGTTCGGGTCGGGCGGAGCGGCTGCTCGTGGTGTGAGCGCGCGAGGC 122
 DB 472 GCTGGAGTTCGGGTCGGGCGGAGCGGCTGCTCGTGGTGTGAGCGCGCGAGGC 531
 QY 123 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCAGTGGGTCGCTTAGGG 182
 DB 532 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCGCTGGGTCGCTTAGGG 591
 QY 183 CCAGAGCCCCCAGCGGCTCCAAAAGTCCCA-GGGCTTCCCGAGCGCGGTG--CTC 239
 DB 592 GCCAAAGCCCCCAGCGGCTCCAAAAGTCCCA-GGGCTTCCCGAGCGCGGTG--CTC 651
 QY 240 GGGCTTCCCTT--CGTCTGAAAGTCGCCCTGGGCGGAGTTCGTCCTCC 286
 DB 652 GGGCTTCCCTTCCCGGCAAAAGTCTCCCTGGGCGGCGCGGCTCC 700

RESULT 5
 CNS006XK/c
 LOCUS
 DEFINITION CNS006XK 935 bp DNA linear GSS 03-JUN-1999
 Drosophila melanogaster genome survey sequence T7 end of BAC #
 BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL066051
 VERSION AL066051.1 GI:4945019
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 935)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Herkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see http://www.fruitfly.org The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mammoser in Pister de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 Location/Qualifiers
 1..935
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACR14N09"

FEATURES
 source


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ORIGIN
Query Match      14.2%; Score 53.2; DB 9; Length 2243;
Best Local Similarity 51.0%; Pred. No. 0.016; Mismatches 0; Indels 0; Gaps 0;
Matches 100; Conservative

QY 24 CCTTGGCGCAACGACGAGCGAGGCGCGAGTGGAGTTCGGAGTTCGGGGTGGCG 83
Db 1905 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1964
QY 84 GCGAGGCGACTGTCCTGCTGCTAGCGCGCGCGCGAGCGCGCGCGCGAGCGCTGATCG 143
Db 1965 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2024
QY 144 CTCCTCTCAACTGGGAGGTCCAGTGGGTTCGCTTAGGGCCCAAGCCCGCCGCTC 203
Db 2025 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2084
QY 204 CAAAGCTCCAGGCG 219
Db 2085 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG

RESULT 8
AG060136/c
LOCUS
DEFINITION Pan troglodytes DNA, clone: PTB-047116.F, genomic survey sequence.
ACCESSION AG060136
VERSION AG060136.1 GI:16611366
KEYWORDS
SOURCE Pan troglodytes (chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 693)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpanzee@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB. This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
FEATURES
source
Location/Qualifiers
1. .693
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-047116.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match      14.1%; Score 53; DB 9; Length 693;
Best Local Similarity 49.4%; Pred. No. 0.017;
Matches 131; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

QY 28 GGGCGCAACGACGAGCGAGGCGCGAGTGGAGTTCGGGGTGGCGGGA 87
```

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Db 647 GGGGCGGCGCGCGCGCGCGGTTTGGGNGGCGCGCGTGCCTGGCGGGGGGGGCG 588
QY 88 GGGCACTGTCGTGCTGAGCGCGCGAGAGCGGCGCGAGCGGCTGATCGGCTCC 147
Db 587 GGGGGGGGGCGCGGGGGGGCGCGCGCCGNNCTGGCCGCGCGCGCGGGCGGCG 528
QY 148 CTCGAACCTGGGAGGTCCAGTGGGTTCGCTTAGGGCCCAAGCCCGCCGCTCAAA 207
Db 527 GGTCTCGTGGGGGGCGCGGGGGCGGGGGTGGCGGGGGGGGGGGCGCGCG 468
QY 208 AGCTCCAGGCGCTCCCGAGGCAACCGTCTCGGCCCTTCTTTCGTCGAGAAAGTCGCC 267
Db 467 TGGGGGGGGGGCGCGCGCGCGCGGGGCGGGCGCCCTCTCCGCGGCGCGCGGNG 408
QY 268 CTGGGGGGCAGTTCGTCCTCCAAAGGG 292
Db 407 GCGGGGGGGCGTGGGGGGCGCGGGG 383

CNS006XK 935 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BAC14N09 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL066051
AL066051.1 GI:4945019
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoler in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain v2; cn bw ap, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
source
Location/Qualifiers
1. .935
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BAC14N09"
/clone_lib="RPCI-98"
/note="end : T7"

ORIGIN
Query Match      13.8%; Score 51.8; DB 9; Length 935;
Best Local Similarity 33.2%; Pred. No. 0.033;
Matches 86; Conservative 58; Mismatches 115; Indels 0; Gaps 0;

QY 28 GGGCGCAACGACGAGGCGGCGAGTGGAGTTCGGGGTGGCGGGA 87
Db 669 GGGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 728
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QY      88  GCGGACTGCTCGGTGCTGACGCGCGCGAGCGGCGCGGCGGTGATCGCTCC 147
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      729  CSSGSGSCSCCSCGSCSSSGSCCGCGCMSCGCGSGCGCGCGCGCGCGCG 788
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      148  CTCGAATCTGGGAGGTTCAGTTCGGTTCAGTTCAGTTCAGTTCAGTTC 207
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      789  CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 848
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      208  AGCTCCAGGGCTCCCGAGGACCGGCTGCTCGGCGCTTCCTTCGTCGAAAGTCGCC 267
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      849  SCGCGSGSGSCCGSGCGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 908
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      268  CTGCGGGGCGTTCGTCC 286
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      909  CSCGCGCGCGSCSSSCSC 927
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
CNS0091P/c
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BAC1916 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL053013
VERSION
AL053013.1 GI:4934461
KEYWORDS
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 925)
Genoscope.
AUTHORS
Direct Submission
TITLE
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoler in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source
1..925
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR1916"
/clone_lib="RPCI-98"
/note="end : TET3"

ORIGIN
Query Match 13.8%; Score 51.6; DB 9; Length 925;
Best Local Similarity 13.4%; Pred. No. 0.037;
Matches 37; Conservative 136; Mismatches 104; Indels 0; Gaps 0;

QY      2  CCTCCTTCGAGCTGAGTTCCTCGGCGCAACGACGAGCGCGCGGCGGAGTGA 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      869  SSSSSGTSACVKNVASSCCCGCMABCWCSSSSCCGASARGVKVRASGAGKR 810
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      62  AGCTGAGATTCGGGGTGGCGGGAGGCGACTGTCGTGCTGAGCGCGCGGAGAG 121
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      809  GGGSGGASASHSSSACBSSSSCSASCSWSASSSSASSSRSRSGGAGGSGASSRSS 750
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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QY      122  CGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCAGTGGGTCGCTTAGG 181
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      749  SSSSAGSVSSASSSSSSSSSVSCSVASSMSCSSBSSSSASASSSSSSASCASC 690
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      182  GCCCAAGCCGCCCGCTCCAAAGCTCCAGGGCTCCCGAGGACCGGTCGCTCGG 241
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      699  SCCCTTSCSCSTASMSAARSSSSSSSSSSSWSSASSSSASSSSSSSSSSSSSGS 630
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      242  CCCTTCCTTCGTCGAGAAAGTCGCCCTCGGGCGAG 278
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      629  ACBSMSSGGSGSVSASSGMSVSSVSSGGRSSGSG 593
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
CNS0091P
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BAC1916 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL053013
VERSION
AL053013.1 GI:4934461
KEYWORDS
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Metazoa; Arthropoda; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 925)
Genoscope.
AUTHORS
Direct Submission
TITLE
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoler in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source
1..925
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR1916"
/clone_lib="RPCI-98"
/note="end : TET3"

ORIGIN
Query Match 13.5%; Score 50.6; DB 9; Length 925;
Best Local Similarity 12.5%; Pred. No. 0.066;
Matches 42; Conservative 158; Mismatches 135; Indels 0; Gaps 0;

QY      5  CCCTTCGAGCTGAGTTCCTCGGCGCAACGACGAGCGCGGCGCGGAGTGAAGC 64
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      572  CSCSCSCSCSSSCSCBCCCCCSCSYCCSSBSKSSSTBSKSCCCSKSVCGTSC 631
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      65  TGAAGTTCGGGGTGGCGGGGAGCGACTGTCCTGCTGCTGACGCGCGGAGAGCGG 124
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      632  SSSSSCSSSSSSSTSSSTSSSSSSSSSSSSSSSTTSKSTASGSGSWAGGSGS 691
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      125  GCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCAGTGGGTCGCTTAGGCGC 184
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```



```
Db 692 TGSTSSSSSSSTSTSSSVSSGSKSTBSGSSBSSSSSSSTSSBBSCTSTSSSSSS 751
QY 185 CAAAGCCCCACCCCGGCTCAAAAGCTCCAGGCGCTCCCGAGCACCGGTGTCGCGCC 244
Db 752 SYSSSTCCCTCCCSYSTSTSSSTSSSTGSGSSSVGTSSSDSTSTCCSCCCYM 811
QY 245 TTCCTCGGTGAGAAAGTCGCCCCCTGGGGGACGTTCGTCCTCAAAAGGTTCTCTCGAAAG 304
Db 812 CTCSTYBMCYTSTSCGSSSSSGKGVTKCGCGGSSSTGMBGTSSACSSSSSSCS 871
QY 305 AATCTGAGAGGGCGCAGTCTTGACCGAGGGAATC 339
Db 872 SSSVSSSSKSSASSSVSSSGSGSGVSSNSSSASKS 906

RESULT 12
LOCUS CL493826 890 bp DNA linear GSS 01-APR-2004
DEFINITION SAIL_586_F04.v1 SAIL Collection Arabidopsis thaliana genomic clone
ACCESSION SAIL_586_F04.v1, genomic survey sequence.
VERSION CL493826
KEYWORDS CL493826.1 GI:45982408
SOURCE GSS.
ORGANISM Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 890)
AUTHORS Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
Mitzel,T., Katagiri,P., Glazebrook,J., Law,M. and Goff,S.A.
A high-throughput Arabidopsis reverse genetics system
Plant Cell 14 (12), 2985-2994 (2002)
22356987
12468722
COMMENT Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com
ABRC Stock Number CS824955; T-DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: TDNA tagged.
FEATURES
source Location/Qualifiers
1..890
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="SAIL_586_F04.v1"
/clone_lib="SAIL Collection"
/notes="T-DNA left border sequences were isolated using a
modified TAIL-PCR strategy"
ORIGIN
Query Match 13.4%; Score 50.4; DB 9; Length 890;
Best Local Similarity 48.6%; Pred. No. 0.073;
Matches 126; Conservative 0; Mismatches 133; Indels 0; Gaps 0;
QY 28 GCGCGCAACACGAGGCGAGCGGCGGCGAGTGGAGCTGCGGGTGGCGGGGA 87
Db 615 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 674
QY 88 GGGGACTGTCGCTGAGCGCGCGCGAGAGCGGCGGAGCGGCTGATCGGCTCC 147
Db 675 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 734
QY 148 CTCGAACTGGGGAGGTTCAGTGGGGTGGCTTAGGGGCCCAAGACCCCGCGCTCAA 207
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Db 735 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 794
QY 208 AGCTCCAGAGGCTCCCGAGGACCGGTGTCGCGCCCTCTTCGCGTACAGAAAGTCGCC 267
Db 795 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 854
QY 268 CTTGGGGGCGAGTTCGTCCC 286
Db 855 CGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 873

RESULT 13
LOCUS AG127812 964 bp DNA linear GSS 04-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-138M14.R, genomic survey sequence.
ACCESSION AG127812
VERSION AG127812.1 GI:16656977
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 964)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
[E-mail:chimps@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170]
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI,
Location/Qualifiers
1..964
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-138M14.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN
Query Match 13.3%; Score 50; DB 9; Length 964;
Best Local Similarity 48.1%; Pred. No. 0.092;
Matches 116; Conservative 0; Mismatches 125; Indels 0; Gaps 0;
QY 38 GAGCGAGGCGGCGCGAGTGGAGCTGGAGTTCGCGGGTGGCGGAGCGACTGTC 97
Db 340 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 399
QY 98 CGTGTGCTGAGCGCGCGAGAGCGGCGCGAGCGGTGATCGGCTCCCTCGAACTGG 157
Db 400 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 459
QY 158 GGNAGTTCAGTGGGGTTCGCTTAGGGGCCCAAGACCCCGCGCTCCAAAGTCCAGG 217
Db 460 GNGGGGNGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 519
```

```

QY 218 GCCTCCCGGACCGGTCTGGCTTCCGTCAGAAAGTCGCCCCCTGGGGGCA 277
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
520 GCCCGAAAAAAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 579

QY 278 G 278
Db 580 G 580

RESULT 14
BG809572 888 bp mRNA linear EST 22-MAY-2001
LOCUS mgct001xa14f Magnaporthe grisea Appressorium Stage cDNA Magnaporthe
DEFINITION grisea cDNA clone mgct001xa14f 5', mRNA sequence.
ACCESSION BG809572
VERSION BG809572.1 GI:14180552
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
REFERENCE 1 (bases 1 to 888)
AUTHORS Choi, W. and Dean, R.A.
TITLE Construction and sequence analysis of an appressorium stage cDNA
JOURNAL library in the rice blast fungus, Magnaporthe grisea
COMMENT Unpublished (2001)
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph_dean@ncsu.edu
Seq primer: T3 primer (AATTAACTCTCACTAAAGGG).
FEATURES
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    1..888
        /organism="Magnaporthe grisea"
        /mol_type="mRNA"
        /strain="70-15"
        /db_xref="taxon:148305"
        /clone="mgct001xa14f"
        /dev_stage="Germinated conidia on appressorium-inductive
        surface"
        /clone_lib="Magnaporthe grisea Appressorium Stage cDNA"
        /note="Vector: pBluescript SK(+); Vector; Site 1: EcoRI;
        Site 2: XhoI; The appressorium formation-specific cDNA
        library was constructed from conidia germinated for 5-8 hr
        on an inductive surface. The library contains over 55,000
        clones with average insert size of 1.5 kbp."
ORIGIN
    Query Match 13.3%; Score 49.8; DB 4; Length 888;
    Best Local Similarity 50.8%; Pred. No. 0.1;
    Matches 128; Conservative 0; Mismatches 123; Indels 1; Gaps 1;

QY 28 GGGCGCAACGACGAGGAGGGGCGGAGTGAAGTTCGGGGTGGGGGGA 87
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
176 GGGGGGGGGGGGNGGGGGGGGGGNGGNGGNGGNGGGGGGGGGGGGGGGG 235

QY 88 GGGCGACTGTCTGTGTGTCTGAGCGCGGCGGAGAGCGGCGGTGATCGGCTCC 147
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
236 GCGCGGGNCGGGGGGGGGGGCGCGCGGGGCGGGGCGGGGGCGCGGGC 294

QY 148 CTCGAACTGGGGAGGTCCAGTGGGGTGTCTTAGGGCCCAAGCCCAACCCGGCTCAAA 207
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
295 CGGCGCGCGCGCGCGCGCGCGCGGGGCGGCGCGCGCGCGCGCGCGCGCG 354

QY 208 AGCTCCAGGGCTCCCGAGGCACCGGTGCTCGGCCCTTCCTTCGATCAGAAAGTCGCCC 267
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
355 CGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 414

QY 268 CTGGGGGCGAGT 279
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Db 415 GGGGGCGGGGGGT 426

RESULT 15
CNS00720Q/c 932 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC #
DEFINITION BACr14B09 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL066742
VERSION AL066742.1 GI:4945205
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 932)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
    source
    1..932
        /organism="Drosophila melanogaster"
        /mol_type="genomic DNA"
        /db_xref="taxon:7227"
        /clone="BACR14B09"
        /clone_lib="RPCI-98"
        /note="end : T7"
ORIGIN
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    Best Local Similarity 32.3%; Pred. No. 0.12;
    Matches 80; Conservative 60; Mismatches 108; Indels 0; Gaps 0;

QY 1 CCCTCCCTTCCGAGCTTGAGCTTACCTGGCGCAACAGCAGGCGGGCGGAGTGG 60
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
800 SSCSCGCGSSCGSCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGSGSGGS 741

QY 61 AAGCTGAGATTCCGGGGTGGCGGGAGGCGACTGTCTGTGTGTGACGCGCGGCGAGA 120
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
740 GGGGSGSGGGGCGSGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGSGCGSS 681

QY 121 GCGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGTTCGTTAG 180
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
680 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 621

QY 181 GGGCCCAAGCGCCCCCGCGGTCCAAAAGCTCCCCAGGGGCTCCCCCAGGACCGGGTCTCG 240
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
620 CGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 561

QY 241 GCCTTTC 248
Db ||| ||| |||
560 SCMSGCC 553

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Search completed: April 7, 2005, 14:55:34
Job time : 2245.21 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 07:44:40 ; Search time 3090.98 Seconds
(without alignments)
10158.276 Million cell updates/sec

Title: US-09-977-579-4_COPY_376_1023

Perfect score: 648

Sequence: 1 atgcctgcctcattagatt.....cggtagcaggaggaggaatag 648

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	648	100.0	1261	6 AR359850	AR359850 Sequence
2	648	100.0	1261	6 AX039100	AX039100 Sequence
3	648	100.0	1261	9 HSA243396	AJ243396 Homo sapi
4	646.4	99.8	5306	9 AB032984	AB032984 Homo sapi
5	627.2	96.8	3296	9 AB097521	AB097521 Macaca fa
6	592.4	91.4	606	6 CQ728741	CQ728741 Sequence
7	537.2	82.9	670	10 AY049036	AY049036 Mus muscu
8	536.6	82.8	2220	6 AR359849	AR359849 Sequence
9	536.6	82.8	2220	6 AX039099	AX039099 Sequence
10	536.6	82.8	2220	10 RNO243395	AJ243395 Rattus no
11	536.6	82.8	2632	6 AX048005	AX048005 Sequence
12	536.6	82.8	3107	10 AF378093	AF378093 Rattus no
13	536.6	82.8	3108	6 AX047984	AX047984 Sequence
14	536.6	82.8	4025	10 AK173115	AK173115 Mus muscu
15	536.6	82.8	4169	10 BC053919	BC053919 Mus muscu
16	536.6	82.8	4176	10 BC058636	BC058636 Mus muscu
17	534.6	82.5	645	6 AX048004	AX048004 Sequence
18	533.4	82.3	3910	10 BC070899	BC070899 Rattus no
19	422	65.1	471	6 BD059018	BD059018 Secreted

20	368	56.8	922	5 BX935227	BX935227 Gallus ga
21	332.2	51.3	912	5 BX931708	BX931708 Gallus ga
22	264.6	40.8	1654	5 BC077295	BC077295 Xenopus l
23	229.6	35.4	127347	2 AF000682	AF000682 Homo sapi
24	229.6	35.4	172546	2 AC024604	AC024604 Homo sapi
25	229.6	35.4	178169	9 AP002765	AP002765 Homo sapi
26	229.6	35.4	178431	2 AP002749	AP002749 Homo sapi
27	229.6	35.4	181471	9 AC069539	AC069539 Homo sapi
28	228	35.2	144833	2 AC063921	AC063921 Homo sapi
29	228	35.2	149800	2 AC021981	AC021981 Homo sapi
30	204.2	31.5	174285	2 AC145484	AC145484 Lemur cat
31	179	27.6	140307	2 AC135353	AC135353 Mus muscu
32	179	27.6	238861	2 AC148331	AC148331 Mus muscu
33	174.2	26.9	214306	2 AC128723	AC128723 Rattus no
34	167.8	25.9	144833	2 AC063921	AC063921 Homo sapi
35	148.2	22.9	657	4 OC035382	U35382 Oryctolagus
36	148.2	22.9	657	6 AX048006	AX048006 Sequence
37	145.4	22.4	1404	9 HUMSCN1BA	LI0338 Human sodiu
38	143.8	22.2	617	6 CQ722293	CQ722293 Sequence
39	143.8	22.2	1335	9 HUMVGSCLB	LI6242 Homo sapien
40	143.8	22.2	1525	9 BC067122	BC067122 Homo sapi
41	138.6	21.4	1125	10 MMU46681	U46681 Mus musculu
42	138.6	21.4	1340	10 MMU85786	U85786 Mus musculu
43	138.6	21.4	1490	6 AX401978	AX401978 Sequence
44	138.6	21.4	1490	10 RATSCHB1B	N91808 Rattus norv
45	138.6	21.4	1557	10 BC039140	BC039140 Mus muscu

ALIGNMENTS

RESULT 1
LOCUS AR359850 1261 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 4 from patent US 6593565.
ACCESSION AR359850
VERSION AR359850.1 GI:33766660
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1261)
AUTHORS Heslin,P. and Lynam,N.R.
TITLE Vehicle interior rearview mirror assembly including an accessory-containing housing
JOURNAL Patent: US 6593565-A 4 15-JUL-2003;
FEATURES Location/Qualifiers
source 1. 1261
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match	100.0%;	Score 648;	DB 6;	Length 1261;
Best Local Similarity	100.0%;	Pred. No. 2.1e-142;		
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Qy	1	ATGCCTGCCTTCAATAGATTGTTTCCCTCGCTTCTCTCGTCTTCTACTGGTCAGT	60	
Db	376	ATGCCTGCCTTCAATAGATTGTTTCCCTCGCTTCTCTCGTCTTCTACTGGTCAGT	435	
Qy	61	GTCTGCTTCCCTGTGTGTGGAAAGTCCCTCGGAGACGGAGCGCGTCGAGGGCAACCCC	120	
Db	436	GTCTGCTTCCCTGTGTGTGGAAAGTCCCTCGGAGACGGAGCGCGTCGAGGGCAACCCC	495	
Qy	121	ATGAAGTCGGCTGCATCTCTCGATGAAGAGAGAGGTGGAGGCCACACCGTGGTG	180	
Db	496	ATGAAGTCGGCTGCATCTCTCGATGAAGAGAGAGGTGGAGGCCACACCGTGGTG	555	
Qy	181	GAATGGTTCTACAGGCGCGGATTTCTTATTTTACGAGTATCGGAATGGC	240	
Db	556	GAATGGTTCTACAGGCGCGGATTTCTTATTTTACGAGTATCGGAATGGC	615	
Qy	241	CACCAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTTCGATGGAATGTCAGCAGGACCTG	300	

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Db 616 CACCAGGAGTGGAGAGCCCTTTTCAGGGCGCTGCTCACTGGATGGCAGCAGGACCTG 675
Qy 301 CAGGAGTGTCCATCATCTGTGCTCAACGTCACCTGGAACGACTCTGGCCCTCTACACCTGC 360
Db 676 CAGGAGTGTCCATCATCTGTGCTCAACGTCACCTGGAACGACTCTGGCCCTCTACACCTGC 735
Qy 361 AATGTGTCCTGGGAGTTTGAAGTTTGAAGGCGCATCGGCCCTTTTGTGAAGACGACGGGCTG 420
Db 736 AATGTGTCCTGGGAGTTTGAAGTTTGAAGGCGCATCGGCCCTTTTGTGAAGACGACGGGCTG 795
Qy 421 ATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGGACTTCACCTCTGTGCTCTCAGAAATC 480
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Qy 481 ATGATGTACATCCTTCTGCTCTTCTCACCCTGTGGCTGCTCATCGAGATGATATATTCG 540
Db 856 ATGATGTACATCCTTCTGCTCTTCTCACCCTGTGGCTGCTCATCGAGATGATATATTCG 915
Qy 541 TACAGAAAGGTCTCAAAAGCCGAGAGGAGGCCCAAGAAACGCGTCTGACTTACCTTGCC 600
Db 916 TACAGAAAGGTCTCAAAAGCCGAGAGGAGGCCCAAGAAACGCGTCTGACTTACCTTGCC 975
Qy 601 ATCCCATCTGAGAACAGGAGAACTCTGCGGTACCACTGCGAGGAATAG 648
Db 976 ATCCCATCTGAGAACAGGAGAACTCTGCGGTACCACTGCGAGGAATAG 1023

RESULT 2
AX039100
LOCUS AX039100 1261 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 4 from Patent WO0063367.
ACCESSION AX039100
VERSION AX039100.1 GI:11229276
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Cox, P., Dixon, A., Jackson, A. and Morgan, K.
JOURNAL A novel family of beta sub-unit proteins from a voltage-gated sodi
diagnostic uses there of
Patent: WO 0063367-A 4 26-OCT-2000;
WARNER-LAMBERT COMPANY (US) ; Cambridge University Technical
SERVICES Limited (GB)
FEATURES
Location/Qualifiers
source 1..1261
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 100.0%; Score 648; DB 6; Length 1261;
Best Local Similarity 100.0%; Pred. No. 2.1e-142; Indels 0; Gaps 0;
Matches 648; Conservative 0; Mismatches 0;

Qy 1 ATGCGCTGCTCAATAGATTGTTTCCCTGGCTTCTCGTCTTACTTACTGGGTCACT 60
Db 376 ATGCGCTGCTCAATAGATTGTTTCCCTGGCTTCTCGTCTTACTTACTGGGTCACT 435
Qy 61 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGGAGACGAGGCGCTGAGGGCAACCC 120
Db 436 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGGAGACGAGGCGCTGAGGGCAACCC 495
Qy 121 ATGAAGCTGGCTGCATCTCTCGATGAGAGAGGAGTGGAGCCACCGGTGCTG 180
Db 496 ATGAAGCTGGCTGCATCTCTCGATGAGAGAGGAGTGGAGCCACCGGTGCTG 555
Qy 181 GAATGTTCTTACAGGCCCGGAGGCGGTGAAGATTTCTTTATTTACGAGTATCGGAATGCG 240
Db 556 GAATGTTCTTACAGGCCCGGAGGCGGTGAAGATTTCTTTATTTACGAGTATCGGAATGCG 615
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Qy 241 CACCAGGAGTGGAGAGCCCTTTTCAGGGCGCTGCTCACTGGATGGCAGCAGGACCTG 300
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Qy 301 CAGGAGTGTCCATCATCTGTGCTCAACGTCACCTGGAACGACTCTGGCCCTCTACACCTGC 360
Db 676 CAGGAGTGTCCATCATCTGTGCTCAACGTCACCTGGAACGACTCTGGCCCTCTACACCTGC 735
Qy 361 AATGTGTCCTGGGAGTTTGAAGTTTGAAGGCGCATCGGCCCTTTTGTGAAGACGACGGGCTG 420
Db 736 AATGTGTCCTGGGAGTTTGAAGTTTGAAGGCGCATCGGCCCTTTTGTGAAGACGACGGGCTG 795
Qy 421 ATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGGACTTCACCTCTGTGCTCTCAGAAATC 480
Db 796 ATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGGACTTCACCTCTGTGCTCTCAGAAATC 855
Qy 481 ATGATGTACATCCTTCTGCTCTTCTCACCCTGTGGCTGCTCATCGAGATGATATATTCG 540
Db 856 ATGATGTACATCCTTCTGCTCTTCTCACCCTGTGGCTGCTCATCGAGATGATATATTCG 915
Qy 541 TACAGAAAGGTCTCAAAAGCCGAGAGGAGGCCCAAGAAACGCGTCTGACTTACCTTGCC 600
Db 916 TACAGAAAGGTCTCAAAAGCCGAGAGGAGGCCCAAGAAACGCGTCTGACTTACCTTGCC 975
Qy 601 ATCCCATCTGAGAACAGGAGAACTCTGCGGTACCACTGCGAGGAATAG 648
Db 976 ATCCCATCTGAGAACAGGAGAACTCTGCGGTACCACTGCGAGGAATAG 1023

RESULT 3
HSA243396
LOCUS HSA243396 1261 bp mRNA linear PRI 13-MAR-2000
DEFINITION Homo sapiens mRNA for voltage-gated sodium channel beta-3 subunit
(scn3b gene).
ACCESSION AJ243396
VERSION AJ243396.2 GI:7242612
KEYWORDS scn3b gene; voltage-gated sodium channel beta-3 subunit.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Morgan, K., Stevens, E.B., Shaw, B., Cox, P., Dixon, A.K., Lee, K.,
Pinnock, R.D., Hynes, J., Richardson, P.J., Mizuguchi, K. and
Jackson, A.P.
JOURNAL beta 3: an additional auxiliary subunit of the voltage-sensitive
sodium channel that modulates channel gating with distinct kinetics
Proc. Natl. Acad. Sci. U.S.A. 97 (5), 2308-2313 (2000)
MEDLINE 20160948
PUBMED 10688874
AUTHORS Morgan, K.
JOURNAL Direct Submission
TITLE Submitted (28-JUN-1999) Morgan K., Biochemistry, University of
Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
REMARK Revised by [4]
REFERENCE 3 (bases 1 to 1261)
AUTHORS Morgan, K.
JOURNAL Direct Submission
TITLE Submitted (13-MAR-2000) Morgan K., Biochemistry, University of
Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
COMMENT On Mar 14, 2000 this sequence version replaced gi:7160974.
FEATURES
Location/Qualifiers
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<1..375
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REFERENCE 1
 AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
 TITLE Kits, such as nucleic acid arrays, comprising a majority of human exons or transcripts, for detecting expression and other uses thereof
 JOURNAL Patent: WO 02068579-A 14675 06-SEP-2002;
 PE Corporation (NY) (US)
 FEATURES Location/Qualifiers
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 Query Match 91.4%; Score 592.4; DB 6; Length 606;
 Best Local Similarity 99.8%; Pred. No. 2.9e-129;
 Matches 593; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 55 GTGAGTGTCTGCTCCCTGCTGTGTGTAAGTGCCTCGGAGACGAGGCGGTGCAGGCG 114
 DB 13 GTGAGTGTCTGCTCCCTGCTGTGTGTAAGTGCCTCGGAGACGAGGCGGTGCAGGCG 72
 QY 115 AACCCCATGAAGTGCCTGCTGCTGCTGATGAAGAGAGAGAGGAGGAGGCGGACCAAG 174
 DB 73 AACCCCATGAAGTGCCTGCTGCTGCTGATGAAGAGAGAGAGGAGGAGGCGGACCAAG 132
 QY 175 GTGAGTGTCTGCTCCCTGCTGTGTGTAAGTGCCTCGGAGACGAGGCGGTGCAGGCG 234
 DB 133 GTGAGTGTCTGCTCCCTGCTGTGTGTAAGTGCCTCGGAGACGAGGCGGTGCAGGCG 192
 QY 235 AATGGCCACAGAGGAGGAGGCGGCTTTTCAGGGCGGCTGAGTGCAGTGCAGTGCAGGAG 294
 DB 193 AATGGCCACAGAGGAGGAGGCGGCTTTTCAGGGCGGCTGAGTGCAGTGCAGTGCAGGAG 252
 QY 295 GACCTGACGAGGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 354
 DB 253 GACCTGACGAGGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 312
 QY 355 ACCTGCAATGTCTCCGGAGTTGAGTTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGG 414
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 QY 415 CGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGAGGAGGAGTTCACCTCTGTTGGTCTCA 474
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 QY 475 GAAATCATGATGATACCTCTTCTGCTTCTCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 534
 DB 433 GAAATCATGATGATACCTCTTCTGCTTCTCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 492
 QY 535 TATTGCTACGAAAGTGTCAAAAGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 594
 DB 493 TATTGCTACGAAAGTGTCAAAAGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 552
 QY 595 CTGCGCATCCATCTGAGAACAGGAGGAGTCTGCGGTACAGTGGAGGAGGAGGAGGAGGAGGAGGAG 648
 DB 553 CTGCGCATCCATCTGAGAACAGGAGGAGTCTGCGGTACAGTGGAGGAGGAGGAGGAGGAGGAGGAG 606

RESULT 7
 LOCUS AY049036 570 bp mRNA linear ROD 01-OCT-2001
 DEFINITION Mus musculus brain and heart sodium channel beta 3 subunit mRNA, complete cds.
 ACCESSION AY049036
 VERSION AY049036.1 GI:15822811
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 670)

AUTHORS Chen, C., Avery, C., Kazen-Gillespie, K. and Isom, L.L.
 TITLE Mouse brain and heart beta 3 sodium channel cDNA
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 670)
 AUTHORS Chen, C., Avery, C., Kazen-Gillespie, K. and Isom, L.L.
 TITLE Direct Submission
 JOURNAL Submitted (30-JUL-2001) Pharmacology, University of Michigan, 1301 MSRB III, Box 0632, Ann Arbor, MI 48109-0632, USA
 FEATURES Location/Qualifiers
 source 1..670
 /organism="Mus musculus"
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 /db_xref="GI:15822812"

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 Query Match 82.9%; Score 537.2; DB 10; Length 670;
 Best Local Similarity 89.3%; Pred. No. 3.1e-116;
 Matches 578; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 ATGCTGCTCCCTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTCTTATCTACTGGGTGAGT 60
 DB 18 ATGCTGCTCCCTCAACAGATTGTTTCCCTAGTCTTCTAGTGTCTCATCTACTGGGTGAGT 77
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 DB 138 ATGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 197
 QY 181 GAATGTTTACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
 DB 198 GAGTGGTTCACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 257
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 DB 258 CACGAGGAGTGCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 317
 QY 301 CAGGAGGAGTGCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
 DB 318 CAGGAGGAGTGCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 377
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LOCUS          Rattus norvegicus mRNA for voltage-gated sodium channel beta-3
DEFINITION     subunit.
ACCESSION      AJ243395
VERSION        AJ243395.2 GI:7242802
KEYWORDS       scn3b gene; voltage-gated sodium channel beta-3 subunit.
SOURCE         Rattus norvegicus (Norway rat)
ORGANISM       Rattus norvegicus
               Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
               Rattus.
REFERENCE      1
AUTHORS        Morgan, K., Stevens, E.B., Shaw, B., Cox, P., Dixon, A.K., Lee, K.,
               Pincock, R.D., Hughes, J., Richardson, P.J., Mizuguchi, K. and
               Jackson, A.P.
TITLE          beta 3: an additional auxiliary subunit of the voltage-sensitive
JOURNAL        Proc. Natl. Acad. Sci. U.S.A. 97 (5), 2308-2313 (2000)
MEDLINE        20160948
PUBMED         10688874
REFERENCE      2
AUTHORS        Morgan, K.
TITLE          Direct Submission
JOURNAL        Submitted (28-JUN-1999) Morgan K., Biochemistry, University of
               Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
REMARK         Revised by [3]
REFERENCE      3 (bases 1 to 2220)
AUTHORS        Morgan, K.
TITLE          Direct Submission
JOURNAL        Submitted (09-MAR-2000) Morgan K., Biochemistry, University of
               Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
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ACCESSION      AX048005
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               Rattus.
REFERENCE      1
AUTHORS        Curtis, R.A.
TITLE          Gene encoding a sodium channel beta-3 subunit protein
JOURNAL        Patent: WO 0069912-A 22 23-NOV-2000;
               Millennium Pharmaceuticals, Inc. (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Rattus.

1 Curtis, R.A.
Gene encoding a sodium channel beta-3 subunit protein
Patent: WO 0069912-A 1 23-NOV-2000;
Millennium Pharmaceuticals, Inc. (US)
JOURNAL
TITLE
PREDICTION OF THE CODING SEQUENCES OF MOUSE HOMOLOGUES OF KIAA
Gene: IV. The Complete Nucleotide Sequences of 500 Mouse
KIAA-Homologous cDNAs Identified by Screening of Terminal Sequences
of cDNA Clones Randomly Sampled from Size-Fractionated Libraries
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (19-MAY-2004) Hisashi Koga, Kazusa DNA Research
Institute, Laboratory for Genome Informatics; 2-6-7
Kazusa-kamata, Kisarazu, Chiba 292-0818, Japan
[E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918]
The CREATE program supported by Japan science and technology
corporation; cDNA full insert sequencing; Kazusa DNA Research
Institute; cDNA library construction, clone selection and 5'- &
3'-end one pass sequencing.
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QY 1 ATGCTGCTTCAATAGATTGTTCCCTGGCTTCTCTGCTTATCTACTGGTCAGT 60
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DEFINITION Mus musculus mRNA for mKIAA1158 protein.
ACCESSION AKI73115
VERSION AKI73115.1 GI:50510814
KEYWORDS FLI_CDNA.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Rattus.

1 Okazaki, N., Kikuno, R.F., Ohara, R., Inamoto, S., Koseki, H., Hiraoka, S., Suga, Y., Seino, S., Nishimura, M., Kaisho, T., Hoshino, K., Kitamura, H., Nagase, T., Ohara, O. and Koga, H.
Prediction of the Coding Sequences of Mouse Homologues of KIAA
Gene: IV. The Complete Nucleotide Sequences of 500 Mouse
KIAA-Homologous cDNAs Identified by Screening of Terminal Sequences
of cDNA Clones Randomly Sampled from Size-Fractionated Libraries
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (19-MAY-2004) Hisashi Koga, Kazusa DNA Research
Institute, Laboratory for Genome Informatics; 2-6-7
Kazusa-kamata, Kisarazu, Chiba 292-0818, Japan
[E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918]
The CREATE program supported by Japan science and technology
corporation; cDNA full insert sequencing; Kazusa DNA Research
Institute; cDNA library construction, clone selection and 5'- &
3'-end one pass sequencing.
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Best Local Similarity 89.3%; Pred. No. 4.1e-116;
Matches 578; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 1 ATGCTGCTTCAATAGATTGTTCCCTGGCTTCTCTGCTTATCTACTGGTCAGT 60
DB 290 ATGCTGCTTCAACAGATTGTTCCCTAGTCTCTAGTCTCATCTACTGGTCAGT 349
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QY 301 CAGGAGGTGTCATCATCTGCTGCTCAACGCTCTCTGAAACGACTCTGCGCTCTACCTG 360

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 06:13:29 ; Search time 470.712 Seconds
(without alignments)
8149.338 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	646.4	99.8	1510	4 AAF84146	Aaf84146 Human nov
5	646.4	99.8	4052	6 ABA93727	Aba93727 Human sig
6	585	90.3	1045	4 AAK52345	Aak52345 Human pol
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8	570.2	88.0	978	13 ADS11487	Adsl1487 Human the
9	536.6	82.8	2220	3 AAC67836	Aac67836 Rat beta3
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33	72.6	11.2	855	10 ADG15041	Adg15041 Human SEC
34	49	7.6	243	12 ACH83019	Ach83019 Human gen
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39	47	7.3	509	4 AA193385	Aa193385 Human pol
40	45.4	7.0	1645	3 AAA88851	Aaa88851 Maize ger
41	45.4	7.0	1645	12 ADI36508	Adi36508 Corn gera
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ALIGNMENTS

RESULT 1

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ID AAC67837 standard; CDNA; 1261 BP.

XX AAC67837;

DT 15-FEB-2001 (first entry)

XX Human beta3 CDNA.

DE Human; beta sub-unit; beta3; analgesic; anticonvulsant;

KW cerebroprotective; vasotropic; cardiact; nootropic; cytostatic;
KW dermatological; gene therapy; voltage-gated sodium channel; pain;
KW epilepsy; stroke; ischaemia; heart disease; Jacobsen Syndrome;
KW familial nonchromaffin paraganglioma; phenylketonuria;
KW Charcot Marie Tooth disease; ss.
XX Homo sapiens.
OS WO200063367-A1.
PN 26-OCT-2000.
XX 24-FEB-2000; 2000WO-EP001783.
XX 15-APR-1999; 99US-0129473P.
XX (WARN) WARNER LAMBERT CO.
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX Cox P, Dixon A, Jackson A, Morgan K;
XX WPI; 2000-665241/64.
XX P-PSDB; AAB36002.
XX Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium
XX channel, and their corresponding polypeptides, useful for detecting and
XX treating sodium channel-associated conditions, e.g. pain, epilepsy and
XX stroke.
XX Claim 10; Page 70-71; 88pp; English.
XX The present sequence is given in the claims of a specification relating

CC to a novel family of beta sub-unit proteins from a voltage-gated sodium
CC channel. Human and rat beta sub-units, which have been collectively
CC identified as beta3, have been isolated. The polynucleotides and
CC polypeptides are useful for screening for agonists and antagonists of
CC sodium channels. The agonists, antagonists, proteins and nucleic acids
CC may be used diagnosing of treating diseases or conditions associated with
CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,
CC heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma,
CC Phenylketonuria and Charcot Marie Tooth disease
XX
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Best Local Similarity 100.0%; Pred. No. 3.9e-165;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 796 ATCCCTTAAAGTACCGAGAGGCTGAGAGGATTCACCTCTGTGTCTCAGAAATC 855
Db |||||||
QY 481 ATGATGTACATCTTCTGTGTCTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db |||||||
QY 856 ATGATGTACATCTTCTGTGTCTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 915
Db |||||||
QY 541 TACAGAAAGGTCTCAAAAGCCGAGGAGGCGCCCAAGAAACCGCTCTGACTTACCTTGGC 600
Db |||||||
QY 916 TACAGAAAGGTCTCAAAAGCCGAGGAGGCGCCCAAGAAACCGCTCTGACTTACCTTGGC 975
Db |||||||
QY 601 ATCCATCTGAGAACCAAGGAGAACTCTGCGGTACCAAGTGGAGAAATAG 648
Db |||||||
QY 976 ATCCATCTGAGAACCAAGGAGAACTCTGCGGTACCAAGTGGAGAAATAG 1023
Db |||||||

RESULT 2
ACF57870
ID ACF57870 standard; cDNA; 1261 BP.
XX
AC ACF57870;
XX
AC ACF57870;
DT 15-JAN-2004 (first entry)
XX
DE Human SCN3B protein encoding cDNA.
XX
DE SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
KW neuroprotective; anesthetic; cyostatic; cerebroprotective; cardiant;
KW

hypotensive; gene therapy; SCN3B; human; gene; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 376..1023
FT /*tag= a
FT /*product= "SCN3B"
XX
PN WO2003072751-A2.
XX
PD 04-SEP-2003.
XX
PF 25-FEB-2003; 2003WO-US006010.
XX
PR 25-FEB-2002; 2002US-0359382P.
XX
XX (UYVA-) UNIV VANDERBILT.
XX
PI George AL, Lessin C;
XX
DR WPI; 2003-712725/67.
DR P-PSDB; ABR83183.
XX
PT Recombinantly expressed sodium channel type 1 alpha subunit, useful in
screening for modulators, for treating e.g. epilepsy.
XX
PS Disclosure; Page 145-147; 176pp; English.
XX
CC The invention relates to a recombinantly expressed and isolated human
SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
CC incorporated into a cell, is used to screen for specific modulators,
CC potentially useful as anticonvulsant, antiepileptic, neuroprotective,
CC analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
CC epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
CC motor endplate diseases, hypertension, congestive heart failure and
CC muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
CC and metastatic cancer cell lines). These activities can also be provided
CC by gene therapy vectors that express (I) or the modulators. The
CC modulators, also antibodies directed against (I), are used to detect
CC sodium channel polypeptides. The present sequence represents a human
CC SCN3B protein encoding cDNA
XX
SQ Sequence 1261 BP; 263 A; 366 C; 372 G; 260 T; 0 U; 0 Other;

Query Match 100.0%; Score 648; DB 10; Length 1261;
Best Local Similarity 100.0%; Pred. No. 3.9e-165;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTGCTTATCTACTGGGTCAGT 60
Db |||||||
QY 376 ATGCCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTGCTTATCTACTGGGTCAGT 435
Db |||||||
QY 61 GTCTGCTTCCCTGTGTGTGGAGTGCCTTCGAGACGAGGCGCTGAGGSCAACCC 120
Db |||||||
QY 436 GTCTGCTTCCCTGTGTGTGGAGTGCCTTCGAGACGAGGCGCTGAGGSCAACCC 495
Db |||||||
QY 121 ATGAAGCTGGCTGCATCTCTCTCATAGAGAGAGAGGTGGAGCCACCGTGGTG 180
Db |||||||
QY 496 ATGAAGCTGGCTGCATCTCTCTCATAGAGAGAGAGGTGGAGCCACCGTGGTG 555
Db |||||||
QY 181 GAATGCTTCTACAGGCGGAGGCGGTAAAGATTCTCTTATTTACAGTATCGAATGGC 240
Db |||||||
QY 556 GAATGCTTCTACAGGCGGAGGCGGTAAAGATTCTCTTATTTACAGTATCGAATGGC 615
Db |||||||
QY 241 CACGAGAGGTGAGAGCCCTTTCAGGGCGCTTCAGTGGAAATGGCAGGACCTG 300
Db |||||||
QY 616 CACGAGAGGTGAGAGCCCTTTCAGGGCGCTTCAGTGGAAATGGCAGGACCTG 675
Db |||||||
QY 301 CAGGAGGTGCATCACTGTCTCAAGTCACTCTGAAGTCTGCTGCTTACACCTGC 360
Db |||||||
QY 676 CAGGAGGTGCATCACTGTCTCAAGTCACTCTGAAGTCTGCTGCTTACACCTGC 735
Db |||||||

QY 361 AATGTGTCCCGGAGTTTGAGTTTGAGCGGCATCGGCCCTTTGTGAAGACGACGCGCTG 420
 Db |||||
 736 AATGTGTCCCGGAGTTTGAGTTTGAGCGGCATCGGCCCTTTGTGAAGACGACGCGCTG 795
 QY 421 ATCCCCCTAGAGTACCGGAGGCTGGAGAGCTTCACTCTGTGGTCTGAGAAATC 480
 Db |||||
 796 ATCCCCCTAGAGTACCGGAGGCTGGAGAGCTTCACTCTGTGGTCTGAGAAATC 855
 QY 481 ATGATGTACATCTCTCTGCTCTCTCACTCACTGCTGGCTGCTCATCGAGATGATATATTC 540
 Db |||||
 856 ATGATGTACATCTCTCTGCTCTCTCACTCACTGCTGGCTGCTCATCGAGATGATATATTC 915
 QY 541 TACAGAAAGGTCTCAAAAGCCGAGAGGCGCCCAAGAAACCGCTGTGACTACCTTTGCC 600
 Db |||||
 916 TACAGAAAGGTCTCAAAAGCCGAGAGGCGCCCAAGAAACCGCTGTGACTACCTTTGCC 975
 QY 601 ATCCCATCTGAGACAGGAGAACTCTGCGGTACCACTGAGGAGATAG 648
 Db |||||
 976 ATCCCATCTGAGACAGGAGAACTCTGCGGTACCACTGAGGAGATAG 1023

RESULT 3

ADB78651

ID ADB78651 standard; cDNA; 1261 BP.

XX

AC ADB78651;

XX

DT 04-DEC-2003 (first entry)

XX

DE Human ion channel subunit cDNA mutant SCNIAR exon 1 SEQ ID NO:22.

XX

KW ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;
 KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
 KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
 KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
 KW ion channel dysfunction; human.

XX

OS Synthetic.

OS

OS Homo sapiens.

XX

PN WO2003008574-A1.

XX

PD 30-JAN-2003.

XX

XX 08-JUL-2002; 2002WO-AU000910.

XX

XX 18-JUL-2001; 2001AU-00006452.

PR

PR 05-MAR-2002; 2002AU-00000910.

PR

PR 13-MAY-2002; 2002AU-00002292.

XX

XX (BION-) BIONOMICS LTD.

PA

PA (WALL) WALLACE R W.

XX

XX Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;

PI

PI Berkovic SF, Scheffer IE;

XX

XX WPI; 2003-239332/23.

DR

XX Identifying predisposition to an ion channel dysfunction, such as

PT

PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
 PT schizophrenia, anxiety and depression, by detecting encoding-gene
 PT mutation events.

PT

XX Claim 6; SEQ ID NO 22; 106pp; English.
 PS The invention relates to a novel method for identifying a subject
 CC predisposed to a disorder associated with ion channel dysfunction. The
 CC method comprises ascertaining if at least one of the genes encoding ion
 CC channel subunits (ICS) has undergone a mutation event so that a cDNA
 CC derived from the subject has any of 134 nucleotide sequences. The method
 CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
 CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
 CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and

RESULT 4

AAF84146

ID AAF84146 standard; cDNA; 1510 BP.

XX

CC ophthalmological activity. A polynucleotide of the invention acts as an
 CC ion channel agonist, or ion channel antagonist. The methods, isolated
 CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
 CC modulator of an ion channel, cells and genetically modified non-human
 CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
 CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
 CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
 CC myasthenia, cardiac arrhythmias, myotonias, malignant hyperthermia,
 CC disease, Parkinson's disease, schizophrenia, episodic ataxia, migraine, Alzheimer's
 CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
 CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
 CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
 CC fibrosis, congenital stationary night blindness and total colour
 CC blindness. The present sequence represents a mutant cDNA of the
 CC invention. The sequence data for this patent is not represented in the
 CC printed specification, but was obtained in electronic format directly
 CC from wipo at ftp.wipo.int/pub/published_pat_sequences.

XX

SQ Sequence 1261 BP; 263 A; 365 C; 372 G; 261 T; 0 U; 0 Other;

Query Match 99.8%; Score 646.4; DB 10; Length 1261;

Best Local Similarity 99.8%; Pred. No. 1.1e-164;

Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTATCTACTGGGTGAGT 60

Db |||||

376 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTATCTACTGGGTGAGT 435

QY 61 GTCTGCTTCCCTGTGTGTGGAAAGTCCCTCGAGACGGAGCGGTGCGAGGCAACCCC 120

Db |||||

436 GTCTGCTTCCCTGTGTGTGGAAAGTCCCTCGAGACGGAGCGGTGCGAGGCAACCCC 495

QY 121 ATCAAGCTGCGTGCATCTCTCATGAGAGAGAGAGGTGAGGCGCCACACGGTGGTG 180

Db |||||

496 ATGAAGCTGCGTGCATCTCTCATGAGAGAGAGAGGTGAGGCGCCACACGGTGGTG 555

QY 181 GAATGTTTCTACAGGCGCGGCGGTAAAGATTTCTTATTTACGAGTATCGGAATGGC 240

Db |||||

556 GAATGTTTCTACAGGCGCGGCGGTAAAGATTTCTTATTTACGAGTATCGGAATGGC 615

QY 241 CACGAGAGGTGGAGAGCCCTTTTCAAGGCGCGCTGCGAGTGGAAATGCGCAGGACCTG 300

Db |||||

616 CACGAGAGGTGGAGAGCCCTTTTCAAGGCGCGCTGCGAGTGGAAATGCGCAGGACCTG 675

QY 301 CAGGAGGTGTCATCACTGTCTCAACGCTCTGAACGACCTCTGSCCTCTACACCTGC 360

Db |||||

676 CAGGAGGTGTCATCACTGTCTCAACGCTCTGAACGACCTCTGSCCTCTACACCTGC 735

QY 361 AATGTTTCCCGGAGTTTGAAGTTTGAAGCGCATCGGCCCTTTTGTGAAGACGACGCGCTG 420

Db |||||

736 AATGTTTCCCGGAGTTTGAAGTTTGAAGCGCATCGGCCCTTTTGTGAAGACGACGCGCTG 795

QY 421 ATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGGACTTCACTCTGTGGTCTCAGAAATC 480

Db |||||

796 ATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGGACTTCACTCTGTGGTCTCAGAAATC 855

QY 481 ATGATGTACATCTCTCTGCTTCTTCTCACCTGCTGCTCATCGAGATGATATATTC 540

Db |||||

856 ATGATGTACATCTCTCTGCTTCTTCTCACCTGCTGCTCATCGAGATGATATATTC 915

QY 541 TACAGAAAGGTCTCAAAAGCCGAGAGGCGCCCAAGAAACCGCTGTGACTACCTTTGCC 600

Db |||||

916 TACAGAAAGGTCTCAAAAGCCGAGAGGCGCCCAAGAAACCGCTGTGACTACCTTTGCC 975

QY 601 ATCCCATCTGAGACAGGAGAACTCTGCGGTACCACTGAGGAGATAG 648

Db |||||

976 ATCCCATCTGAGACAGGAGAACTCTGCGGTACCACTGAGGAGATAG 1023

AC AAF84146;
XX 07-SEP-2001 (first entry)
DT Human novel sodium channel betal-like subunit encoding cDNA.
DE Sodium channel; sensory neurone specific channel; betal-like subunit;
KW SNS; therapeutic; pain; analgesic; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 213..860
FT /*tag= a
FT /product= "sodium channel betal-like subunit"
XX WO200144293-A2.
XX 21-JUN-2001.
XX 14-DEC-2000; 2000WO-GB004802.
XX 17-DEC-1999; 99GB-00029970.
XX (GLAX) GLAXO GROUP LTD.
XX Plumpton M, Powell AJ, Sanseau P;
XX WPI; 2001-398129/42.
XX P-PSDB; AAB85206.
XX Novel sub-unit for voltage-gated sodium channel proteins for producing
PT agents useful for treating pain.
XX Claim 4; Page 29-30; 31pp; English.
XX The invention provides a novel betal-like sub-unit for voltage-gated
CC sodium ion channel polypeptide, specifically a sensory neurone specific
CC channel (SNS) subunit. The novel betal-like subunit is useful for
CC producing a therapeutic agent which is useful treating pain in a patient.
CC The subunit can be expressed by standard recombinant methodology. The
CC present sequence represents a human novel sodium channel betal-like
CC subunit encoding cDNA
XX Sequence 1510 BP; 350 A; 410 C; 414 G; 336 T; 0 U; 0 Other;
SQ
Query Match 99.8%; Score 646.4; DB 4; Length 1510;
Best Local Similarity 99.8%; Pred. No. 1.1e-164;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGCCTGCCTTCAATAGATTGTTCCCTGGCTTCTCTCGTGTATCTACTGGGTCAGT 60
DB |||||||
DB 213 ATGCCTGCCTTCAATAGATTGTTCCCTGGCTTCTCTCGTGTATCTACTGGGTCAGT 272
QY 61 GTCGTCTTCCCTGTGTGGAAGTCCCTCGGACGAGCGCGTGCAGGSCAACCC 120
DB |||||||
DB 273 GTCGTCTTCCCTGTGTGGAAGTCCCTCGGACGAGCGCGTGCAGGSCAACCC 332
QY 121 ATGAAGCTGCGTGCATCTCTGTCATGAAGAGAGAGAGGTGGAGCCACCGGTGGTG 180
DB |||||||
DB 333 ATGAAGCTGCGTGCATCTCTGTCATGAAGAGAGAGAGGTGGAGCCACCGGTGGTG 392
QY 181 GAATGTTCTACAGCCCGGCGGTAAAGATTCTTATTACGAGTATGGAAATGCG 240
DB |||||||
DB 393 GAATGTTCTACAGCCCGGCGGTAAAGATTCTTATTACGAGTATGGAAATGCG 452
QY 241 CACGAGAGGTGAGAGCCCTTTACAGGCGCGCTCAGTGAATGCGAGCAAGGACCTG 300
DB |||||||
DB 453 CACGAGAGGTGAGAGCCCTTTACAGGCGCGCTCAGTGAATGCGAGCAAGGACCTG 512
QY 301 CAGGAGGTGTCATCACTGTGCTCAACGTCACCTCTGAACGACTCTGGCCTCTACACCTGC 360
DB |||||||
DB 513 CAGGAGGTGTCATCACTGTGCTCAACGTCACCTCTGAACGACTCTGGCCTCTACACCTGC 572

QY 361 AATGTGTCCGGAGTTTGAAGTTCGAGCGCATCGCCCTTTGTGAGAGACGCGGCTG 420
DB |||||||
DB 573 AATGTGTCCGGAGTTTGAAGTTCGAGCGCATCGCCCTTTGTGAGAGACGCGGCTG 632
QY 421 ATCCCCCTTAAGAGTCAACGAGGAGCTGGAGAGGACTTCACCTCTGTGTCTCAGAAATC 480
DB |||||||
DB 633 ATCCCCCTTAAGAGTCAACGAGGAGCTGGAGAGGACTTCACCTCTGTGTCTCAGAAATC 692
QY 481 ATGATGTACATCCTTCTGTGTCTTCTCACCCTGTGTGTCTCATCGAGATGATATTCG 540
DB |||||||
DB 693 ATGATGTACATCCTTCTGTGTCTTCTCACCCTGTGTGTCTCATCGAGATGATATTCG 752
QY 541 TACAGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACCGCTCTGACTACCTTGCC 600
DB |||||||
DB 753 TACAGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACCGCTCTGACTACCTTGCC 812
QY 601 ATCCCATCTGAGAACAAAGGAGAACTCTCGGTACCACTGGAGGAATAG 648
DB |||||||
DB 813 ATCCCATCTGAGAACAAAGGAGAACTCTCGGTACCACTGGAGGAATAG 860

RESULT 5

ABA93727

ID ABA93727 standard; cDNA; 4052 BP.

XX ABA93727;

AC ABA93727;

XX 30-APR-2002 (first entry)

XX Human signal transduction cDNA clone amy2_2f18.

DE Human; foetal brain; foetal kidney; melanoma; testis; amygdala;

XX gene therapy; ss.

XX Homo sapiens.

XX WO200198454-A2.

XX 27-DEC-2001.

XX 25-APR-2001; 2001WO-IB002050.

XX 25-APR-2000; 2000US-0199380P.

XX (GEHU-) GERMAN HUMAN GENOME PROJECT.

XX Wiemann S;

XX WPI; 2002-055860/07.

XX P-PSDB; ABB05689.

XX Human cDNA sequences and clones derived from human foetal brain, foetal

XX kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic

XX screening and therapy.

XX Claim 1; Page 174-175; 61pp; English.

XX The present invention describes assemblages and computer readable media

XX comprising novel human cDNA sequences and clones derived from human

XX foetal brain, foetal kidney, melanoma, testis and amygdala cDNA

XX libraries. ABA93702 to ABA93766 represent human cDNA sequences from the

XX present invention which encode the proteins given in ABB05662 to

XX ABB05729. The human cDNA sequences and clones can be used in gene

XX therapy. The clones may be used in a variety of applications, for example

XX they may be used in profiling assays, for providing large arrays of human

XX genetic material for implementing large-scale screening strategies and

XX for treating diseases via gene therapy procedures

XX Sequence 4052 BP; 994 A; 1033 C; 1036 G; 989 T; 0 U; 0 Other;

SQ Query Match 99.8%; Score 646.4; DB 6; Length 4052;

Best Local Similarity 99.8%; Pred. No. 1.6e-164;

Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTGCTCAATAGATGTTTCCCTGCTCTCTCGTGTCTATCTAGTGGTCACT 60
 DB 804 ATGCTGCTCAATAGATGTTTCCCTGCTCTCTCGTGTCTATCTAGTGGTCACT 863
 QY 61 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGGAGACGAGCGCGTGCAGGGCAACCCC 120
 DB 864 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGGAGACGAGCGCGTGCAGGGCAACCCC 923
 QY 121 ATGAAGCTGCTGCTCACTCTCTGATGAAGAGAGAGAGTGGAGGCCACACCGTGGTG 180
 DB 924 ATGAAGCTGCTGCTCACTCTCTGATGAAGAGAGAGAGTGGAGGCCACACCGTGGTG 983
 QY 181 GAATGGTTCTACAGCCCGAGGGCGGTAAAGATTTCTTATTTACAGATATCGGAATGGC 240
 DB 984 GAATGGTTCTACAGCCCGAGGGCGGTAAAGATTTCTTATTTACAGATATCGGAATGGC 1043
 QY 241 CACGAGAGGTGGAGAGCCCTTTTCAGGGGCGCTCGAGTGGATGGCAGCAAGCACTG 300
 DB 1044 CACGAGAGGTGGAGAGCCCTTTTCAGGGGCGCTCGAGTGGATGGCAGCAAGCACTG 1103
 QY 301 CAGAGCTGCTCACTCACTGCTCAAGTCACTCTGAAGAGCTCTGGCCTCTACACCTGC 360
 DB 1104 CAGAGCTGCTCACTCACTGCTCAAGTCACTCTGAAGAGCTCTGGCCTCTACACCTGC 1163
 QY 361 AATGTGTCCCGGAGTTTGTAGTTTGGAGCGCATCGGCCCTTTGTGAAGACGACGCGCTG 420
 DB 1164 AATGTGTCCCGGAGTTTGTAGTTTGGAGCGCATCGGCCCTTTGTGAAGACGACGCGCTG 1223
 QY 421 ATCCCCCTAAGAGTCAACGAGGAGGCTGGAGAGCTTCACTCTGTGGTCTCAGAATC 480
 DB 1224 ATCCCCCTAAGAGTCAACGAGGAGGCTGGAGAGCTTCACTCTGTGGTCTCAGAATC 1283
 QY 481 ATGATGTACATCTTCTGTGTTCTCCTCACTGTGGTCTGCTCATCGAGATGATATATGC 540
 DB 1284 ATGATGTACATCTTCTGTGTTCTCCTCACTGTGGTCTGCTCATCGAGATGATATATGC 1343
 QY 541 TACAGAAAGGTCTCAAAAGCCGAGAGGAGCGCCCAAGAAACGCTCTGACTACCTTTGCC 600
 DB 1344 TACAGAAAGGTCTCAAAAGCCGAGAGGAGCGCCCAAGAAACGCTCTGACTACCTTTGCC 1403
 QY 601 ATCCCATCTGAGAACAGGAGAACTCTGCGGTACCACTGGAGGAATAG 648
 DB 1404 ATCCCATCTGAGAACAGGAGAACTCTGCGGTACCACTGGAGGAATAG 1451

RESULT 6
 AAK52345
 ID AAK52345 standard; cDNA; 1045 BP.
 AC AAK52345;
 XX
 XX
 DE 06-NOV-2001 (first entry)
 XX
 XX Human polynucleotide SEQ ID NO 890.
 XX
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation; ss.
 XX
 XX Homo sapiens.
 XX
 PN W0200157190-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 05-FEB-2001; 2001WO-US004098.
 XX
 XX 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00724822.
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y,
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI; 2001-476283/51.
 DR P-PSDB; AAM79212.
 XX
 XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 PT
 XX Claim 1; Page 2934-2935; 6221pp; English.
 XX
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 SQ Sequence 1045 BP; 222 A; 289 C; 314 G; 220 T; 0 U; 0 Other;
 Query Match 90.3%; Score 585; DB 4; Length 1045;
 Best Local Similarity 99.2%; Pred. No. 4.2e-148;
 Matches 588; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGCTGCTTCAATAGATGTTTCCCTGCTCTCTCGTGTCTATCTAGTGGTCACT 60
 DB 302 ATGCTGCTTCAATAGATGTTTCCCTGCTCTCTCGTGTCTATCTAGTGGTCACT 361
 QY 61 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGGAGACGAGCGCGTGCAGGGCAACCCC 120
 DB 362 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGGAGACGAGCGCGTGCAGGGCAACCCC 421
 QY 121 ATGAAGCTGCTGCTCATCTCTGATGAAGAGAGAGAGTGGAGGCCACACCGTGGTG 180
 DB 422 ATGAAGCTGCTGCTCATCTCTGATGAAGAGAGAGAGTGGAGGCCACACCGTGGTG 481
 QY 181 GAATGGTTCTACAGGCCCGAGCGGTAAAGATTTCTTATTTACAGATATCGGAATGGC 240
 DB 482 GAATGGTTCTACAGGCCCGAGCGGTAAAGATTTCTTATTTACAGATATCGGAATGGC 541
 QY 241 CACGAGAGGTGGAGAGCCCTTTTCAGGGGCGCTCGAGTGGATGGCAGCAAGCACTG 300
 DB 542 CACGAGAGGTGGAGAGCCCTTTTCAGGGGCGCTCGAGTGGATGGCAGCAAGCACTG 601
 QY 301 CAGGAGGTGCTCATCACTGTGCTCAACGTCACTCTGAAACGACTCTGCGCTCTACACCTGC 360
 DB 602 CAGGAGGTGCTCATCACTGTGCTCAACGTCACTCTGAAACGACTCTGCGCTCTACACCTGC 661
 QY 361 AATGTGTCCCGGAGTTTGTAGTTTGGAGCGCATCGGCCCTTTGTGAAGACGACGCGCTG 420
 DB 662 AATGTGTCCCGGAGTTTGTAGTTTGGAGCGCATCGGCCCTTTGTGAAGACGACGCGCTG 721
 QY 421 ATCCCCCTAAGAGTCAACGAGGAGGCTGGAGAGACTTCACTCTGTGGTCTCAGAATC 480
 DB 722 ATCCCCCTAAGAGTCAACGAGGAGGCTGGAGAGACTTCACTCTGTGGTCTCAGAATC 781
 QY 481 ATGATGTACATCTTCTGTGTTCTCCTCACTGTGGTCTGCTCATCGAGATGATATATGC 540

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Db      782 ATGATGTATACCTCTCTGGTCTTCCTCACTTGTGGCTGCTCATCGAGATGATATATGC 841
QY      541 TACAGAAAGGTCTCAAAAGCCGAAGAGGAGCCCAAGAAACCGCTCTGACTA 593
Db      842 TACAGAAAGGTCTCAAAAGCCGAAGAGGAGCCCAAGAAACCGCTAAGTCCA 894

RESULT 7
AAH98320
ID      AAH98320 standard; cDNA; 978 BP.
XX      AC      AAH98320;
XX      DT      12-OCT-2001 (first entry)
XX      DE      Human EST-derived coding sequence SEQ ID NO: 177.
XX      KW      Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW      tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW      diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW      gene therapy; nutrition; ss.
XX      OS      Homo sapiens.
XX      PN      WO200154477-A2.
XX      PD      02-AUG-2001.
XX      PF      25-JAN-2001; 2001WO-US0002687.
XX      PR      25-JAN-2000; 2000US-00491404.
PR      17-JUL-2000; 2000US-00617746.
PR      03-AUG-2000; 2000US-00631451.
PR      15-SEP-2000; 2000US-00663870.
XX      (HYSE-) HYSEQ INC.
XX      Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI      Cao Y, Drmanac RA, Zhang J, Werhman T;
XX      WPI: 2001-476164/51.
DR      P-PSDB; AAM23661.
XX      Isolated polypeptide for treatment of diseases, diagnostics, raising
PT      antibodies and research use.
XX      Claim 1; Page 299-300; 1275pp; English.
XX      The present invention provides the protein and coding sequences of novel
CC      proteins from a variety of organisms, including human, dog, cat, horse,
CC      cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC      urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC      from the organism of interest. They can be used in diagnostics,
CC      forensics, gene mapping, identification of mutations, to assess
CC      biodiversity and for nutritional purposes. The present sequence is a cDNA
CC      of the invention
XX      Sequence 978 BP; 193 A; 283 C; 293 G; 209 T; 0 U; 0 Other;

Query Match      88.0%; Score 570.2; DB 4; Length 978;
Best Local Similarity 94.8%; Pred. No. 4.2e-144;
Matches 612; Conservative 0; Mismatches 33; Indels 2; Gaps 2;

QY      1 ATGCCCTGCCTTCAATAGATTGTTCCCTGGCTTCTCTGCTGCTTACTACTGGGTCACT 60
Db      295 ATGCCCTGCCTTCAATAGATTGTTCCCTGGCTTCTCTGCTGCTTACTACTGGGTCACT 354

QY      61 GTCTGCTTCCCTGTGTGTGGAAAGTGCCTCGAGACGAGCCCTGAGGGCAACCCC 120
Db      355 GTCTGCTTCCCTGTGTGTGGAAAGTGCCTCGAGACGAGCCCTGAGGGCAACCCC 414

QY      121 ATGAAGCTGGCGTGCATCTCTCTCATGAAGAGAGAGGTGGAGGCCACCGTGGTG 180
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Db      415 ATGAAGCTGGCGTGCATCTCTCTCATGAAGAGAGAGGTGGAGGCCACCGTGGTG 474
QY      181 GAATGTTCTTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTATTACGAGTATCGGAATGC 240
Db      475 GAATGTTCTTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTATTACGAGTATCGGAATGC 534
QY      241 CACGAGGAGGTGGAGAGCCCTTTTACAGGGGCCCTGTCAGTGGAAATGGCAGAGGACCTG 300
Db      535 CACGAGGAGGTGGAGAGCCCTTTTACAGGGGCCCTGTCAGTGGAAATGGCAGAGGACCTG 594
QY      301 CAGGAGCTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTCTGGCCTCTACACCTGC 360
Db      595 CAGGAGCTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTCTGGCCTCTACACCTGC 654
QY      361 AATGTGTCCCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGGCGCTG 420
Db      655 AATGTGTCCCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGGCGCTG 714
QY      421 ATCCCTCTTAAGAGTCAACGAGGAGGTGGAGAGGACTTCACCTCTGTGTCTCAGAAATC 480
Db      715 ATCCCTCTTAAGAGTCAACGAGGAGGTGGAGAGGACTTCACCTCTGTGTCTCAGAAATC 774
QY      481 ATGATGTACATCTTCTGTCTTCTCACCCTGTGCTGCTCATCGAGATGATATATG- 539
Db      775 AIGATGTATACCTTCTGTGCTTCTCACCCTGTGCTGCTCATCGAGATGATATATG- 834
QY      540 CTACAGAAAGGTCTCAAAAGCCGAAGAGAGCAGCCCAAGAAACCGGTCTTGACTACC- 598
Db      835 CTACAGAACGGTGTATCAGACAGACGACCGGCCCCCAACAGAAACCGGATGGCTACCTTTG 894
QY      599 CCATCCCTCTCAGAACAGAGAGAACTCTGCGGTACCACTGAGAGGAA 645
Db      895 CGATTCCATTTGAGAACAGGGGAAATTTCTCGGTACCTCGCGGGGGA 941

RESULT 8
ADS11487
ID      ADS11487 standard; DNA; 978 BP.
XX      AC      ADS11487;
XX      DT      16-DEC-2004 (first entry)
XX      DE      Human therapeutic contig DNA - SEQ ID 1724.
XX      KW      antiinflammatory; neuroprotective; antianaemic; cytostatic; vulneryary;
KW      inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW      aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
XX      OS      Homo sapiens.
XX      WO2004080148-A2.
XX      23-SEP-2004.
XX      30-SEP-2003; 2003WO-US030720.
XX      02-OCT-2002; 2002US-0416186P.
XX      (NUVE-) NUVELO INC.
XX      Tang YT, Asundi V, Ren F, Zhang J, Werhman T, Wang Z, Ma Y;
PI      Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX      WPI: 2004-668857/65.
DR      P-PSDB; ADS12085.
XX      New polynucleotide, useful in preparing a composition for diagnosing or
PT      treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT      aplastic anemia or cancer for promoting wound healing.
XX      Example 2; SEQ ID NO 1724; 718pp; English.
PS
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XX The invention relates to a novel isolated polynucleotide and the encoded
 CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
 CC neuroprotective, antianaemic, cytoskeletal and vascular activities and may
 CC be useful in preparing a composition for diagnosing or treating
 CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
 CC disorders, such as aplastic anaemia or cancer, as well as for promoting
 CC wound healing. The molecules may also be utilised during gene therapy
 CC procedures. The current sequence is that of a human therapeutic contig
 CC DNA of the invention. The current sequence is not shown explicitly within
 CC the specification but can be accessed from the WIFO web-site.

XX SQ Sequence 978 BP; 193 A; 283 C; 293 G; 209 T; 0 U; 0 Other;

Query Match 88.0%; Score 570.2; DB 13; Length 978;
 Best Local Similarity 94.6%; Pred. No. 4.2e-144;
 Matches 612; Conservative 0; Mismatches 33; Indels 2; Gaps 2;

QY 1 ATGCTGCTTCAATAGATTGTTCCCTGGCTTCTCTCGTCTATCTACTGGTCACT 60
 DB ATGCTGCTTCAATAGATTGTTCCCTGGCTTCTCTCGTCTATCTACTGGTCACT 354
 QY 61 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGAGACGAGGCGGTGACGGCAACCCC 120
 DB GTCTGCTTCCCTGTGTGTGAAGTGCCTCGAGACGAGGCGGTGACGGCAACCCC 414
 QY 121 ATGAAGCTGCGCTCATCTCTGATGAAGACGAGGAGGTGGAGGCCACCACTGGTGTG 180
 DB ATGAAGCTGCGCTCATCTCTGATGAAGACGAGGAGGTGGAGGCCACCACTGGTGTG 474
 QY 181 GAATGGTGTCTACAGCCCGGAGGCGGTAAAGATTTCCTATTACGAGTATCGGAATGGC 240
 DB GAATGGTGTCTACAGCCCGGAGGCGGTAAAGATTTCCTATTACGAGTATCGGAATGGC 534
 QY 241 CACAGAGGTGGAGAGCCCTTTTCAGGGGCGCTGAGTGAATGGAGCAAGCACTG 300
 DB CACAGAGGTGGAGAGCCCTTTTCAGGGGCGCTGAGTGAATGGAGCAAGCACTG 594
 QY 301 CAGAGCTGTCCATCACTGTGCTCAAGTCACTGTAACGACTCTGGCCTTACACCTGC 360
 DB CAGAGCTGTCCATCACTGTGCTCAAGTCACTGTAACGACTCTGGCCTTACACCTGC 654
 QY 361 AATGTGTCGCGGAGTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGCGCTG 420
 DB AATGTGTCGCGGAGTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGCGCTG 714
 QY 421 ATCCCCCTAAGATCAACGAGGAGGCTGGAGAGCTTACCTCTGTGGTCTCAGAAATC 480
 DB ATCCCCCTAAGATCAACGAGGAGGCTGGAGAGCTTACCTCTGTGGTCTCAGAAATC 774
 QY 481 ATGATGTACATCTTCTGTGTTCTTCTCACTGTTGGCTGCTCATCGAGATGATATTCG- 539
 DB ATGATGTACATCTTCTGTGTTCTTCTCACTGTTGGCTGCTCATCGAGATGATATTCG- 834
 QY 540 CTACAGAAAGGTCTCAAAAGCCGAGGAGGCGCCCAAGAAAACCGCTCTGACTACC- 598
 DB CTACAGAAAGGTCTCAAAAGCCGAGGAGGCGCCCAAGAAAACCGCTCTGACTACC- 894
 QY 599 CCATCCCATCTGAGAACAGAGAGAACTCTGCGGTACCACTGGAGGAA 645
 DB CGATTCCATTTGAGAACAGAGGAAATTTCTTGGTACCTCGGGGGGA 941

RESULT 9

AAC67836
 ID AAC67836 standard; cDNA; 2220 BP.

XX AC AAC67836;

XX 15-FEB-2001 (first entry)

XX DE Rat beta3 subunit cDNA.

KW Rat; beta sub-unit; beta3; analgesic; anticonvulsant; cerebroprotective;
 KW vasotrophic; cardiant; nootropic; cytoskeletal; dermatological;
 KW gene therapy; voltage-gated sodium channel; pain; epilepsy; stroke;
 KW ischaemia; heart disease; Jacobsen Syndrome;
 KW familial nonchromaffin paraganglioma; phenylketonuria;
 KW Charcot Marie Tooth disease; ss.

OS Rattus sp.

XX WO2000063367-A1.

XX 26-OCT-2000.

XX 24-FEB-2000; 2000WO-EP001783.

XX 15-APR-1999; 99US-0129473P.

XX (WARN) WARNER LAMBERT CO.

XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX Cox P, Dixon A, Jackson A, Morgan K;

XX WPI; 2000-665241/64.

XX P-PSDB; AAB36001.

PT Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium
 PT channel, and their corresponding polypeptides, useful for detecting and
 PT treating sodium channel-associated conditions, e.g. pain, epilepsy and
 PT stroke.

XX Claim 6; Page 69-70; 88pp; English.

XX The present sequence is given in the claims of a specification relating
 CC to a novel family of beta sub-unit proteins from a voltage-gated sodium
 CC channel. Human and rat beta sub-units, which have been collectively
 CC identified as beta3, have been isolated. The polynucleotides and
 CC polypeptides are useful for screening for agonists and antagonists of
 CC sodium channels. The agonists, antagonists, proteins and nucleic acids
 CC may be used in diagnosing or treating diseases or conditions associated with
 CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,
 CC heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma,
 CC Phenylketonuria and Charcot Marie Tooth disease

XX SQ Sequence 2220 BP; 573 A; 557 C; 561 G; 529 T; 0 U; 0 Other;

Query Match 82.8%; Score 536.6; DB 3; Length 2220;
 Best Local Similarity 89.3%; Pred. No. 7.2e-135;
 Matches 578; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 ATGCTGCTTCAATAGATTGTTCCCTGGCTTCTCTCGTCTATCTACTGGTCACT 60
 DB ATGCTGCTTCAATAGATTGTTCCCTGGCTTCTCTCGTCTATCTACTGGTCACT 422
 QY 61 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGAGACGAGGCGGTGACGGCAACCCC 120
 DB GTCTGCTTCCCTGTGTGTGAAGTGCCTCGAGACGAGGCGGTGACGGCAACCCC 482
 QY 121 ATGAAGCTGCGCTCATCTCTGATGAAGACGAGGAGGTGGAGGCCACCACTGGTGTG 180
 DB ATGAAGCTGCGCTCATCTCTGATGAAGACGAGGAGGTGGAGGCCACCACTGGTGTG 542
 QY 181 GAATGGTGTCTACAGCCCGGAGGCGGTAAAGATTTCCTATTACGAGTATCGGAATGGC 240
 DB GAATGGTGTCTACAGCCCGGAGGCGGTAAAGATTTCCTATTACGAGTATCGGAATGGC 602
 QY 241 CACAGAGGTGGAGAGCCCTTTTCAGGGGCGCTGAGTGAATGGAGCAAGCACTG 300
 DB CACAGAGGTGGAGAGCCCTTTTCAGGGGCGCTGAGTGAATGGAGCAAGCACTG 662
 QY 301 CAGAGCTGTCCATCACTGTGCTCAAGTCACTGTAACGACTCTGGCCTTACACCTGC 360
 DB CAGAGCTGTCCATCACTGTGCTCAAGTCACTGTAACGACTCTGGCCTTACACCTGC 722

Db 643 GGTGGAAATGGTTCTACAGGCCCGGCGGTAAAGATTTCTTATTTACAGATATCGGAA 702
 QY 237 TGGCCACCGAGAGGTGGAGAGCCCTTTTCAGGGGCGCCTTGCAGTGGAAATGGCAGCAAGGA 296
 Db 703 TGGCCACCGAGAGGTGGAGAGCCCTTTTCAGGGGCGCCTTGCAGTGGAAATGGCAGCAAGGA 762
 QY 297 CTTGCAAGGAGGTGTCATCTGTGCTCAACGTCACCTTGAACGACTCTGGGCTCTACAC 356
 Db 763 CTTGCAAGGAGGTGTCATCTGTGCTCAACGTCACCTTGAACGACTCTGGGCTCTACAC 822
 QY 357 CTGCAATGTCTCCGGGAGTTTGAGTTTTCAGGGCGCATCGGCCCTTTTGTGAAGACGACGCG 416
 Db 823 CTGCAATGTCTCCGGGAGTTTGAGTTTTCAGGGCGCATCGGCCCTTTTGTGAAGACGACGCG 882
 QY 417 GCTGATCCCTTAAGAGTCAACGAGGAGGTGGAGAGGACTTACCTCTGTGTCTCACA 476
 Db 883 GCTGATCCCTTAAGAGTCAACGAGGAGGTGGAGAGGACTTACCTCTGTGTCTCACA 942
 QY 477 AATCATGATGTACATCTTCTGTGCTCTTCTCACCCTGTGGCTCTCATCGAGATGATATA 536
 Db 943 AATCATGATGTACATCTTCTGTGCTCTTCTCACCCTGTGGCTCTCATCGAGATGATATA 1002
 QY 537 TTGCTACAGAAAGGTCTCAAAAGCCGAAGAGGCGAGCCCAAGAAACGCGTCTGACTAC 594
 Db 1003 TTGCTACAGACAGGTCTCAAAAGCCGAAGAGGCGAGCCCAAGAAACGCGCCAGGAAC 1060

RESULT 13

AAC90601
 ID AAC90601 standard; cDNA; 645 BP.
 XX
 AC AAC90601;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Rat sodium channel beta3 protein Alrxa94h5 partial coding sequence.
 XX
 KW Rat; sodium channel beta3 protein; Alrxa94h5; pain; sleep disorder;
 KW neurodegenerative disorder; mood disorder; muscle contraction; ss.
 XX
 OS Rattus sp.
 XX
 PN WO200069912-A1.
 XX
 PD 23-NOV-2000.
 XX
 PF 12-MAY-2000; 2000WO-US013144.
 XX
 PR 14-MAY-1999; 99US-0134198P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Curtis RAJ;
 XX
 DR WPI; 2001-122743/13.
 XX

PT New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
 PT root ganglion cDNA library for use in chromosome mapping, forensic
 PT medicine, monitoring clinical trials and therapeutics.
 XX
 PS Claim 1; Page 40-41; 145pp; English.
 XX
 CC The present invention provides the protein and coding sequences of the
 CC rat sodium channel beta3 protein, designated Alrxa94h5. This protein is
 CC involved in the generation of pain and other sensory or perceptible nerve
 CC impulses, in the establishment and endurance of mood, neurodegenerative
 CC and sleep disorders, and in the control of muscle contraction, including
 CC movements such as the heartbeat, digestion and vascular tone. The
 CC sequences can be used in predictive medicine, screening and diagnostic
 CC assays, and in pharmacogenomics
 XX
 SQ Sequence 645 BP; 155 A; 154 C; 181 G; 155 T; 0 U; 0 Other;

Query Match 82.5%; Score 534.6; DB 5; Length 645;
 Best Local Similarity 89.3%; Pred. No. 1.6e-134;
 Matches 576; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
 QY 1 ATGCGCTGCCCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTATCTACTTGGGTCACT 60
 Db 1 ATGCGCTGCCCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTATCTACTTGGGTCACT 60
 QY 61 GTCTGCTTCCCTTGTGTGTGGAAGTGCCTTCGAGACGAGGCGGTGAGGCAACCC 120
 Db 61 GTCTGCTTCCCTTGTGTGTGGAAGTGCCTTCGAGACGAGGCGGTGAGGCAACCC 120
 QY 121 ATGAAGCTGCGTGCATCTCTGATGAAGAGAGGAGGTGAGGCAACCC 180
 Db 121 ATGAAGCTGCGTGCATCTCTGATGAAGAGAGGAGGTGAGGCAACCC 180
 QY 181 GAATGTTTCTACAGGCGCGGTAAAGATTTCTTATTTACGAGTATCGGAATGGC 240
 Db 181 GAATGTTTCTACAGGCGCGGTAAAGATTTCTTATTTACGAGTATCGGAATGGC 240
 QY 241 CACGAGAGGTGGAGAGCCCTTTTCAGGGGCGCTGCACTGGAATGGCAGCAAGCACTG 300
 Db 241 CACGAGAGGTGGAGAGCCCTTTTCAGGGGCGCTGCACTGGAATGGCAGCAAGCACTG 300
 QY 301 CAGGAGGTGCTCATCTCACTGCTCAACGTCACCTCTGAAAGCGCTCTGACCTTACAC 360
 Db 301 CAGGAGGTGCTCATCTCACTGCTCAACGTCACCTCTGAAAGCGCTCTGACCTTACAC 360
 QY 361 AATGTGTCCTCGGAGTTTTCAGTTTTCAGGGCGCATCGGCCCTTTTGTGAAGACGCGGCTG 420
 Db 361 AATGTGTCCTCGGAGTTTTCAGTTTTCAGGGCGCATCGGCCCTTTTGTGAAGACGCGGCTG 420
 QY 421 ATCCCTTTCAGAGTCAACGAGGAGGTGGAGAGGACTTCACTCTGTGTCTCAGAAATC 480
 Db 421 ATCCCTTTCAGAGTCAACGAGGAGGTGGAGAGGACTTCACTCTGTGTCTCAGAAATC 480
 QY 481 ATGATGTACATCTTCTGTGTCTTCTCCTCACCCTGTGCTCTCATCGAGATGATATATTC 540
 Db 481 ATGATGTACATCTTCTGTGTCTTCTCCTCACCCTGTGCTCTCATCGAGATGATATATTC 540
 QY 541 TACAGAAAGGTCTCAAAAGCCGAAGAGGCGAGCCCAAGAAACGCGTCTGACTACCTTGGC 600
 Db 541 TACAGAAAGGTCTCAAAAGCCGAAGAGGCGAGCCCAAGAAACGCGTCTGACTACCTTGGC 600
 QY 601 ATCCCTTTCAGAGCAACGAGGAGACTTCTGCGGTACCACTGAGGAGAA 645
 Db 601 ATCCCTTTCAGAGCAACGAGGAGACTTCTGCGGTACCACTGAGGAGAA 645

RESULT 14

ADS10151
 ID ADS10151 standard; DNA; 953 BP.
 XX
 AC ADS10151;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Human therapeutic DNA - SEQ ID 388.
 XX
 KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnary;
 KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
 KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
 XX
 OS Homo sapiens.
 XX
 PN WO2004080148-A2.
 XX
 PD 23-SEP-2004.
 XX
 PF 30-SEP-2003; 2003WO-US030720.
 XX
 PR 02-OCT-2002; 2002US-0416186P.
 XX

PA (NUVE-) NUVELO INC.
XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX WPI; 2004-668857/65.
DR P-PSDB; ADS10835.
XX New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.
XX Claim 1; SEQ ID NO 388; 718pp; English.
XX The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic DNA of
CC the invention. The current sequence is not shown explicitly within the
CC specification but can be accessed from the WIPO web-site.
XX
SQ Sequence 953 BP; 180 A; 279 C; 290 G; 204 T; 0 U; 0 Other;
Query Match 77.8%; Score 504; DB 13; Length 953;
Best Local Similarity 99.0%; Pred. No. 3.6e-126;
Matches 507; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ATGCTGCTCCCTCAATAGATTGTTTCCCTGGCTTCTCGTCTTACTACTGGTCAGT 60
DB 327 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCGTCTTACTACTGGTCAGT 386
QY 61 GTCTGCTTCCCTGTGTGTGAAGTCCCTCGAGACGAGCGCGTGCAGGGCAACCCC 120
DB 387 GTCTGCTTCCCTGTGTGTGAAGTCCCTCGAGACGAGCGCGTGCAGGGCAACCCC 446
QY 121 ATGAAGCTGCTGCTCATCTCTCGATGAAGAGAGAGGTGGAGGCCACCGGTGGTG 180
DB 447 ATGAAGCTGCTGCTCATCTCTCGATGAAGAGAGAGGTGGAGGCCACCGGTGGTG 506
QY 181 GAATGTTTCTACAGCCCGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC 240
DB 507 GAATGTTTCTACAGCCCGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC 566
QY 241 CACGAGAGTGGAGAGCCCTTTTCAGGGCGCTCGAGTGGGAATGCGACGAGACCTG 300
DB 567 CACGAGAGTGGAGAGCCCTTTTCAGGGCGCTCGAGTGGGAATGCGACGAGACCTG 626
QY 301 CAGGAGTGTCCATCACTGTGCTCAAGTCACTCTGAACGACTCTGCGCTCTACACCTGC 360
DB 627 CAGGAGTGTCCATCACTGTGCTCAAGTCACTCTGAACGACTCTGCGCTCTACACCTGC 686
QY 361 AATGTGTCCCGGAGTTTGAAGTTTGAAGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 420
DB 687 AATGTGTCCCGGAGTTTGAAGTTTGAAGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 746
QY 421 ATCCCTTAAAGATCAACGAGGAGGTGGAGAGACATTCACCTCTGTGTGTTTCAAGAAATC 480
DB 747 ATCCCTTAAAGATCAACGAGGAGGTGGAGAGACATTCACCTCTGTGTGTTTCAAGAAATC 806
QY 481 ATGATGTACATCTTCTGTGTTTCTTCCCTCACCCCT 512
DB 807 ATGATGTACATCTTCTGTGTTTCTTCCCTCACCCCT 838
RESULT 15
AAV86895
ID AAV86895 standard; cDNA; 471 BP.
XX
AC AAV86895;
XX
XX 27-APR-1999 (first entry)
XX EST clone BM4.
DE
XX Expressed sequence tag; secreted protein; haematopoiesis regulator;
KW tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
OS Homo sapiens.
XX WO9845435-A2.
PN
XX 15-OCT-1998.
XX
XX 10-APR-1998; 98WO-US006954.
PF
XX 10-APR-1997; 97US-00835913.
PR
XX (GEMY) GENETICS INST INC.
PA
XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Spaulding V, Agostino MU;
PI WPI; 1999-070076/06.
XX
XX New polynucleotides encoding human secreted proteins - derived from e.g.
PT human blood, kidney, foetal lung, placenta, testes, brain, ovary,
PT pituitary, retina and colon cDNA libraries.
XX
XX Claim 1; Page 383-384; 633pp; English.
PS
XX This sequence represents an expressed sequence tag (EST), and is a
CC polynucleotide of the invention. The polynucleotides of the invention are
CC all secreted EST sequences isolated from a variety of human tissue
CC sources. The EST sequences and proteins encoded by them are predicted to
CC have useful biological activities which would make them suitable for
CC treating, preventing or ameliorating medical conditions in humans and
CC animals, although no supporting data is given. Suggested activities
CC include nutritional activity, immune stimulating or suppressing activity,
CC haematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity. The EST sequences are also stated to be useful for gene therapy
XX
SQ Sequence 471 BP; 93 A; 126 C; 143 G; 108 T; 0 U; 1 Other;
Query Match 65.1%; Score 422; DB 2; Length 471;
Best Local Similarity 99.5%; Pred. No. 4.6e-104;
Matches 433; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCGTCTTACTACTGGTCAGT 60
DB 29 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCGTCTTACTACTGGTCAGT 88
QY 61 GTCTGCTTCCCTGTGTGTGAAGTCCCTCGAGACGAGCGCTCGAGGGCAACCCC 120
DB 89 GTCTGCTTCCCTGTGTGTGAAGTCCCTCGAGACGGA -GCCGTGACGAGCAACCCC 147
QY 121 ATGAAGCTGCTGCTCATCTCTCGATGAAGAGAGAGGTGGAGGCCACCGGTGGTG 180
DB 148 ATGAAGCTGCTGCTCATCTCTCGATGAAGAGAGAGGTGGAGGCCACCGGTGGTG 207
QY 181 GAATGTTTCTACAGCCCGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC 240
DB 208 GAATGTTTCTACAGCCCGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC 267
QY 241 CACGAGAGTGGAGAGCCCTTTTCAGGGCGCTCGAGTGGGAATGCGACGAGACCTG 300
DB 268 CACGAGAGTGGAGAGCCCTTTTCAGGGCGCTCGAGTGGGAATGCGACGAGACCTG 327

QY 301 CAGGACGTGTCATCACTGTGCTCAACGTCACCTCTGACGACTCTGGCCTCTACACCTGC 360
 Db |||||
 QY 328 CAGGACGTGTCATCACTGTGCTCAACGTCACCTCTGACGACTCTGGCCTCTACACCTGC 387
 Db |||||
 QY 361 AATGTGTCCCGGAGTTTGAGTTTGAGGGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 420
 Db |||||
 QY 388 AATGTGTCCCGGAGTTTGAGTTTGAGGGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 447
 Db |||||
 QY 421 ATCCCCCTAAGAGTC 435
 Db |||||
 QY 448 ATCCCCCTAAGAGTC 462
 Db |||||

Search completed: April 7, 2005, 11:09:35
 Job time : 475.712 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
C	1	143.8	22.2	617	4	US-09-949-016-2369	Sequence 2369, Ap
	2	51	7.9	11174	4	US-09-949-016-14111	Sequence 14111, A
	3	48.6	7.5	30337	4	US-09-949-016-13053	Sequence 13053, A
	4	45.4	7.0	1645	4	US-09-023-587A-5	Sequence 5, Appli
	5	44.8	6.9	1053	4	US-09-902-540-2666	Sequence 2666, Ap
	6	44.8	6.9	13706	4	US-09-902-540-1124	Sequence 1124, Ap
	7	42.4	6.5	2133	4	US-09-902-540-4106	Sequence 4106, Ap
	8	42.4	6.5	23738	4	US-09-902-540-1203	Sequence 1203, Ap
	9	41.6	6.4	696	4	US-09-489-039A-3591	Sequence 3591, Ap
	10	40.6	6.3	2943	4	US-09-902-540-3929	Sequence 3929, Ap
C	11	40.6	6.3	21295	4	US-09-902-540-1194	Sequence 1194, Ap
	12	40.4	6.2	1533	4	US-09-902-540-7877	Sequence 7877, Ap
	13	40.4	6.2	5228	4	US-09-902-540-789	Sequence 789, App
	14	39.2	6.0	732	4	US-09-902-540-3806	Sequence 3806, Ap
	15	39.2	6.0	6202	4	US-09-774-528-120	Sequence 120, App
	16	39.2	6.0	18551	4	US-09-902-540-1187	Sequence 1187, Ap
	17	38.6	6.0	513	4	US-09-902-540-8812	Sequence 8812, Ap
	18	38.6	6.0	1407	4	US-09-902-540-6215	Sequence 6215, Ap
	19	38.6	6.0	8122	4	US-09-902-540-937	Sequence 937, App
	20	38.6	6.0	13332	4	US-09-902-540-1047	Sequence 1047, Ap
C	21	38.2	5.9	1437	4	US-09-902-540-8578	Sequence 8578, Ap
	22	38.2	5.9	9081	4	US-09-902-540-905	Sequence 905, App
	23	37.4	5.8	711	4	US-09-902-540-6903	Sequence 6903, Ap
	24	37.4	5.8	4169	4	US-09-902-540-590	Sequence 590, App
	25	37	5.7	597	4	US-09-902-540-3561	Sequence 3561, Ap
	26	37	5.7	19019	4	US-09-902-540-1171	Sequence 1171, Ap
	27	36.8	5.7	6267	4	US-09-902-540-5649	Sequence 5649, Ap

Db 469 CGAGTGGACCGCATCTGTGGCGGCGGACCGGCGCAACTCTCGGTGGCCAAACGACATGGG 528
QY 234 GAATGGCCACACGAGGTGGAGAGCCCTTTTCAGGGGCGGCTGCAGTGAATGGCAGCAA 293
Db 529 CGCGGGCGACTAGAGTACCCATCGGTTCAGAGCGCGGTCAAGATCCCGACGACAA 588
QY 294 GGACCTGCAGGAGGTGTCCATCACTGTGTCTCAAGCTCACTCTGAACGACTCTGGCCTCTA 353
Db 589 GATGGTGTACTACGAGGAGCGCGGAGATGTACGTGGCGGACGACGCTCTCTCCGACTT 648
QY 354 CACTGCAATGTGTCCCGGAGTTGA 380
Db 649 CTACGGCTGGGTGTTCCTCCCAAGTCCGA 675

RESULT 5

US-09-902-540-2666
; Sequence 2666, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 2666
; LENGTH: 1053
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-2666

Query Match 6.9%; Score 44.8; DB 4; Length 1053;
Best Local Similarity 52.1%; Pred. No. 0.0076;
Matches 100; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
QY 61 GTCTGCTCCCTGTGTGTGGAGTCCCTCGAGACGAGGCGGTCGAGGCAACCCC 120
Db 151 GACTTCTCCACGACCTGTGTGGACCTCGCTCGAAGATGACGACGCGGAGCGCCACTC 210
QY 121 ATGAAGTGGCTGCATCTCTCATGAAGAGAGAGGAGTGGAGCCACACCGTGGT 180
Db 211 ATCCACCGCTGTGTGGCTTCTTCGCGACGGGTGACAGCATCGTCGGCAACACCTGGT 270
QY 181 GAATGGTCTTACAGGCGGCGGTAAAGATTTCCTTATTACGAGTATCGAATGGC 240
Db 271 CTGAACCTCTACAAGCACCTGAAGCCCTCGAGGCGGATGTACCTGTGCGGCCAGCTC 330
QY 241 CACGAGAGGTG 252
Db 331 TACGAGGAGGCG 342

RESULT 6

US-09-902-540-1124/c
; Sequence 1124, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1124
; LENGTH: 13706
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1124

Query Match 6.9%; Score 44.8; DB 4; Length 13706;
Best Local Similarity 52.1%; Pred. No. 0.027;
Matches 100; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 61 GTCTGCTCCCTGTGTGTGGAGTCCCTCGAGACGAGGCGGTCGAGGCAACCCC 120
Db 4948 GACTTCTCCACGACCTGTGTGGACCTCGCTCGAAGATGACGACGCGGAGCGCCACTC 4899
QY 121 ATGAAGTGGCTGCATCTCTCATGAAGAGAGAGGAGTGGAGCCACACCGTGGT 180
Db 4888 ATCCACCGCTGTGTGGCTTCTTCGCGACGGGTGACAGCATCGTCGGCAACACCTGGT 4829
QY 181 GAATGGTCTTACAGGCGGCGGTAAAGATTTCCTTATTACGAGTATCGAATGGC 240
Db 4828 CTGAACCTCTACAAGCACCTGAAGCCCTCGAGGCGGATGTACCTGTGCGGCCAGCTC 4769
QY 241 CACGAGAGGTG 252
Db 4768 TACGAGGAGGCG 4757

RESULT 7

US-09-902-540-4106/c
; Sequence 4106, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4106
; LENGTH: 2133
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4106

Query Match 6.5%; Score 42.4; DB 4; Length 2133;
Best Local Similarity 51.6%; Pred. No. 0.053;
Matches 97; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 87 GCCTTCGAGACGAGGCGGTGAGGGCAACCCCATGAAGCTGGCTGCATCTCTCAT 146
Db 1813 GGCCAGGATGATGGCGGCGCCATCCCGTTTGAAGACGCGTGAAGCGCGCGTGCAG 1754
QY 147 GAAGAGAGGAGGTGGAGCCACCAACCGTGGTGGATGTGTTTACAGGCGCGGCGG 206
Db 1753 GAAGCGGCGGCGGAGTTCGGACACGCTGGGCGTGGGACCGCTTCCAGACCAAGTGT 1694
QY 207 TAAAGATTTCTTATTACGAGTATCGAATGCGCACGAGAGTGGAGAGCCCTTTCA 266
Db 1693 GGGTGAAGCGCTCGGTACGAGATCTGCGCGGACTCCAGCTCGGACAGCGCGGTGCA 1634
QY 267 GGGCGGCC 274
Db 1633 GCTCCGCC 1626

RESULT 8

US-09-902-540-1203

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; Sequence 1203, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1203
; LENGTH: 23738
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1203

Query Match      6.5%; Score 42.4; DB 4; Length 23738;
Best Local Similarity 51.6%; Pred. No. 0.17;
Matches 97; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 87 GCGCTCGAGACGGAGCGCGTCAGGGCAACCCCATGAAGCTGCGCTGCATCTCTGCAT 146
DB 4191 GCGCAGGATGATGGCGGCGCCCATCCCGTTTGAAGACGCGTGAAGCGCGCGTGCAG 4250

QY 147 GAAGAGAGAGGAGTGGAGGCCACACACGCTGGTGAATGGTTCTACAGGCCCGAGGGCGG 206
DB 4251 GAAGCGGCGCGGAGTGGACACGCTGGCGTGGACCGCTTCCAGCACCACTGTCTGT 4310

QY 207 TAAAGATTTCCTTATTACAGTATCGGAATGCCACACAGGAGTGGAGAGCCCTTTCA 266
DB 4311 GCGTGAAGCGCTCCGCTACAGGATCTGGCGGACTCCAGCTCGGACAGCGCGGTGCA 4370

QY 267 GGGGGGCC 274
DB 4371 GCTCCGCC 4378

RESULT 9
US-09-489-039A-3591
; Sequence 3591, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3591
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3591

Query Match      6.4%; Score 41.6; DB 4; Length 696;
Best Local Similarity 48.3%; Pred. No. 0.053;
Matches 116; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 83 AAGTGCCTCGAGACGGAGCGCGTCAGGGCAACCCCATGAAGCTGCGCTGCATCTCT 142
DB 92 AGCGCGCACTCGCGAGGCGGTGCTGGCAAGCTGCCGAAGCGCGCTATCGCACT 151

QY 143 GCATGAAGAGAGAGGAGTGGAGGCCACCAACCGTGTGGAATGGTTCTACAGGCCGCGAGG 202
DB 152 ACCTGCCGTTCAACAGCGTTGACGGTATCCCGCTGATCAGGGGATTCGGCTGTGTTCC 211
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QY 203 GCGTAAAGATTTCCTTATTACAGTATCGAATGGCCACAGAGGTGGAGAGCCCT 262
DB 212 CCGGCGCGAACTCCTTTTACCGGGGAAGATGTCTTTGAGCTGCAGGGCCACCGGCGCCGG 271

QY 263 TTCAGGGGCGCTCGAGTGGATGCGACGAGCACTGCAGGACGCTGTCCATCATCTGTCG 322
DB 272 TCATTCTGACCTGCTGCTTAAACGTATTCTGACCTGCGGGCTTGCATCGCAGCG 331

RESULT 10
US-09-902-540-3929
; Sequence 3929, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3929
; LENGTH: 2943
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3929

Query Match      6.3%; Score 40.6; DB 4; Length 2943;
Best Local Similarity 48.9%; Pred. No. 0.21;
Matches 109; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 85 GTGCGCTCGAGACGGAGCGCGTGCAGGCAACCCCATGAAGCTGCGCTGCATCTCTCGC 144
DB 1831 GTGCTGGAAGAGTGGAGCGCGCTGCGGAGCTGCGGCTGATGCGCGCGAGGCCCGC 1890

QY 145 ATGAAGAGAGAGGAGTGGAGGCCACACGCGTGGTGGATGGTTCTACAGGCCCGAGGCG 204
DB 1891 ATGGCTACGGCGCAGGAGCTGAAGGCCCGCGTGGAGGGCGCGCCAGGTGAAGCGC 1950

QY 205 GGTAAAGATTTCCTTATTACAGTATCGAATGCCACAGGAGTGGAGAGCCCTTT 264
DB 1951 GCCTATGACCCGCTCCTCGACGTTGCGACGCTTCGACCGCGCGCTGGAGCGCTGGTG 2010

QY 265 CAGGGGCGCTCGAGTGGATGGCAAGGACCAAGGACCTGCAGGAGC 307
DB 2011 AAGCGCGCCAGGAGCGCATGGGCATCGAGGCCGAGGAGG 2053

RESULT 11
US-09-902-540-1194
; Sequence 1194, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1194
; LENGTH: 21295
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1194
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Query Match	6.2%	Score 40.4;	DB 4;	Length 5228;
Best Local Similarity	47.9%;	Pred. No. 0.31;		
Matches 116: Conservative	0;	Mismatches 126;	Indels 0;	Gaps 0;

Qy	232	CGGAATGGCCAC	CCAGGAGGTGGAGAGCCCTTCTTCAGGGGCGCTGCAGTGGAAATGGCAGC	291
Db	3057	CGGGATCCCGCAGCAGT	TGAGTCTCCGAGGGAGGGCTCGTCTCTCGCGGATGGGGAC	3116
Qy	292	AAGGACCTGCAGACG	TGTCATCACTGTGCTCAACGTCACTCTGAACAGCACTCTGGGCTC	351
Db	3117	ACGAGCTGCAGACCT	TGGTGGCGCGTACCAGGTGACGCCGGCTGGGTCCACGTGGGC	3176
Qy	352	TACACCTGCAANTG	TCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACG	411
Db	3177	TTCCAGCGCACCCAT	GCCTGCGCTCGTGGAGGGGCGCTGGCGCAACGTGGGGCATCACC	3236
Qy	412	ACCGGCTGATCCCT	TAAAGTACCGAGGAGGCTCGAGAGGACTTCACTCTGTGGTCTC	471
Db	3237	GTGCTGTTCGGCT	TGCTTTCACCGCGCGGCGCTTCTCTGTGCAGCCGCCCATCGT	3296
Qy	472	TC	473	
Db	3297	TC	3298	

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RESULT 14
US-09-902-540-3806
; Sequence 3806, Application US/09902540
; Patent No. 683347
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3806
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3806

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Query: Match	6.0%	Score 39.2;	DB 4;	Length 732;
Best Local Similarity	49.5%;	Pred. No. 0.27;		
Matches 101;	Conservative	0;	Mismatches 103;	Indels 0; Gaps 0;
QY	297	CCTGCAGGACGTTCCATCACTGTGCTCAACGTCACACTCTGGCCTTCACAC	356	
Db	480	CCTGAGGACATGTCGAGACACTGAAGATCGCGCGGCTCAAGCGCTGGCGCTTTCAA	539	

357	QY	CTGCAATGTGTCGGGAGTTTGATTGAGGCCATCGGCCCTTGTGAGAGCAGCGC	416
540	Db	GTAAGAGCGGCGCGAGCCCATCTGAAGTCTCACCAGCAGACGAGCTCGCCG	599
417	QY	GCTGATCCCCCTAAGAGTCAACGAGGAGGCTGGAGAGGAATTCACTGTGTGTTCTCAGA	476
600	Db	GGTGACAGCTCCGTACTCAGCGCGCTGGCGAAGTGGGTTCTCCGTGGAGGGCTACCG	659
477	QY	AATCATGATGTACATCCTCTCTGGT	500
660	Db	GGAGAAGGTGGAGCGCGTCTGTTGTT	683

RESULT 15

US-09-774-528-120
; Sequence 120, Application US/09774528

FACEID NO. 0743015
GENERAL INFORMATION:

APPLICANT: Tanq, Y. Tom

APPLICANT: Zhou, Ping

APPLICANT: Goodrich, Ryle

; APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Ren, Feiyan

APPLICANT: Zhang, Jie

; APPLICANT: Zhao, Qing A.

; APPLICANT: Yang, Yonghong

; APPLICANT: Xue, Aidong

; APPLICANT: Wehrman, Tom

; APPLICANT: Wang, Jian-Ru

; APPLICANT: Wang, Dunrui

APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. 67436

6743619e1 Nucleic Acids and Polymptides

; TITLE OF INVENTION: Polypeptides
 : FILE REFERENCE: 802

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; FILE REFERENCE: 802
: CURRENT APPLICATION

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;; CURRENT APPLICATION NUMBER: US/09/774,528
: CURRENT FILING DATE: 2001-01-30

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; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441

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; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt FL genes Version 2.0

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; SOFTWARE: PC-
; SEQ ID NO 120

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; SEQ ID NO 120
; LENGTH: 6202

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; LENGTH: 0202
; TYPE: DNA

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ORGANISM: Homo sapiens

FEATURE:

; NAME/KEY: CDS

; LOCATION: (49)

Query Match	6.0%;	Score 39.2;	DB 4;	Length 6202;
Best Local Similarity	47.24;	Pred. No. 0.76;		
Matches 119;	Conservative 0;	Mismatches 133;	Indels 0;	Gaps 0;
QY	93	GGAGACGGAGGCGGTG	CAGGGCAACCCATGAAGCTCGCTGCGATCTCTGCGATGAAGAG	152
Db	2418	GCACAGGAGCTCGGGAGAGGCACGGTGACATCTCTGAAGCGCAAGCGGAGCTGGAGGA	2477	
QY	153	AGAGGAGGTGGAGGCCACACCGTGTGTGGAATGGTTCTACAGGCCCGAGGGCGGTAAAGA	212	
Db	2478	CGGGGAGAAGGTTGTGACCACTGAGCGAGAGGCGCTGCACGAGGACGAGGACAACAGC	2537	
QY	213	TTTTCCTATTATTACGAGTATCGGAATCGGCACACGAGGAGTGGAGAGCCCTTTTCAGGGGCG	272	
Db	2538	CCTCGCCATGGCGAGAACAGAGGCTGCGGGGCGAGCTGCACAGGCTCAATTTCTTGCA	2597	
QY	273	CCTGCGATGAAATGGCAGCAGAGNACCTCGAGGACGTGTCCATCACTGTGCTCAACGTAC	332	
Db	2598	CCACCAGCTGAAGGGGGAGTACGAGGAGCTGACGCCCAACACCAAGAGCTGAAACCTC	2657	
QY	333	TCTGAACGACTC	344	
Db	2658	ACTGAACAACGC	2669	

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OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 10:54:05 ; Search time 580.168 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

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Maximum Match 100%

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCRU5_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	648	100.0	1261	11	US-09-977-579-4
2	536.6	82.8	2220	13	US-09-977-579-3
3	536.6	82.8	2632	13	US-10-029-191-22
4	536.6	82.8	3108	13	US-10-029-191-1
5	534.6	82.5	645	13	US-10-029-191-21
6	148.2	22.9	657	13	US-10-029-191-23
7	143.8	22.2	1335	18	US-10-723-860-2247
8	142.2	21.9	1414	18	US-10-477-272-1
9	141	21.8	407	17	US-10-276-774-718
10	138.6	21.4	1490	9	US-09-917-800A-1654
11	81.4	12.6	807	17	US-10-401-916-12
12					Sequence 4, Appli
13					Sequence 3, Appli
14					Sequence 22, Appli
15					Sequence 1, Appli
16					Sequence 21, Appli
17					Sequence 23, Appli
18					Sequence 2247, Ap
19					Sequence 1, Appli
20					Sequence 718, App
21					Sequence 1654, Ap
22					Sequence 12, Appli

12	81.4	12.6	974	17	US-10-401-916-13	Sequence 13, Appli
13	49	7.6	243	16	US-10-029-386-16214	Sequence 16214, A
14	49	7.6	569	16	US-10-029-386-2514	Sequence 2514, Ap
15	48.6	7.5	3583	18	US-10-723-860-6471	Sequence 6471, Ap
16	45.4	7.0	876	18	US-10-767-701-10747	Sequence 10747, A
17	45.2	7.0	954	18	US-10-425-115-100998	Sequence 100998, A
18	44.8	6.9	921	17	US-10-369-493-43050	Sequence 43050, A
19	43.8	6.8	1434	17	US-10-259-194A-622	Sequence 622, App
20	43.8	6.8	1720	17	US-10-425-114-19213	Sequence 19213, A
21	43.8	6.8	1764	17	US-10-425-114-15538	Sequence 15538, A
22	43.8	6.8	1794	17	US-10-425-114-25057	Sequence 25057, A
23	43.8	6.8	2029	18	US-10-425-115-15984	Sequence 15984, A
24	42.8	6.6	1298	18	US-10-437-963-21288	Sequence 21288, A
25	41.6	6.4	1362	17	US-10-282-122A-23492	Sequence 23492, A
26	40.2	6.2	779	17	US-10-425-114-26163	Sequence 26163, A
27	39.8	6.1	1884	18	US-10-437-963-53366	Sequence 53366, A
28	39.2	6.0	5973	17	US-10-094-466-63	Sequence 63, Appl
29	39.2	6.0	6202	17	US-10-120-988-120	Sequence 120, Appl
30	39	6.0	1798	18	US-10-437-963-50269	Sequence 50269, A
31	38.6	6.0	922	18	US-10-437-963-82867	Sequence 82867, A
32	38.6	6.0	1052	18	US-10-425-115-154932	Sequence 154932, A
33	38.6	6.0	1179	9	US-09-815-242-7698	Sequence 7698, Ap
34	38.6	6.0	1179	17	US-10-282-122A-30011	Sequence 30011, A
35	38.6	6.0	1311	17	US-10-369-493-42998	Sequence 42998, A
36	38.6	6.0	1536	17	US-10-425-114-35508	Sequence 35508, A
37	38.6	6.0	2139	17	US-10-369-493-32177	Sequence 32177, A
38	38.6	6.0	2720	18	US-10-425-115-99348	Sequence 99348, A
39	38.4	5.9	3252	18	US-10-437-963-102169	Sequence 102169, A
40	38.4	5.9	4143	18	US-10-437-963-102168	Sequence 102168, A
41	38.2	5.9	1455	18	US-10-767-701-14341	Sequence 14341, A
42	38	5.9	1689	16	US-10-102-622-11	Sequence 9, Appli
43	38	5.9	1689	16	US-10-102-622-11	Sequence 11, Appli
44	38	5.9	2692	17	US-10-104-047-1554	Sequence 1554, Ap
45	37.6	5.8	1776	18	US-10-437-963-42691	Sequence 42691, A

ALIGNMENTS

RESULT 1

- US-09-977-579-4
- Sequence 4, Application US/09977579
- Publication No. US20040248240A1
- GENERAL INFORMATION:
- APPLICANT: Cambridge University Technical Services
- TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
- TITLE OF INVENTION: channel
- TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses th
- FILE REFERENCE: 674558-2001
- CURRENT APPLICATION NUMBER: US/09/977,579
- CURRENT FILING DATE: 2001-10-15
- PRIOR APPLICATION NUMBER: PCT/EP00/01783
- PRIOR FILING DATE: 2000-02-24
- PRIOR APPLICATION NUMBER: 60,129,473
- PRIOR FILING DATE: 2000-02-24
- NUMBER OF SEQ ID NOS: 47
- SOFTWARE: PatentIn version 3.1
- SEQ ID NO 4
- LENGTH: 1261
- TYPE: DNA
- ORGANISM: Homo sapiens
- US-09-977-579-4

Query Match	100.0%	Score 648;	DB 11;	Length 1261;
Best Local Similarity	100.0%;	Pred. No. 1e-200;		
Matches 648;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGCTGCTTCAATAGATTGTTCCCTGGCTTCTCTCGTGTCTATCTACTGGGTGAGT	60	
Db	376	ATGCTGCTTCAATAGATTGTTCCCTGGCTTCTCTCGTGTCTATCTACTGGGTGAGT	435	
QY	61	GTCTGCTTCCCTGTGTGTGTGGAAGTGCCTCGGACGAGCGCGTGCAGGCAACCCC	120	

Db 436 GTCTGCTTCCCTGTGTGTGGAGTGCCTCGGAGACGAGGCCGTGACGGCAACCC 495
QY 121 ATGAAGCTGCGTGCATCTCTGCATGAAGAGAGAGAGGTGAGGCCACCAACGGTGGTG 180
Db 496 ATGAAGCTGCGTGCATCTCTGCATGAAGAGAGAGAGGTGAGGCCACCAACGGTGGTG 555
QY 181 GAATGCTTCTACAGGCCGAGGGCGGTAAAGATTTCTTATTTACAGATATCGGAATGCG 240
Db 556 GAATGCTTCTACAGGCCGAGGGCGGTAAAGATTTCTTATTTACAGATATCGGAATGCG 615
QY 241 CACGAGAGGTGAGAGCCCTTTTCAGGGCGCGCTCGAGTGGAAATGGCAGCAGACCTG 300
Db 616 CACGAGAGGTGAGAGCCCTTTTCAGGGCGCGCTCGAGTGGAAATGGCAGCAGACCTG 675
QY 301 CAGGAGGTGCTCACTGTGCTCAACGTCACTCTGAACGACTCTGGCTCTACACCTGC 360
Db 676 CAGGAGGTGCTCACTGTGCTCAACGTCACTCTGAACGACTCTGGCTCTACACCTGC 735
QY 361 AATGTGTCGGGAGTTTGAATTTGAGGGCGCATCGGCCCTTTGTGAAGACGACGGGCTG 420
Db 736 AATGTGTCGGGAGTTTGAATTTGAGGGCGCATCGGCCCTTTGTGAAGACGACGGGCTG 795
QY 421 ATCCCTTAAAGTCAACGAGAGGTGAGAGGACTTCACTCTCTGCTCTCAGAAATC 480
Db 796 ATCCCTTAAAGTCAACGAGAGGTGAGAGGACTTCACTCTCTGCTCTCAGAAATC 855
QY 481 ATGATGTACATCTCTGCTCTTCTCAACCTGTGCTCTCATCGAGATATATTGC 540
Db 856 ATGATGTACATCTCTGCTCTTCTCAACCTGTGCTCTCATCGAGATATATTGC 915
QY 541 TACAGAAAGGTCTCAAAAGCGAGAGGCGAGCCCAAGAAACCGCTCTGACTTGTCC 600
Db 916 TACAGAAAGGTCTCAAAAGCGAGAGGCGAGCCCAAGAAACCGCTCTGACTTGTCC 975
QY 601 ATCCCTTAAAGTCAACGAGAGGACTCTGGGTACCACTGAGGAGATAG 648
Db 976 ATCCCTTAAAGTCAACGAGAGGACTCTGGGTACCACTGAGGAGATAG 1023

RESULT 2

US-09-977-579-3
; Sequence 3, Application US/0977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodium channel
; TITLE OF INVENTION: channel
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977,579
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: rat
US-09-977-579-3

Query Match 82.8%; Score 536.6; DB 11; Length 2220;

Best Local Similarity 89.3%; Pred. No. 3.1e-164;

Matches 578; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 ATGCTGCTTCAATAGATTTTCCCTGGCTTCTCTGCTGCTTATCTACTGGGTCACT 60
Db 363 ATGCTGCTTCAACAGATTTGCTTCCCTAGCTTCTTCTAGTGTCTATCTACTGGGTCA 422
QY 61 GTCTGCTTCCCTGTGTGTGGAGTGCCTCGGAGACGAGGCCGTGACGGCAACCC 120

Db 423 GTCTGCTTCCCTGTGTGTGGAGTGCCTCGGAGACGAGCGGTGACGGCAATCCC 482
QY 121 ATGAAGCTGCGTGCATCTCTGCATGAAGAGAGAGAGGTGAGGCCACCAACGGTGGTG 180
Db 483 ATGAAGCTGCGTGCATCTCTGCATGAAGAGAGAGAGGTGAGGCCACCAACGGTGGTG 542
QY 181 GAATGCTTCTACAGGCCGAGGGCGGTAAAGATTTCTTATTTACAGATATCGGAATGCG 240
Db 543 GAATGCTTCTACAGGCCGAGGGCGGTAAAGATTTCTTATTTACAGATATCGGAATGCG 602
QY 241 CACGAGAGGTGAGAGCCCTTTTCAGGGCGCGCTCGAGTGGAAATGGCAGCAGACCTG 300
Db 603 CACGAGAGGTGAGAGCCCTTTTCAGGGCGCGCTCGAGTGGAAATGGCAGCAGACCTG 662
QY 301 CAGGAGGTGCTCACTGTGCTCAACGTCACTCTGAACGACTCTGGCTCTACACCTGC 360
Db 663 CAGGAGGTGCTCACTGTGCTCAACGTCACTCTGAACGACTCTGGCTCTACACCTGC 722
QY 361 AATGTGTCGGGAGTTTGAATTTGAGGGCGCATCGGCCCTTTGTGAAGACGACGGGCTG 420
Db 723 AATGTGTCGGGAGTTTGAATTTGAGGGCGCATCGGCCCTTTGTGAAGACGACGGGCTG 782
QY 421 ATCCCTTAAAGTCAACGAGAGGTGAGAGGACTTCACTCTCTGCTCTCAGAAATC 480
Db 783 ATACCTTTGCGAGTCACTGAAGAGGGGAGAGACTTCACTCTCTGCTCTCAGAAATC 842
QY 481 ATGATGTACATCTCTGCTCTTCTCAACCTGTGCTCTCATCGAGATATATTGC 540
Db 843 ATGATGTACATCTCTGCTCTTCTCAACCTGTGCTCTCATCGAGATATATTGC 902
QY 541 TACAGAAAGGTCTCAAAAGCGAGAGGCGAGCCCAAGAAACCGCTCTGACTTGTCC 600
Db 903 TACAGAAAGGTCTCAAAAGCGAGAGGCGAGCCCAAGAAACCGCTCTGACTTGTCC 962
QY 601 ATCCCTTAAAGTCAACGAGAGGACTCTGGGTACCACTGAGGAGATAG 647
Db 963 ATCCCTTAAAGTCAACGAGAGGACTCTGGGTACCACTGAGGAGATAG 1009

RESULT 3

US-10-029-191-22
; Sequence 22, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/501
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2632
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-22

Query Match 82.8%; Score 536.6; DB 13; Length 2632;

Best Local Similarity 89.3%; Pred. No. 3.3e-164;

Matches 578; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 ATGCTGCTTCAATAGATTTTCCCTGGCTTCTCTGCTGCTTATCTACTGGGTCACT 60
Db 78 ATGCTGCTTCAACAGATTTGCTTCCCTAGCTTCTTCTAGTGTCTATCTACTGGGTCA 137
QY 61 GTCTGCTTCCCTGTGTGTGGAGTGCCTCGGAGACGAGGCCGTGACGGCAACCC 120
Db 138 GTCTGCTTCCCTGTGTGTGGAGTGCCTCGGAGACGAGGCCGTGACGGCAATCCC 197

Db 121 ATGAAGCTGAGGTGCATCTCTGTCATGAAGAGGAGAGGTGAGGCCACCACTGTGGTG 180
QY 181 GAATGTTCTACAGGCCGAGGCGGTAAAGATTTCTTTATTTACAGATATCGGAATGCG 240
Db 181 GAGTGGTCTACAGGCTGAGGCGGTAAAGATTTCTTTATATATGAGTATCGGAATGCG 240
QY 241 CACGAGAGGTGAGAGCCCTTTACGGGCGCTGCACTGAGTGAATGCGAGGAGCACTG 300
Db 241 CACGAGAAAGTGAGAGCCCTTTCAAGGCGCTGCACTGAGTGAATGCGAGGAGCACTG 300
QY 301 CAGGAGGTGCATCACTGTGCTCAACGTCACCTGAAAGACTCTGCGCTCTACACCTGC 360
Db 301 CAGGAGTATCACTCACTGTGCTCAACGTCACCTGAAAGACTCTGCGCTCTACACCTGC 360
QY 361 AATGTCTCCGGAGTTTGAAGTGAAGGCGCATCGGCCCTTTGTGAAGACGAGCGGCTG 420
Db 361 AATGTCTCAGGAGTTTGAAGTGAAGGCGCATCGGCCCTTTGTGAAGACGAGACTG 420
QY 421 ATCCCTTAAGAGTACCGAGGAGGCTGAGAGGACTTCACCTCTGTGTCTCAGAAATC 480
Db 421 ATACCTTTGCGAGTCACTGAAGGCGGAGAGACTTCACCTCTGTGTCTCAGAAATC 480
QY 481 ATGATGTACATCTCTGTCTCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 481 ATGATGTACATCTCTGTCTCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 TACAGAAAGTCTCAAAAGCCGAGAGGAGGCGCCCAAGAAAGCGCTGCTGCTGCTGCTG 600
Db 541 TACAGAAAGTCTCTAAGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
QY 601 ATCCCATCTGAGAACAGAGAGACTCTGCGTACAGTGGAGAA 645
Db 601 ATCCCTTACAGAGAACAGAGAGACTCTGCGTACAGTGGAGAA 645

RESULT 6

US-10-029-191-23
; Sequence 23, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Lepus Sp.
US-10-029-191-23

Query Match 22.9%; Score 148.2; DB 13; Length 657;
Best Local Similarity 57.7%; Pred. No. 1.4e-37;
Matches 333; Conservative 0; Mismatches 223; Indels 21; Gaps 3;

QY 76 TGTGTGGAAGTGCCTTCGAGAGCGGAGGCGCTGTCAGGGCAACCCCATGAAGCTGCGCTGC 135
Db 61 TCGTGGAGTGGACTTCGAGAGCGGAGCGGTGTACGGGATGACCTTCAAAATTTCTGTGC 120
QY 136 ATCTCTGATGAGAGAGAGGAGGTGGAGGCCACACCGTGTGGAATGTTCTACAG 195
Db 121 ATCTCTGAAAGCGCCGAGAGGAGCCACCGGCGAGACCTTCACGAGTGGACCTTCCGC 180
QY 196 CCGAGGCGGTAAAGATT-----TCCTTATTTACAGTATCGGAATGCGCACCAAG 246

Db 181 CAGAAGGCACTGAGGAGTTTCTCAAGATCTCGCTATGAGAACGAGGTGCTGCAGCTG 240
QY 247 GAGGTGGAGAGCCCTTTTCAGGGGCGCTGCAAGTGAATGGCAG-----CAAGGAC 297
Db 241 GAGGAAGACGAGCGCTTTGAGGGCGCGTGTGTGAACGCGCAGCGCGGCGCACCAAGGAC 300
QY 298 CTGAGGAGCGTCTCATCTGCTCAACGTCACCTCTGAACGACTCTGGCCTCTACACC 357
Db 301 CTGAGGAGCGTCTCATCTTCACTCAATGTCCTCAACCACTCTGCGGCGACTACCAAG 360
QY 358 TCATATGTGTCGCGGAGTTTGAAGTGAAGGCGCATCGGCCCTTTGTGAAGACGAGCGCG 417
Db 361 TGCCATGTCTACCGCTGCTCTCTTCGAAACTACGAGCAACACACGAGCTCGTCAAG 420
QY 418 CTGATCCCTTAAGAGTACCGAGAGGCTGAGAGGACTTCACCTCTGTGTCTCAGAA 477
Db 421 AAGATCCACTCGAGGTGTGCAAGCAAGGCAACAGAGACATGGCATCCATCGTGTGCGAG 480
QY 478 ATCATGATGTACATCTCTGCTCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 537
Db 481 ATCATGATGTACATCTCTGCTCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 538 TCCTACAGAAAGTCTCAAAAGCCGAGAGGCA---GCCCAAGAAACCGCTCTGACTAC 594
Db 541 TCCTACAGAAAGTCTCGGCGCCGACGAGGCGCAGCGGCGCAGGAGACCGCTCGGAATAC 600
QY 595 CTGTCATCCCATCTGAGAACAAAGAGAGACTCTGCGG 631
Db 601 TTGGCCATCACCCTCAGAAAGCAAGAAATTCACGG 637

RESULT 7

US-10-723-860-2247
; Sequence 2247, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2247
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2247

Query Match 22.2%; Score 143.8; DB 18; Length 1335;
Best Local Similarity 56.9%; Pred. No. 5.1e-36;
Matches 334; Conservative 0; Mismatches 232; Indels 21; Gaps 3;

QY 66 CTTCTCTGTGTGTGGAAGTGCCTTCGAGAGCGGAGGCGCTGTCAGGGCAACCCCATGAA 125
Db 75 CTGCGGGGCTCGGTGGAGTGGACTCGGAGACCGAGGCGGTGTATGGATGACCTTCAA 134
QY 126 GCTGCGCTGCTCTCTGCTGATGAAGAGAGAGGTGGAGGCCACACCGTGTGGAATG 185
Db 135 AATTCTTTGCTCTCTGCAAGCGCGCAGGAGACCAACGCTGAGACCTTCACCGAGTG 194
QY 186 GTTCTACAGGCGCGGAGGCGGTAAAGATT-----TCCTTATTTACAGTATCGGAA 236
Db 195 GACCTTCCGAGAGGCGACTGAGAGTTTGTCAAGATCTTCGCTATGAGAAAGT 254
QY 237 TGGCCACCAAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTGCAAGTGAATGGCAG----- 290
Db 255 GTTGCAGCTGGAGGAGGATGAGCGCTTCGAGGGCGCGTGTGTGGAATGGCAGCGCGG 314

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; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-272-1

Query Match      21.9%;   Score 142.2;  DB 18;  Length 1414;
Best Local Similarity 56.7%;  Pred. No. 1.7e-35;
Matches 333; Conservative 0; Mismatches 233; Indels 21; Gaps 3;

Qy      66  CTTCCCTGTGTGTGGAAATGCCCTCGAGACGAGGCGCGTGCAGGCGCAACCCCATGAA 125
      151  CTGGGGGGCTGCGTGGAGGTGGACTCGAGACCGAGGCGGTGTATGGATGACCTTCAA 210

Qy      126  GCTGCGGTGCATCTCTGTCATGAAGAGAGAGGAGGTGGAGCCACCAAGGTGGTGGATG 185
      211  AATTCCTTTGTCATCTCTGTCGAAGCCCGAGCGAGACCAACGCTGAGACCTTTCACCGAGTG 270

Qy      186  GTTCTCAGGCGCCGAGGGCGGTAAAGATT-----TCCTTATTACGAGTATCGGAA 236
      271  GACCTTCGCGCCAGAAAGGCATGAGGAGTTGTCAAGATCCTCGCTATGAGATGAGGT 330

Qy      237  TGGCCACAGGAGGTGGAGAGCCCTTTTCAGGGCGCGCTGCAGTGGAAATGGCAG----- 290
      331  GTTGCACTGGAGGAGGATGAGTGCTTCGAGGGCGCGTGTGTGGAAATGGCAACCGGG 390

Qy      291  ---CAAGGACTCGAGGACGTGTCATCTGCTCAACGTCACCTCTGAACGACTCTGG 347
      391  CACCAAGAAGCTGCAGGATCTGTCTATCTTCATCACCNAATGTCACCTACACCACTCGGG 450

Qy      348  CCTCTACACCTGCAATGTGTCCCGGAGTTTGAATGTTTGGCGCGCATCGGCCCTTTTGGAA 407
      451  CGACTACAGGTGCCACGCTCTACCGCCTGCTCTTCTTCGAAAACTACGAGCAACACCCAG 510

Qy      408  GACGACGCGGTGATCCCCCTTAAGAGTCACCGAGGAGGCTGGAGGAGACTTTCACCTCTGT 467

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; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1654
; LENGTH: 1490
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_017288
US-09-917-800A-1654

Query Match          21.4%; Score 138.6; DB 9; Length 1490;
Best Local Similarity 56.7%; Pred. No. 2.6e-34;
Matches 327; Conservative 0; Mismatches 229; Indels 21; Gaps 3;

QY 76 TGTGTGGAAGTGCCTCGAGCGGAGCGGTGCGAGGCAACCCCATGAAGCTGCGCTCG 135
Db 280 TGGGTGGAGGTGAATCTGAGACCGGAGGAGTATGGGATGACCTTCAAAATCCTGTGT 339
QY 136 ATCTCTGTCATGAAGAGAGAGAGGTGAGAGGCCACCAACCGTGTGGAATGGTTCTACAG 195
Db 340 ATCTCTGTGAAGGTGTAGTGAGACCAACCGCGAGACCTTCACGGAGTGGACCTTCGCG 399
QY 196 CCGAGGCGGTTAAAGATT-----TCCTTATTTAGAGTATCGGAATGGCCACCGAG 246
Db 400 CAGAAGGCGACAGAGGAATTTGTCAAGATCCTACGCTATGAGAATGAGGTGCTGCGAGCTG 459
QY 247 GAGGTGAGAGGCCCTTTCAGGGGCGCTGCGAGTGAATGGCG-----CAAGGAC 297
Db 460 GAGGAAGATGAGCGCTTTGAGGCGCGTGTGTGTGAACGTTAGTCGGGCGACCAAGGAC 519
QY 298 CTGAGGAGGTGTCCATCACTGTGCTCAAGCTCACTCTGAACGACTCTGGCCTCTACACC 357
Db 520 CTGAGGACCTGTCCATCTTCATCAACCAATGTCAACCTACACCACTCTGGCGACTACGAA 579
QY 358 TGAATGTGTCCGGGAGTTTGAAGTTTGAAGCGCATCGGCGCTTTGTGAAGAGCGCGG 417
Db 580 TGTCAAGTCTACCGTCTCCTCTCTTTGTATTAATTACGAGCACAAACCAGCGCTGCTCAAG 639
QY 418 CTGATCCCTTAAGACTCACCGAGGAGGCTGAGAGGACTTCACCTCTGTGTTCTCAGAA 477
Db 640 AAGATCCACTGGAGTGTGGCAAGGCCAACAGAGATGATGCAATCCATCGTGTGTCAGAG 699
QY 478 ATCATGATGTACATCTCTTCTGTTCTTCTCACCCTGTGGTGTCTCATCGAGATGATATAT 537
Db 700 ATCATGATGTACGTCTCATTTGTTGTTTAAACCATATGGCTGTGGCGAGATGGTGTAC 759
QY 538 TGTCTACAGAAAGTGTCTAAAGGCC----GAAGGCGAGCCCGAGAAACCGGTCTGACTAC 594
Db 760 TGTCTACAGAAAGTGTCTGTGTCAGCGAAGTGTGTCACAGAGAAATGCTCTCGGAATAC 819
QY 595 CTTGCGCATCCATCTCAGAACCAAGGAGAACTCTGCGG 631
Db 820 CTGGCCATTACTTCCGAGAGCAAGAGAACTGTACAG 856
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RESULT 11
US-10-401-916-12

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; Sequence 12, Application US/10401916
; Publication No. US20040002439A1
; GENERAL INFORMATION:
; APPLICANT: Qin, Ning
; APPLICANT: Codd, Ellen
; APPLICANT: D'Andrea, Michael
; TITLE OF INVENTION: DNAs encoding human betala sodium channel subunit
; FILE REFERENCE: ORT-1221
; CURRENT APPLICATION NUMBER: US/10/401,916
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/875,456A
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-401-916-12

Query Match          12.6%; Score 81.4; DB 17; Length 807;
Best Local Similarity 57.5%; Pred. No. 1e-15;
Matches 195; Conservative 0; Mismatches 126; Indels 18; Gaps 2;

QY 66 CTTCCCTGTGTGTGTGGAAGTCCCTCGGAGACGAGGCGCGTGCAGGCAACCCCATGAA 125
Db 51 CTGCGGGGCTGCGTGGAGGTGACTCGGAGACCGGAGCGCGTGTATGGGATGACCTTCAA 110
QY 126 GCTGGCGTGCATCTCTCTGATGAAGAGAGAGAGGTGAGGCGCACCCACCGTGTGGAATG 185
Db 111 AATTCTTTCATCTCTCTCAAGCGCGCAGCGACCAACGCTGAGACCTTCACCGAGTG 170
QY 186 GTTCTACAGGCCCGGAGCGGGTAAGATT-----TCCTTATTTAGAGTATCGGAA 236
Db 171 GACCTTCCGCCAAGAGGCACTGAGGAGTTTGTCAAGATCTCTCGCTATGAGAATGAGGT 230
QY 237 TGGCCACAGGAGGTGAGAGCGCCCTTTCAGGGGCGCTTCAGTGGAAATGGCGAG----- 290
Db 231 GTTGCAGCTTGGAGAGGATGAGCGCTTCGAGGCGCGCTGTGGAATGGCGAGCGGG 290
QY 291 ---CAAGGACCTGCGAGGAGCTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTGG 347
Db 291 CACCAAGACCTGCGAGGATCTGTCTATCTTCATCAACCAATGTCACTCAACCACTCGGG 350
QY 348 CTTCTACACTGCAATGTGTCCGGGAGTTGAGTTGA 386
Db 351 CGACTACGAGTGCACGCTACCGCTGCTCTTCTTCTGA 389
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RESULT 12

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US-10-401-916-13
; Sequence 13, Application US/10401916
; Publication No. US20040002439A1
; GENERAL INFORMATION:
; APPLICANT: Qin, Ning
; APPLICANT: Codd, Ellen
; APPLICANT: D'Andrea, Michael
; TITLE OF INVENTION: DNAs encoding human betala sodium channel subunit
; FILE REFERENCE: ORT-1221
; CURRENT APPLICATION NUMBER: US/10/401,916
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/875,456A
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-401-916-13
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Query Match 12.6%; Score 81.4; DB 17; Length 974;
Best Local Similarity 57.5%; Pred. No. 1.1e-15;


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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (294)..(315)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1696)..(1712)
; OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-6471

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Query Match      7.5%; Score 48.6; DB 18; Length 3583;
Best Local Similarity 63.0%; Pred. No. 9.1e-05;
Matches 75; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY      454 GACTTCACCTCTGTGGTCTCAGAAATCATGATCATCTTCTGGTCTTCTCACCCTG 513
Db      2229 GACATGGCATCCATCGTGTCTGAGATCATGATGTGTGTCATTGGTGTGACCATA 2288

QY      514 TGGCTGCTCATCGAGATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAAAGGCGAGC 572
Db      2289 TGGCTGCTGCGCAGAGATGATTTACTGCTACAGAGAGATGCTGCCGCCACGAGAGACTGC 2347

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Search completed: April 7, 2005, 15:19:35
Job time : 583.168 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 08:50:34 ; Search time 3865.9 Seconds
(without alignments)
6380.306 Million cell updates/sec

Title: US-09-977-579-4_COPY_376_1023
Perfect score: 648
Sequence: 1 atgcctgcctcaatagatt.....cggtagcaggaggagaatg 648

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_hic.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_gss1.*
- 9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	646.4	99.8	648	9	AY419145	AY419145 Homo sapi
2	646.4	99.8	2555	3	CR609664	CR609664 full-leng
3	646.4	99.8	4052	3	HSM801563	AL136589 Homo sapi
4	646	99.7	1052	5	EX420015	EX420015 BX420015
5	624.4	96.4	975	5	EX445002	EX445002 BX445002
6	546.8	84.4	582	9	BP200910	BP200910 BP200910
7	536.6	82.8	648	9	AY419147	AY419147 Mus muscu
8	536.6	82.8	1359	3	AK076466	AK076466 Mus muscu
9	536.6	82.8	3549	3	AK049747	AK049747 Mus muscu
10	525.6	81.1	4149	3	AK049286	AK049286 Mus muscu
11	518	79.9	636	5	BM933157	BM933157 UI-M-BH3-
12	510.8	78.8	672	2	BB614118	BB614118 BB614118
13	508.2	78.4	4105	3	BC058083	BC058083 Mus muscu
14	468	72.2	950	4	BG294174	BG294174 602391245
15	465	71.8	584	9	AY419146	AY419146 Pan trogl
16	461.4	71.2	584	5	BP361278	BP361278 BP361278
17	447.6	69.1	723	6	CA749311	CA749311 UI-M-FY0-
18	420.8	64.9	927	5	BP311484	BP311484 BP311484
19	408.4	63.0	927	5	BQ713131	BQ713131 AGENCOURT
20	385.2	59.4	825	5	BQ745919	BQ745919 UI-M-EXO-
21	382.4	59.0	846	6	CD355879	CD355879 UI-M-FY0-
22	370.4	57.2	1069	5	BM928131	BM928131 AGENCOURT
23	357.8	55.2	742	6	CB526211	CB526211 UI-M-FY0-
24	351	54.2	986	5	BU118914	BU118914 603142291

25	348.4	53.8	845	6	CA327438	CA327438 UI-M-FY0-
26	345.2	53.3	692	7	CN219870	CN219870 WLA010B08
27	343.6	53.0	700	4	BI739617	BI739617 603361873
28	336.2	51.9	652	2	BB652801	BB652801 BB652801
29	330.6	51.0	892	5	BU368614	BU368614 603790206
30	326	50.3	595	5	BU368531	BU368531 603788820
31	310	47.8	450	6	CB787935	CB787935 AMGNNUC:N
32	303.2	46.8	823	7	CO428886	CO428886 UI-M-HXO-
33	302.8	46.7	734	7	CK367344	CK367344 AGENCOURT
34	301.6	46.5	712	6	CB526257	CB526257 UI-M-FY0-
35	299.6	46.2	780	5	BQ770528	BQ770528 UI-M-FY0-
36	294.6	45.5	582	5	BP202832	BP202832 BP202832
37	291.6	45.0	750	6	CD349206	CD349206 UI-M-FY0-
38	286	44.1	895	5	EX743834	EX743834 BX743834
39	281.6	43.5	714	7	CF531573	CF531573 UI-M-FY0-
40	273	42.1	669	5	BM951151	BM951151 UI-M-RHO-
41	266.4	41.1	471	6	CB732717	CB732717 AMGNNUC:N
42	258.8	39.9	705	6	CD349958	CD349958 UI-M-FY0-
43	255.8	39.5	798	7	CF290312	CF290312 AGENCOURT
44	248.8	38.4	544	7	CN666608	CN666608 A0842F07-
45	248.8	38.4	650	7	CN665870	CN665870 A0832C11-

ALIGNMENTS

AY419145 Homo sapiens HCM6793 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. 648 bp DNA linear GSS 12-DEC-2003

AY419145 GSS. GI:39775105

AY419145 Homo sapiens (human)

REFERENCE 1 (bases 1 to 648)

AUTHORS Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 648)

AUTHORS Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT These sequences were made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1..648

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

<1..>648

/locus_tag="HCM6793"

Query Match 99.8%; Score 646.4; DB 9; Length 648;
Best Local Similarity 99.8%; Pred. No. 2.3e-163;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCCTGCCTCAATAGATTGTTCCCTGGCTCTCTCGTCTTACTTCTGGTGGTCACT 60
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DB 1 ATGCCTGCCTCAATAGATTGTTCCCTGGCTCTCTCGTCTTACTTCTGGTGGTCACT 60
|||||

[illegible]

```
CONSRM      The German cDNA Consortium
TITLE       Direct Submission
JOURNAL     Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
           Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
           Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
           sequenced by Medigenomix (Martinried/Germany) within the cDNA
           sequencing Consortium of the German Genome Project.
           This clone (DKFZp761F182) is available at the RZPD Deutsches
           Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
           Please contact RZPD for ordering:
           http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp761F182
           Further information about the clone and the sequencing project is
           available at http://mips.gsf.de/projects/cdna/.

FEATURES             Location/Qualifiers
     source            1..4052
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                     /mol_type="mRNA"
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                     /db_xref="taxon:9606"
                     /clone="DKFZp761F182"
                     /tissue_type="amygdala"
                     /clone_lib="761 (synonym: hamy2). Vector pSport1; host
                     DH10B; sites NotI + SalI"
                     /dev_stage="adult"
                     /note="voltage-gated sodium channel beta-3 subunit"
     gene              1..4052
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     CDS               804..1451
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                     /codon_start=1
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                     /protein_id="CAB66524.1"
                     /db_xref="GI:13276681"
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                     /db_xref="UniProt/Swiss-Prot:Q9NY72"
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                     VITVLNVLTANDSLGVTCNVSREFFEFHAPFPVKTTLPLRVTEAGEDFTSVSEI
                     MMVILLVFLTLMLLIEMIYCYRKVKRAEAAQENASDYLALPSENKENSAPVEE"

ORIGIN
Query Match      99.8%; Score 646.4; DB 3; Length 4052;
Best Local Similarity 99.8%; Pred. No. 3.6e-163;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ATGCTGCTCCCTCAATAGATTGTTTCCCTCGCTTCTCTCGTCTATCTACTGGTCAGT 60
DB      804 ATGCTGCTCCCTCAATAGATTGTTTCCCTCGCTTCTCTCGTCTATCTACTGGTCAGT 863

QY      61  GTCTGCTTCCCTGTGTGTGGAAAGTGCCCTCGGAGACGAGCGCGTGCAAGGCAACCCC 120
DB      864 GTCTGCTTCCCTGTGTGTGGAAAGTGCCCTCGGAGACGAGCGCGTGCAAGGCAACCCC 923

QY      121 ATGAAGCTGCGCTGCATCTCTCTGCATGAAGAGAGAGAGGTGGAGGCCACACGGTGGTG 180
DB      924 ATGAAGCTGCGCTGCATCTCTCTGCATGAAGAGAGAGAGGTGGAGGCCACACGGTGGTG 983

QY      181 GAATGTTTACAGGCCCGGAGGGCGTAAAGATTCTTATTACAGTATCGAATGGC 240
DB      984 GAATGTTTACAGGCCCGGAGGGCGTAAAGATTCTTATTACAGTATCGAATGGC 1043

QY      241 CACGAGAGGTGGAGAGCCCTTTTCAGGGCGCGCTGCAGTGGAAATGGCAGCAGGACCTG 300
DB      1044 CACGAGAGGTGGAGAGCCCTTTTCAGGGCGCGCTGCAGTGGAAATGGCAGCAGGACCTG 1103

QY      301 CAGGACGTGTCATCACTGTGCTCAACGTCATCTGTAACGACTCTGGCCCTCTACACCTGC 360
DB      1104 CAGGACGTGTCATCACTGTGCTCAACGTCATCTGTAACGACTCTGGCCCTCTACACCTGC 1163

QY      361 AATGTGTCGGGAGTTGATTTGAGCGCGATCGGCCCTTTGTGAAGACGACGCGGCTG 420
DB      1164 AATGTGTCGGGAGTTGATTTGAGCGCGATCGGCCCTTTGTGAAGACGACGCGGCTG 1223
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QY      421 ATCCCTTAAGAGCTCACCGAGGAGGCTTGGAGAGGACTTACCTCTGTGTCTCAGAAATC 480
DB      1224 ATCCCTTAAGAGCTCACCGAGGAGGCTTGGAGAGGACTTACCTCTGTGTCTCAGAAATC 1283

QY      481 ATGATGTACATCCTTCTGTGTTCTTCTCACCTGTGGCTGTCTATCGAGATGATATATTC 540
DB      1284 ATGATGTACATCCTTCTGTGTTCTTCTCACCTGTGGCTGTCTATCGAGATGATATATTC 1343

QY      541 TACAGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGGCTGTGACTACCTTGGC 600
DB      1344 TACAGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGGCTGTGACTACCTTGGC 1403

QY      601 ATCCCATCTGAGAACAAAGGAGAACTCTCGGTACCAGTGGAGGAATAG 648
DB      1404 ATCCCATCTGAGAACAAAGGAGAACTCTCGGTACCAGTGGAGGAATAG 1451

RESULT 4
BX420015 LOCUS          1062 bp      mRNA      linear      EST 01-MAY-2004
DEFINITION BX420015 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
ACCESSION  CS0DF023YA09 5-PRIME, mRNA sequence.
VERSION     BX420015
KEYWORDS    BX420015.2 GI:46929710
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 1062)
AUTHORS    Li, W.-B., Gruber, C., Jesse, J. and Polaves, D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL    Unpublished (2001)
COMMENT    On May 13, 2003 this sequence version replaced gi:30646738.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 6147.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?8=CS0DF023AA05QP1&c=6147.r.

FEATURES             Location/Qualifiers
     source            1..1062
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DF023YA09"
                     /tissue_type="FETAL BRAIN"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."

ORIGIN
Query Match      99.7%; Score 646; DB 5; Length 1062;
Best Local Similarity 99.7%; Pred. No. 3.3e-163;
Matches 646; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1  ATGCTGCTCCCTCAATAGATTGTTTCCCTCGGCTTCTCTCGTCTATCTACTGGTCAGT 60
DB      234 ATGCTGCTCCCTCAATAGATTGTTTCCCTCGGCTTCTCTCGTCTATCTACTGGTCAGT 293

QY      61  GTCTGCTTCCCTGTGTGTGGAAAGTGCCCTCGGAGACGAGCGCGTGCAAGGCAACCCC 120
DB      1164 GTCTGCTTCCCTGTGTGTGGAAAGTGCCCTCGGAGACGAGCGCGTGCAAGGCAACCCC 120
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294 GTCTGCTCCCTGTGTGTGGAGTGCCTCGGAGACGAGGCGCTGAGGGCAACCCC 353
 121 ATGAAGCTCGCTGCATCTCTCTGATGAAGAGAGAGAGGTGGAGCCACCAACGCTGGTG 180
 354 ATGAAGCTCGCTGCATCTCTCTGATGAAGAGAGAGAGGTGGAGCCACCAACGCTGGTG 413
 181 GAATGTTCTACAGGCGCGAGGCGGTAAAGATTTCTTTATACAGATATCGGAATGCG 240
 414 GAATGTTCTACAGGCGCGAGGCGGTAAAGATTTCTTTATACAGATATCGGAATGCG 473
 241 CACAGAGGTGGAGAGCCCTTTACGGGCGCTGCAATGGAATGGAGAGGAGACCTG 300
 474 CACAGAGGTGGAGAGCCCTTTACGGGCGCTGCAATGGAATGGAGAGGAGACCTG 533
 301 CAGAGAGGTGCATCATCTGTCTCAACGTCATCTGAAAGAGCTCTGACCTCTACACCTGC 360
 534 CAGAGAGGTGCATCATCTGTCTCAACGTCATCTGAAAGAGCTCTGACCTCTACACCTGC 593
 361 ATGTGTCGGGAGTTGAGTTGAGGCGCATCGGCGCTTTGGAAGACGAGCGGCTG 420
 594 ATGTGTCGGGAGTTGAGTTGAGGCGCATCGGCGCTTTGGAAGACGAGCGGCTG 653
 421 ATCCCTCAAGAGTCAACGAGGAGGCTGGAGAGGACTTCACTCTGTGCTCTCAGAAATC 480
 654 ATCCCTCAAGAGTCAACGAGGAGGCTGGAGAGGACTTCACTCTGTGCTCTCAGAAATC 713
 481 ATGATGATCATCTCTGTCTCTCTCACTCTGCTGTGCTCTCATGAGATGATATATGCG 540
 714 ATGATGATCATCTCTGTCTCTCTCACTCTGCTGTGCTCTCATGAGATGATATATGCG 773
 541 TACAGAAAGGTCTCAAAAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
 774 TACAGAAAGGTCTCAAAAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 833
 601 ATCCATCTGAGAAACGAGAGGAGTCTGCGGTACCAAGTGGAGGAGATAG 648
 834 ATCSATCTGAGAAACGAGAGGAGTCTGCGGTACCAAGTGGAGGAGATAG 881

RESULT 5
 BX445002
 LOCUS
 DEFINITION
 BX445002 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 CSODP023YA09 5-PRIME, mRNA sequence.
 BX445002.2 GI:47009181
 EST.
 Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 975)
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 15, 2003 this sequence version replaced gi:30782286.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 6147.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CSIAF0062E05QPl&c=6147.r.
 1. .975
 Location/Qualifiers

FEATURES
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 /mol_type="mRNA"
 /db_xref="taxon:9606"

/clone="CSODP023YA09"
 /tissue_type="FETAL BRAIN"
 /dev_stage="fetal"
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 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Query Match 96.4%; Score 624.4; DB 5; Length 975;
 Best Local Similarity 98.8%; Pred No. 2.2e-157;
 Matches 636; Conservative 3; Mismatches 4; Indels 1; Gaps 1;
 QY 1 ATGCTGCTCCCTCAATAGATTTGTTCCCTCGGCTTCTCTGCTCTTATCTACCTGGTCACT 60
 DB 235 ATGCTGCTCCCTCAATAGATTTGTTCCCTCGGCTTCTCTGCTCTTATCTACCTGGTCACT 294
 QY 61 GTCTGCTCCCTGTGTGTGGAAGTGCCTCGGAGACGAGGCGCTGAGGGCAACCCC 120
 DB 295 GTCTGCTCCCTGTGTGTGGAAGTGCCTCGGAGACGAGGCGCTGAGGGCAACCCC 354
 QY 121 ATGAAGCTCGCTGCATCTCTCTGATGAAGAGAGGAGGTGGAGCCACCAACGCTGGTG 180
 DB 355 ATGAAGCTCGCTGCATCTCTCTGATGAAGAGAGGAGGTGGAGCCACCAACGCTGGTG 414
 QY 181 GAATGTTCTACAGGCGCGAGGCGGTAAAGATTTCTTTATACGAGTATCGGAATGCG 240
 DB 415 GAATGTTCTACAGGCGCGAGGCGGTAAAGATTTCTTTATACGAGTATCGGAATGCG 474
 QY 241 CACAGAGGTGGAGAGCCCTTTACGGGCGCTTGCAGTGAATGGAGGAGGAGGAGGAGG 300
 DB 475 CACAGAGGTGGAGAGCCCTTTACGGGCGCGCTTGCAGTGAATGGAGGAGGAGGAGG 534
 QY 301 CAGGAGCTGTCCATCACTGTGCTCAACGTCATCTGAAAGAGTCTGCGCTCTACACCTGC 360
 DB 535 CAGGAGCTGTCCATCACTGTGCTCAACGTCATCTGAAAGAGTCTGCGCTCTACACCTGC 594
 QY 361 AATGTGTCGGGAGTTGAGTTGAGGCGCATCGGCGCTTTGTGAAGACGAGCGGCTG 420
 DB 595 AATGAAGTTCGGGAGTTGAGTTGAGGCGCATCGGCGCTTTGTGAAGACGAGCGGCTG 654
 QY 421 ATCCCTCAAGAGTCAACGAGGAGGCTGGAGAGGACTTCACTCTGTGCTCTCAGAAATC 480
 DB 655 ATCCCTCAAGAGTCAACGAGGAGGCTGGAGAGGACTTCACTCTGTGCTCTCAGAAATC 714
 QY 481 ATGATGATCATCTCTGTGCTCTCTCACTCTGCTGTGCTCTCATGAGATGATATATGCG 540
 DB 715 ATGATGATCATCTCTGTGCTCTCTCACTCTGCTGTGCTCTCATGAGATGATATATGCG 774
 QY 541 TACAGAAAGGTCTCAAAAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
 DB 775 TACAGAAAGGTCTCAAAAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 834
 QY 601 ATCCATCTGAGAAACGAGAGGAGTCTGCGGTACCAAGTGGAGGAGATAG 644
 DB 835 ATCCATCTGAGAAACGAGAGGAGTCTGCGGTACCAAGTGGAGGAGATAG 877

RESULT 6

BP200910
 LOCUS
 DEFINITION
 BP200910 Sugano cDNA library, amygdala Homo sapiens cDNA clone
 AMR03894, mRNA sequence.
 ACCESSION
 VERSION
 BP200910
 KEYWORDS
 EST.
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 582)

AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yezuzuki@ims.u-tokyo.ac.jp.

FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="AMR03894"
 /tissue_type="amygdala"
 /clone_lib="Sugano cDNA library, amygdala"

ORIGIN

Query Match	84.4%;	Score 546.8;	DB 5;	Length 582;
Best Local Similarity	99.6%;	Pred. No. 1.8e-136;		
Matches 548;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	3	GCCTGCCCTTCAATAGATGTTTCCCTGGCTCTCTCGTCTTATCTACTGGGTCACTGT	62
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Qy	63	CTGCTTCCCTGTGTGTGGAGTGCCTCGGAGACGGAGCCGTGAGGGCAACCCCAT	122
Db	93	CTGCTTCCCTGTGTGTGGAGTGCCTCGGAGACGGAGCCGTGAGGGCAACCCCAT	152
Qy	123	GAAGCTCGCTGCATCTCCTGCATGAAGAGAGAGAGGTGAGGCCACACCGTGTGGGA	182
Db	153	GAAGCTCGCTGCATCTCCTGCATGAAGAGAGAGAGGTGAGGCCACACCGTGTGGGA	212
Qy	183	ATGCTTCTCAAGGCCCGAGGGCGTGAAGATTTCTTATTTACAGTATCGGAATGGCCA	242
Db	213	ATGCTTCTCAAGGCCCGAGGGCGTGAAGATTTCTTATTTACAGTATCGGAATGGCCA	272
Qy	243	CCAGGAGTGGAGAGCCCTTTACAGGGCGCTGACGTGGAATGGACGAGACCTTGCA	302
Db	273	CCAGGAGTGGAGAGCCCTTTACAGGGCGCTGACGTGGAATGGACGAGACCTTGCA	332
Qy	303	GGACGTGTCCATCACTGTGTCTCAACGTCACTCTGAACGACTCTGGCTCTACACCTGCAA	362
Db	333	GGACGTGTCCATCACTGTGTCTCAACGTCACTCTGAACGACTCTGGCTCTACACCTGCAA	392
Qy	363	TGTGTCCCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGGGCTGAT	422
Db	393	TGTGTCCCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGGGCTGAT	452
Qy	423	CCCCCTAAGAGTCAACGAGAGGCTGAGAGGACTTCACTCTGTGTCTCAGAAATCAT	482
Db	453	CCCCCTAAGAGTCAACGAGAGGCTGAGAGGACTTCACTCTGTGTCTCAGAAATCAT	512
Qy	483	GATGTACATCCTTCTGTCTTCTTCTTCCATCCCTGTGTGCTCTCATCGAGATGATATTGCTA	542
Db	513	GATGTACATCCTTCTGTCTTCTTCTTCCATCCCTGTGTGCTCTCATCGAGATGATATTGCTA	572
Qy	543	CAGAAAGGTC 552	
Db	573	CAGAAAGGTC 582	

RESULT 7	AV419147	648 bp	DNA	linear	GSS 12-DEC-2003
LOCUS	AV419147				
DEFINITION	Mus musculus HCM6793 gene, VIRTUAL TRANSCRIPT, partial sequence,				
ACCESSION	AV419147				
VERSION	AV419147.1	GI:39775107			
KEYWORDS	GSS.				

Qy 421 ATCCCCCTAAGAGTACCGAGGAGGCTGGAGAGGACTTCACTCTGTGGTCTCAGAAATC 480
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 Db 477 ATACCCCTGCAGTCACTGAAGAGCGGAGAGACTTCACTCTGTGGTCTCAGAAATC 536
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 Qy 481 ATGATGTACATCCTTCTGTCTTCTCACTCCTGTGGTCTCATCGAGATGATATATGTC 540
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 Db 537 ATGATGTACATCCTCCTGTCTTCTCACTCCTGTGGTCTTATTTAGATGATCTATGTC 596
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 Qy 541 TACAGAAAGGTCTCAAGAGCGGAGAGGAGCCCAAGAAACGGTCTGACTACCTTGCC 600
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 Db 597 TACAGAAAGGTCTCTAAGCGCGAGAGGAGCACTCAGGAAATGCGTGTGACTACCTTGCT 656
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 Qy 601 ATCCCATCTGAGAACAGGAGAACTCTCGCGTACAGTGGAGGAATA 647
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 Db 657 ATCCCTTCAGAGAACAGGAGAACTCTGTGTACCTCCGTTGGAGGAATA 703
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RESULT 9
 AK049747
 LOCUS
 DEFINITION
 Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:CS30046E12 product:VOLTAGE-GATED SODIUM CHANNEL BETA-3 SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog [Rattus norvegicus], full insert sequence.

ACCESSION
 AK049747
 VERSION
 HTc; CAP trapper.
 KEYWORDS
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1
 Carninci, P. and Hayashizaki, Y.
 TITLE
 High-efficiency full-length cDNA cloning
 JOURNAL
 Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE
 99279253
 PUBMED
 10349636

REFERENCE
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL
 Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE
 20499374
 PUBMED
 11042159

REFERENCE
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL
 Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE
 20530913
 PUBMED
 11078861

TITLE
 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 JOURNAL
 Functional annotation of a full-length mouse cDNA collection
 NATURE 409, 685-690 (2001)

REFERENCE
 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 NATURE 420, 563-573 (2002)
 JOURNAL
 Nature 420, 563-573 (2002)
 REFERENCE
 6
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL:http://genome.gsc.riken.jp/
 URL:http://fantom.gsc.riken.jp/.

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 Db 292 GTCTGCTTCCCTGTGTGTAGAAAGTACCTCGGAGACAGACGCGTGCAGGGCAATCC 351
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RESULT 10
AK049286
LOCUS
DEFINITION
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clone: C330019103 product: VOLTAGE-GATED SODIUM CHANNEL BETA-3
SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog [Rattus
norvegicus], full insert sequence.

ACCESSION
AK049286
VERSION
AK049286.1 GI:26093400
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
PUBMED

REFERENCE
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
PUBMED

REFERENCE
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Iehi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanishi, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
PUBMED

REFERENCE
4 The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection

JOURNAL
REFERENCE
AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
JOURNAL
REFERENCE
AUTHORS
Nature 409, 685-690 (2001)
5
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
FEATURES
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Matches 578; Conservative 0; Mismatches 69; Indels 1; Gaps 1;
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QY 180 GGAATGGTTCTACAGGCGCCGAGGCGGTAAAGATTTCCTTATTTACAGTATCGGAATGG 239
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RESULT 11

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LOCUS BM933157
DEFINITION UI-M-BH3-bsq-d-04-0-UI.r1 NIH BMAP M S4 Mus musculus cDNA clone
ACCESSION BM933157
VERSION BM933157.1 GI:19392309
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 636)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@nih.gov
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 REVERSE.
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FEATURES

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NIH_BMAP_M_S4 library is a subtracted library of a series,
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hippocampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: NIH_BMAP_M_S4,
NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S1,
NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library
(NIH_BMAP_M_S4) was constructed as follows: PCR amplified
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NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
NIH_BMAP_M_S4 library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)"

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ORIGIN

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Db 307 CAGGAGGTTCCATCACTGTGCTCAACGTCACCTCTGAAGAGCTCTGCGCTCT 366
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Db 367 AATGTTCCCGGAGTTTGAAGGCGCATCGGCGCTTGTGAAGAGGAGCGGCTG 426
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Db 427 ATACCTTCCGAGTCACTGAAGAGGCGGAGAGAGCTTCACTCTCTGCTGCT 486
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RESULT 12
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LOCUS   BB614118 RIKEN full-length enriched, 0 day neonate head Mus
DEFINITION Mus musculus cDNA clone 4833414B02 5', mRNA sequence.
ACCESSION BB614118
VERSION   BB614118.1 GI:16454578
KEYWORDS
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Kira,A.
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamana,K.I.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
Location/Qualifiers
1. 672
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FEATURES
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BC058083
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/clone_lib="RIKEN full-length enriched, 0 day neonate
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGGATCCAGAGCTCTTTTTTTTTTTVN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATTCGAGTTAATAATATCCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FIC I."
ORIGIN
Query Match      78.8%; Score 510.8; DB 2; Length 672;
Best Local Similarity 89.2%; Pred. No. 9.6e-127;
Matches 551; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
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QY      361  AATGTGTCCGGGAGTTTGAGTTTGAGGGCGCATCGGCCCTTTGTGAAGACGAGCGGGCTG 420
Db      415  AATGTGTCCAGGGAGTTTGAGTTTGAGGACACACCGGCCCTTTGTGAAGACCAAGACTA 474
QY      421  ATCCCTCTAAGAGTCACCGAGAGGCTGCGAGAGGACTTTCACCTCTGTGGTCTCGAAATC 480
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QY      481  ATGATGTACATCTCTTGGTCTTCTTCACTCTGAGTGGTGTCTCATCGAGATGATATTGC 540
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DEFINITION Mus musculus sodium channel, voltage-gated, type III, beta, mRNA
(cDNA clone IMAGE:6826414), containing frame-shift errors.
ACCESSION BC058083
VERSION BC058083.1 GI:34784518
KEYWORDS HTc.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schreitz, T.E., Brownstein, M.J., Ustin, T.B., Toshnyuki, S.,
Kernin, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahney, J., Helton, E., Kretzeman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalios, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 4105)
Strausberg, R.
Direct Submission
Submitted (08-SEP-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalios, Michael Smith, Lorraine Spence, Jeff Scott,
Michael Thorne, Miranada Tsai, Natsaja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
Series: IRAK Plate: 126 Row: 1 Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 23943798
This clone has the following problem: frame shifted.
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/tissue_type="Brain, mouse, 13.5,14.5,16.5,17.5 dpc"
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FEATURES
source

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ORIGIN
Query Match 78.4%; Score 508.2; DB 3; Length 4105;
Best Local Similarity 88.7%; Pred. No. 7.6e-126;
Matches 574; Conservative 0; Mismatches 68; Indels 5; Gaps 2;

QY 1 ATCCCTGCCTTCAATAGATTGTTCCCTCGGCTCTCTCGTCTTACTACTGGTCAGT 60
DB 356 ATCCCTGCCTTCAACAGATTGCTTCCCTAGCTCTCTAGTGTCTATCTACTGG- 411
QY 61 GTCTGCTTCCCTGTGTGTGTGGAGTGCCTCCGAGACGAGGCGCGTGCAGGCAACCCC 120
DB 412 GTCTGCTTCCCTGTGTGTGTAGAGTACCTCCGAGACAGAGCCGCTGAGGCAATTCC 471
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DB 592 CACAGGAGGTGAGAGAGCCCTTTCCAAGGTCGTCGAGTGAATGGAGCAAGACCTG 650
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DB 651 CAGGAGGTATCATCATCTGTCTCAATGTCATCTCTGAATGACTCTGGCCTCTACATGT 710
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DB 711 AATGTCGTCAGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTCTGAGAGCAACAAGACTA 770
QY 421 ATCCCTTCAAGAGTCAACGAGGAGGTGAGAGGACTTCACTCTCTGTGTCTCAGAAATC 480
DB 771 ATACCTCTCGAGTCACTGAAGAGGCGGAGAGACTTCACTCTCGTGTCTCGGAATC 830
QY 481 ATGATGTACATCTCTCTGCTTCTCCTCACCCTGTGCTCTCATCGAGATGATATATGC 540
DB 831 ATGATGTACATCTCTCTGCTTCTCTCACCCTGTGCTCTTATTGAGATGATCTATTC 890
QY 541 TACAGAAAGGTCTCAAAAGCCGAGAGGCGAGCCCAAGAAACCGCTCTGACTACCTTGCC 600
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RESULT 14
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LOCUS
DEFINITION 602391245F1 NTH_MGC_94 Mus musculus cDNA clone IMAGE:4503250 5',
mRNA sequence.
ACCESSION BG294174
VERSION BG294174.1 GI:13054543
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.

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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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 High quality sequence stop: 643.
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 Site:2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 3.3 kb. Library enriched for
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 Note: this is a NIH_MGC Library."

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Db	207	ATGAAGCTGAGATGCATCTCTGTCATGAAGAGGGAGGAGGTGGAGGCCACCACTGTAGTG	265
Qy	181	GAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC	240
Db	267	GAGTGGTTCTACAGGCCCTGAGGGCGGTAAAGATTTCCTTATATATGAGTATCGGAATGGC	325
Qy	241	CACCAGAGGTGGAGAGCCCTTTTCAGGGCGCGCTGCAGTGGAAATGCAGCAAGGACCTG	300
Db	327	CACCAGAGGTGGAGAGCCCTTCCAAAGTCTGTGCAGTGGAAATGGAGCAAGACCTG	385
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RESULT 15
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 LOCUS Pan troglodytes HCM6793 gene, VIRTUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.

ACCESSION	AY419146
VERSION	AY419146.1
KEYWORDS	GI:39775106
SOURCE	GSS.
ORGANISM	Pan troglodytes (chimpanzee)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. 1 (bases 1 to 584)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Infering nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2 (bases 1 to 584)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	These sequences were made by sequencing genomic exons and ordering them based on alignment.
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Best Local Similarity	80.1%; Pred. No. 2.2e-114;
Matches 468; Conservative	0; Mismatch 116; Indels 0; Gaps 0
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Dd	1 ATGCTGCCCTTCATAGATTGTTCCTCGTGCCTTCTCGTGCTTATCTACTGGGTCACT 60
Qy	61 GTCTGCTTCCTGTGTGTGGAAAGTGCCTTCGGAGACGGAGCCGTGAGGGCAACCCC 120
Dd	61 GTCTGCTTCCTGTGTGTGGAAAGTGCCTTCGGAGACGGAGCCGTGAGGGCAACCCC 120
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 05:42:10 ; Search time 5458 Seconds
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Searched: 4708233 seqs, 24227607955 residues

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 18	216	17.1	178431	2 AP002749	AP002749 Homo sapi
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c 45	23	1.8	190037	2	CR394567	CR394567 Danio rer

ALIGNMENTS

RESULT 1
LOCUS AR359850 1261 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 4 from patent US 6593565.
ACCESSION AR359850
VERSION AR359850.1 GI:33766660
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1261)
AUTHORS Heslin,P. and Lynam,N.R.
TITLE Vehicle interior rearview mirror assembly including an accessory-containing housing
JOURNAL Patent: US 6593565-A 4 15-JUL-2003;
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/mol_type="genomic DNA"

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Db 1	CCCTCCCTCCGAGCTGAGCTTACCTCTGGCGGCAACGAGCGAGGCGCGAGTGG	60			
Qy 61	AAGCTGGAGTTCGCGGGTGGCGGGGAGGCGGAGTGTCCGTGGTCTGAGCGCGCGAGA	120			
Db 61	AAGCTGGAGTTCGCGGGTGGCGGGGAGGCGGAGTGTCCGTGGTCTGAGCGCGCGAGA	120			
Qy 121	GCGGGCGCGAGCGGCTGATCGGCTCCCTCAACTGGGGAGGTCAGTGGGGTGCCTTAG	180			
Db 121	GCGGGCGCGAGCGGCTGATCGGCTCCCTCAACTGGGGAGGTCAGTGGGGTGCCTTAG	180			
Qy 181	GGCCCCAAAGCCCCACCCGCTCCAAAAGCTCCACAGGCTCCCGAGGCGACCGGTGCTCG	240			
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Db 301 AAAGATCTGAGAGGCGCAGTCCTTGACCGAGGAATCTCTGTGTAGCCTTGAAGC 360
Qy 361 CGCAGCCCGCAGAGATGCTGCTGCTTCAATAGATGTTTCCCTCGGCTTCTCTCGCTT 420
Db 361 CGCAGCCCGCAGAGATGCTGCTGCTTCAATAGATGTTTCCCTCGGCTTCTCTCGCTT 420
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Db 601 GAGTATCGGAATGCCACAGGAGTGGAGAGCCCTTTTCAGGGCGCTGCGAGTGGAA 660
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Qy 1261 G 1261
Db 1261 G 1261
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AX039100
LOCUS 1261 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 4 from Patent WO0063367.
ACCESSION AX039100
VERSION AX039100.1 GI:11229276
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cox, P.; Dixon, A.; Jackson, A. and Morgan, K.
TITLE A novel family of beta sub-unit proteins from a voltage-gated sodi-
um channel, nucleic acids encoding them and therapeutic or
diagnostic uses there of
JOURNAL Patent: WO 0063367-A 4 26-OCT-2000;
WARNER-LAMBERT COMPANY (US) ; Cambridge University Technical
Services Limited (GB)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	721	GGCTCTACACCTCAATGTGTCCCGGAGTTTCAGTTTGGAGGCGCATCGGCCCTTTGTG	780
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Db	1261	G 1261	
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LOCUS			
DEFINITION	HSA243396	1261 bp mRNA linear PRI 13-MAR-2000	
ACCESSION		Homo sapiens mRNA for voltage-gated sodium channel beta-3 subunit	
VERSION	AJ243396	(scn3b gene).	
KEYWORDS	AJ243396.2	GI:7242612	
SOURCE	scn3b gene;	voltage-gated sodium channel beta-3 subunit.	
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REMARK			
REFERENCE			

AUTHORS	Morgan, K.
TITLE	Direct Submission
JOURNAL	Submitted (13-MAR-2000) Morgan K., Biochemistry, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
COMMENT	On Mar 14, 2000 this sequence version replaced gi:7160974.
FEATURES	Location/Qualifiers
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Best Local Similarity	100.0%; Pred. No. 0;
Matches 1261; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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LOCUS AB032984 Homo sapiens mRNA for KIAA1158 protein, partial cds.
DEFINITION AB032984 Homo sapiens mRNA for KIAA1158 protein, partial cds.
ACCESSION AB032984
VERSION AB032984.1 GI:6330135
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 5306)
AUTHORS Hirosewa,M., Nagase,T., Ishikawa,K., Kikuno,R., Nomura,N. and Ohara,O.
TITLE Characterization of cDNA clones selected by the GeneMark analysis from size-fractionated cDNA libraries from human brain
JOURNAL DNA Res. 6 (5), 329-336 (1999)
MEDLINE 20039618
PUBMED 10574461
REFERENCE 2 (bases 1 to 5306)
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AUTHORS Ohara,O., Nagase,T. and Kikuno,R.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge/, Tel:++81-438-52-3913,
Fax:++81-438-52-3914)
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RESULT 5
LOCUS CQ728741 606 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 14675 from Patent WO02068579.
ACCESSION CQ728741
VERSION CQ728741.1 GI:42298386
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE KITS, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 14675 06-SEP-2002;
PE Corporation (NY) (US)
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Best Local Similarity 99.8%; Pred. No. 1.7e-299;
Matches 593; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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LOCUS Homo sapiens chromosome 11 clone CMB9-32A1 map 11q24, WORKING DRAFT
DEFINITION SEQUENCE, 8 unordered pieces.
ACCESSION AP000682
VERSION AP000682.3 GI:9844967
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Tokoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Homo sapiens 127,347 genomic DNA of 11q24
JOURNAL Published Only in DataBase (1999)
REFERENCE 2
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Tokoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
[B-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924]
On Aug 18, 2000 this sequence version replaced gi:8118870.

COMMENT
----- Genome Center
Center: RIKEN Genomic Sciences Center (GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDrafter1
Center clone name: CMB9-32A1
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 124981 bases at least Q40
Consensus quality: 125815 bases at least Q30
Consensus quality: 126286 bases at least Q20
Insert size: 126647; sum-of-contigs
Quality coverage: 12.71x in Q20 bases; sum-of-contigs
-----
```

NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their

order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

1 33532 contig of 33532 bp in length
33533 59223 contig of 25591 bp in length
59224 83007 contig of 23684 bp in length
83108 100196 contig of 17089 bp in length
100297 112313 contig of 12017 bp in length
112414 121043 contig of 8630 bp in length
121144 125917 contig of 4774 bp in length
126018 127347 contig of 1330 bp in length.

* NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 33532: contig of 33532 bp in length
* 33533 33632: gap of 100 bp
* 33633 59223: contig of 25591 bp in length
* 59224 59323: gap of 100 bp
* 59324 83007: contig of 23684 bp in length
* 83108 83107: gap of 100 bp
* 83108 100196: contig of 17089 bp in length
* 100197 100296: gap of 100 bp
* 100297 112313: contig of 12017 bp in length
* 112314 112413: gap of 100 bp
* 112414 121043: contig of 8630 bp in length
* 121044 121143: gap of 100 bp
* 121144 125917: contig of 4774 bp in length
* 125918 126017: gap of 100 bp
* 126018 127347: contig of 1330 bp in length.

FEATURES

source

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112414. .121043
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126018. .127347
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ORIGIN

Query Match 33.9%; Score 428; DB 2; Length 127347;
Best Local Similarity 100.0%; Pred. No. 1.9e-233;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CTCCTTCGAGCTGAGCTTACCTGGCGCGCAACGAGCGAGCGAGGGCGGAGTGGAA 62
Db 29132 CTCCTTCGAGCTGAGCTTACCTGGCGCGCAACGAGCGAGCGAGGGCGGAGTGGAA 29073
QY 63 GTGGAGTTCGGGGTGGGGAGGCGAGCTGTCTCGTGGTGTGAGCGCCCGCGAGAGC 122
Db 29072 GCTGGAGTTCGGGGTGGGGAGGCGAGCTGTCTCGTGGTGTGAGCGCCCGCGAGAGC 29013

QY 123 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTGCCTTAGGG 182
Db 29012 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTGCCTTAGGG 28953
QY 183 CCCAAAGCCCCCACCAGCGCTCCAAAAGTCCCCAGAGGCTCCCGAGCGACCGGTGCTCGGC 242
Db 28952 CCCAAAGCCCCCACCAGCGCTCCAAAAGTCCCGAGGCTCCCGAGCGACCGGTGCTCGGC 28893
QY 243 CTTCTCTTCGGTTCAGAAAGTTCGCCCTGGGGGCGAGTTCTGTCGTCGAGGTTTCTCGAA 302
Db 28892 CTTCTCTTCGGTTCAGAAAGTTCGCCCTGGGGGCGAGTTCTGTCGTCGAGGTTTCTCGAA 28833
QY 303 AGAATCTGAGAGGGCGGCGAGTCTTCGACGAGGGAATCTCTGTGTAGCTTGGAGCGC 362
Db 28832 AGAATCTGAGAGGGCGGCGAGTCTTCGACGAGGGAATCTCTGTGTAGCTTGGAGCGC 28773
QY 363 CCAGCCCCAGAGAGTCCCTGCTCAATAGATGTTTCCCTGGCTTCTCTCGTGTAT 422
Db 28772 CCAGCCCCAGAGAGTCCCTGCTCAATAGATGTTTCCCTGGCTTCTCTCGTGTAT 28713
QY 423 CTACTGGG 430
Db 28712 CTACTGGG 28705

RESULT 7

AC063921/c

LOCUS

AC063921

DEFINITION

Homo sapiens chromosome 3 clone RP11-142P10, WORKING DRAFT

SEQUENCE, 13 unordered pieces.

AC063921

VERSION

HTG; HTGS PHASE1; HTGS_DRAFT.

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 144833)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-ouman, F.R., Allen, C.,

Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayale, M., Banks, T.,

Barbacia, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D.,

Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,

Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,

Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,

Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,

Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,

Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,

Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,

Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,

Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,

Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,

Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,

Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,

Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,

Hernandez, O., Hodgson, A., Hogue, M., Holloway, C., Hollins, B.,

Homs, P., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,

Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,

Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,

Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,

Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulaseg, H.,

Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,

Maneshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,

Massey, M., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Metzger, M.,

Miner, G., Mear, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,

Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,

Nguyen, N., Nickerson, E., Nwokenko, S., Oguh, M., Okwuonu, G.,

Oreguena, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,

Peters, L., Picken, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,

Rivers, M., Rojas, A., Rojokan, I., Rolfe, M., Ruiz, S., Savery, G.,

Scherer, S., Scott, G., Shen, H., Shoshitari, N., Sisson, I.,

Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,

Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,

Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
McDonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
McNeeeters, R., Meldrum, J., Meneus, B., Morrow, J., Naylor, J.,
Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K.,
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
Zimmer, A. and Zody, M.

TITLE Direct Submission

Submitted (23-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 19, 2000 this sequence version replaced gi:6731265.

On Jul 19, 2000 this sequence version replaced qi:6731265.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

web site: <http://www.seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
Contact: sequence_submissions@...

Center project name: I1335

Center project name: L1333
Center clone name: L1C15

CENTER CIOLE NAME: TUCIS
STAFFS
STEWARDS

```
----- summary statistics
sequencing vector: M12: M77815: 100% of reads
```

sequencing vector: M13; M7/815; 100% of reads
Chemist at: Dye-terminator Big Dye; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% o

Assembly program: Phrap; version 0.960731

Consensus quality: 135317 bases at least

Consensus quality: 141872 bases at least

Consensus quality: 144404 bases

Insert size: 121000; agarose-fp

Insert size: 147000; sum-of-contigs

Quality coverage: 4.2 in Q20 bases; agarose-fp

```

-----
Quality coverage: 3.5 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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*	43670	43769: gap of 100 bp
*	43770	49948: contig of 6179 bp in length
*	49949	50048: gap of 100 bp
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*	60960	61059: gap of 100 bp
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* 76430 76529: gap of unknown length
 * 76530 86704: contig of 10175 bp in length
 * 86705 86804: gap of unknown length
 * 86805 103147: contig of 16343 bp in length
 * 103148 103247: gap of unknown length
 * 103248 116343: contig of 13096 bp in length
 * 116344 116443: gap of unknown length
 * 116444 135318: contig of 18875 bp in length
 * 135319 172546: gap of unknown length
 * 135419 172546: contig of 37128 bp in length.

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 /location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="Chromosome 10"
 /clone="RP11-331G19"
 /clone_lib="RPCI-11"

ORIGIN
 Query Match 33.9%; Score 428; DB 2; Length 172546;
 Best Local Similarity 100.0%; Pred. No. 1.9e-233;
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CTCCTTCCGAGCTGAGCTTACCTCGGCGCAACGAGCGAGCGAGGGCGGAGTGGAA 62
 Db 122377 CTCCTTCCGAGCTGAGCTTACCTCGGCGCAACGAGCGAGCGAGGGCGGAGTGGAA 122436
 QY 63 GTTGGAGTTCCGGGTGGGGGAGGCGACTGTCCGTGGTCTGAGCGCGCGCGAGAGC 122
 Db 122437 GCTGGAGTTCCGGGTGGGGGAGGCGACTGTCCGTGGTCTGAGCGCGCGCGAGAGC 122496
 QY 123 GGGCGCGAGCGGCTGATCGGTCCTCGAACTGGGAGGTCAGTGGGGTGCCTTAGGG 182
 Db 122497 GGGCGCGAGCGGCTGATCGGTCCTCGAACTGGGAGGTCAGTGGGGTGCCTTAGGG 122556
 QY 183 CCCAAGCCCCCACCACCGGCTCCAAAGCTCCAGAGGCTCCCGAGCGACCGGTGCTCGGC 242
 Db 122557 CCCAAGCCCCCACCACCGGCTCCAAAGCTCCAGAGGCTCCCGAGCGACCGGTGCTCGGC 122616
 QY 243 CTTCTCTCGGTGAGAAAGTCGCCCCCTCGGGGCGAGTTCGTCCTCCAAAGGTTTCTCGAA 302
 Db 122617 CTTCTCTCGGTGAGAAAGTCGCCCCCTCGGGGCGAGTTCGTCCTCCAAAGGTTTCTCGAA 122676
 QY 303 AGAATCTGAGAGCGCGAGCTCTCTGACCGAGGAATCTCTGTGTAGCCTTGGAGCGC 362
 Db 122677 AGAATCTGAGAGCGCGAGCTCTCTGACCGAGGAATCTCTGTGTAGCCTTGGAGCGC 122736
 QY 363 CCAGCCCCCAGAGATGCGCTTCAATAGATTGTTTCCCTGGCTTCTCTGTGCTTAT 422
 Db 122737 CCAGCCCCCAGAGATGCGCTTCAATAGATTGTTTCCCTGGCTTCTCTGTGCTTAT 122796
 QY 423 CTACTGGG 430
 Db 122797 CTACTGGG 122804

RESULT 10
 AP002765/c
 LOCUS Homo sapiens genomic DNA, chromosome 11q clone.RP11-634B22,
 DEFINITION complete sequence.
 ACCESSION AP002765
 VERSION AP002765.3 GI:16751488
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 Homo sapiens genomic DNA
 TITLE

JOURNAL Published Only in Database (2000)
 REFERENCE 2 (bases 1 to 178169)
 AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (10-JUL-2000) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
 1-7-22 Suenho-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:hattori@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 COMMENT On Nov 5, 2001 this sequence version replaced gi:12381934.
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 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="11"
 /map="11q"
 /clone="RP11-634B22"

ORIGIN
 Query Match 33.9%; Score 428; DB 9; Length 178169;
 Best Local Similarity 100.0%; Pred. No. 1.9e-233;
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CTCCTTCCGAGCTGAGCTTACCTCGGCGCAACGAGCGAGCGAGGGCGGAGTGGAA 62
 Db 107533 CTCCTTCCGAGCTGAGCTTACCTCGGCGCAACGAGCGAGCGAGGGCGGAGTGGAA 107474
 QY 63 GCTGGAGTTCCGGGTGGGGGAGGCGACTGTCCGTGGTCTGAGCGCGCGCGAGAGC 122
 Db 107473 GCTGGAGTTCCGGGTGGGGGAGGCGACTGTCCGTGGTCTGAGCGCGCGCGAGAGC 107414
 QY 123 GGGCGCGAGCGGCTGATCGGTCCTCGAACTGGGAGGTCAGTGGGGTGCCTTAGGG 182
 Db 107413 GGGCGCGAGCGGCTGATCGGTCCTCGAACTGGGAGGTCAGTGGGGTGCCTTAGGG 107354
 QY 183 CCCAAGCCCCCACCACCGGCTCCAAAGCTCCAGAGGCTCCCGAGCGACCGGTGCTCGGC 242
 Db 107353 CCCAAGCCCCCACCACCGGCTCCAAAGCTCCAGAGGCTCCCGAGCGACCGGTGCTCGGC 107294
 QY 243 CTTCTCTCGGTGAGAAAGTCGCCCCCTCGGGGCGAGTTCGTCCTCCAAAGGTTTCTCGAA 302
 Db 107293 CTTCTCTCGGTGAGAAAGTCGCCCCCTCGGGGCGAGTTCGTCCTCCAAAGGTTTCTCGAA 107234
 QY 303 AGAATCTGAGAGCGCGAGCTCTTGAACGAGGAATCTCTGTGTAGCCTTGGAGCGC 362
 Db 107233 AGAATCTGAGAGCGCGAGCTCTTGAACGAGGAATCTCTGTGTAGCCTTGGAGCGC 107174
 QY 363 CCAGCCCCCAGAGATGCGCTTCAATAGATTGTTTCCCTGGCTTCTCTGTGCTTAT 422
 Db 107173 CCAGCCCCCAGAGATGCGCTTCAATAGATTGTTTCCCTGGCTTCTCTGTGCTTAT 107114
 QY 423 CTACTGGG 430
 Db 107113 CTACTGGG 107106

RESULT 11
 AC069539/c
 LOCUS Homo sapiens chromosome 11 clone RP11-321E15, complete sequence.
 DEFINITION AC069539
 ACCESSION AC069539
 VERSION AC069539.5 GI:20270093
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 181471)
 Smith,D.R.
 Genome Therapeutics Corporation Sequencing Center: Human Genome
 Sequence Data
 TITLE

JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 181471)
AUTHORS	Smith,D.R.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA
REFERENCE	3 (bases 1 to 181471)
AUTHORS	Smith,D.R.
TITLE	Direct Submission
JOURNAL	Submitted (19-OCT-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA
REFERENCE	4 (bases 1 to 181471)
AUTHORS	Smith,D.R.
TITLE	Direct Submission
JOURNAL	Submitted (23-APR-2002) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA
COMMENT	On Apr 23, 2002 this sequence version replaced gi:10881056.
FEATURES	Location/Qualifiers 1..181471 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="11" /clone="RP11-32LE15" /clone_lib="RPCI-11"
ORIGIN	
Query Match	33.9%; Score 428; DB 9; Length 181471;
Best Local Similarity	100.0%; Pred.No.1.9e-233;
Matches 428; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	3 CTCCTTCCGAGCTGAGCTTTACCTCGGGGCAAACGAGCGAGGCGAGGGCGCGAGTGGAA 62
Db	79671 CTCCTTCCGAGCTGAGCTTTACCTCGGGGCAAACGAGCGAGGCGAGGGCGCGAGTGGAA 79612
Qy	63 GCTGGAATTCGGGGTGCGGGGAGGCGACTGTCCGTGCTGTGAGCCGCCGGCGAGAGC 122
Db	79611 GCTGGAATTCGGGGTGCGGGGAGGCGACTGTCCGTGCTGTGAGCCGCCGGCGAGAGC 79552
Qy	123 GGGCGGAGCGGCTGATCGGCTCCCTCGAACCCTGGGAGGTCACAGTGGGGTCCAGTGGGTCCGTAGGG 182
Db	79551 GGGCGGAGCGGCTGATCGGCTCCCTCGAACCCTGGGAGGTCACAGTGGGGTCCAGTGGGTCCGTAGGG 79492
Qy	183 CCCAAGCCCCCACCCGGCTCCAAAAGCTCCCAGGGCCTCCCAGGCACCGGTGCTCGGC 242
Db	79491 CCCAAGCCCCCACCCGGCTCCAAAAGCTCCCAGGGCCTCCCAGGCACCGGTGCTCGGC 79432
Qy	243 CTTTCCTTGGTCAGAAAGTCGCCCCCTGGGGCAGTTTGTCTCCCAAAGGTTTTCTCGAA 302
Db	79431 CCTTCTCTCGTTCAGAAAGTCGCCCCCTGGGGCAGTTTGTCTCCCAAAGGTTTTCTCTCGAA 79372
Qy	303 AGAATCTGAGAGGGCGCAGTCCTTGACCGAGGGAATCTCTCTGTGTAGCTTTGGAAGCG 362
Db	79371 AGAATCTGAGAGGGCGCAGTCCTTGACCGAGGGAATCTCTCTGTGTAGCTTTGGAAGCG 79312
Qy	363 CCAGCCCCAGAAGATGCTCGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTAT 422
Db	79311 CCAGCCCCAGAAGTGCCTGCCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTAT 79252
Qy	423 CTACTGGG 430
Db	79251 CTACTGGG 79244
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LOCUS	BD059018 471 bp DNA linear PAT 27-AUG-2002
DEFINITION	Secreted expressed sequence tags (sESTs).
ACCESSION	BD059018
VERSION	BD059018.1 GI:22604624
KEYWORDS	JP 2001519666-A/873.
SOURCE	Zea mays
ORGANISM	Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.

REFERENCE
AUTHORS
Jacobse, K., Mccoy J.M., Lavallie, E.R., Racine, L.A., Merberg, D.,
Treacy, M., Spaulding, V. and Agostino, M.J.
Secreted expressed sequence tags (SESTs)
Patent: JP 2001519666-A 873 23-OCT-2001;
GENETICS INSTITUTE INC

TITLE
JOURNAL
GENETICS INSTITUTE INC

COMMENT
PN JP 2001519666-A/873
PD 23-OCT-2001
PF 10-APR-1998 JP 1998543068
PR 10-APR-1997 US 08/835913
PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLE, LISA A RACIE, PI DAVID MERBERG,
PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC
C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness:
Double;

CC Topology: Linear;
FH Key Location/Qualifiers

FEATURES
source
1..471
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"

ORIGIN

Query Match 25.7%; Score 324; DB 6; Length 471;
Best Local Similarity 100.0%; Pred. No. 1e-173;
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 487 GGCAACCCCATGAAGCTGGCGCTCATCTCTGCATGAAGAGAGAGAGGTTGGAGGCCACC 546
Db 139 GGCAACCCCATGAAGCTGGCGTCACTCTCTGCATGAAGAGAGAGAGGTTGGAGGCCACC 138
Qy 547 ACGGTGTTGGAATTGGTTTCACAGCCCGAGGGCGGTAAAGATTTCTTTATTTACGAGTAT 606
Db 199 ACGGTGTTGGAATTGGTTTCACAGCCCGAGGGCGGTAAAGATTTCTTTATTTACGAGTAT 258
Qy 607 CGGAATGGCCACCAGAGAGTGGAGAGCCCTTTTCAGGGGGCGCTGCAGTGGATGGCAGC 666
Db 259 CGGAATGGCCACCAGAGAGTGGAGAGCCCTTTTCAGGGGGCGCTGCAGTGGATGGCAGC 318
Qy 667 AAGGACTCTGAGGACGTGTCCATCACTGTGCTCAACGTCACCTCGAACGACTCTGGCCCTC 726
Db 319 AAGGACTCTGAGGACGTGTCCATCACTGTGCTCAACGTCACCTCGAACGACTCTGGCCCTC 378
Qy 727 TACACTGCAATGTGTCCCGGAGTTTGATGTTGAGGCGCATCGGCCCTTTGTGAAGACG 786
Db 379 TACACTGCAATGTGTCCCGGAGTTTGATGTTGAGGCGCATCGGCCCTTTGTGAAGACG 438
Qy 787 ACGGGCTGATCCCCCTAAGATC 810
Db 439 ACGGGCTGATCCCCCTAAGATC 462

RESULT 13
AP002749
LOCUS
DEFINITION
Homo sapiens chromosome 11 clone RP11-158J21 map 11q24, WORKING
DRAFT SEQUENCE, 41 unordered pieces.
AP002749
VERSION
AP002749.1 GI:198588
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 178431)

TITLE
JOURNAL
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Homo sapiens 178,431 genomic DNA of 11q24
Published Only in DataBase (2000)

REFERENCE
AUTHORS

2 (bases 1 to 178431)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,I., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (10-JUL-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
(E-mail: hattori@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
Tel: 81-42-778-9923, Fax: 81-42-778-9924)

COMMENT

----- Genome Center
Center: RIKEN Genomic Sciences Center (GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDraft11
Center clone name: RP11-158J21
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 155982 bases at least Q40
Consensus quality: 165758 bases at least Q30
Consensus quality: 170239 bases at least Q20
Insert size: 174431; sum-of-contigs
Quality coverage: 4.20x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of
41 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved.

1
13012 contig of 13012 bp in length
13113 24677 contig of 11565 bp in length
34640 contig of 9863 bp in length
43196 contig of 8456 bp in length
34741 50126 contig of 6830 bp in length
43297 57725 contig of 7499 bp in length
50227 64612 contig of 6287 bp in length
57826 70999 contig of 6287 bp in length
64713 76188 contig of 5089 bp in length
71100 83580 contig of 7292 bp in length
76289 83680 contig of 100 bp
83681 90511 contig of 6831 bp in length
90612 95493 contig of 4882 bp in length
95494 102262 contig of 100 bp
102363 102362 gap of 100 bp
105967 105866 contig of 3504 bp in length
111243 11142 contig of 5176 bp in length
115923 115923 contig of 4681 bp in length
121747 121747 contig of 5724 bp in length
121848 125532 contig of 3685 bp in length
125533 125633 contig of 100 bp
127928 127927 contig of 2295 bp in length
131185 131184 contig of 3157 bp in length
131285 132725 contig of 1441 bp in length
132726 132825 gap of 100 bp
132826 135566 contig of 2741 bp in length
135567 135666 gap of 100 bp
135667 138000 contig of 2334 bp in length
138001 138100 gap of 100 bp
138101 141194 contig of 3094 bp in length
141195 141294 gap of 100 bp
141295 143619 contig of 2325 bp in length
143620 143719 gap of 100 bp
143720 146448 contig of 2729 bp in length
146549 146548 gap of 100 bp
146549 149531 contig of 2983 bp in length
149532 149631 gap of 100 bp
149632 152157 contig of 2526 bp in length
152158 152257 gap of 100 bp
152258 155623 contig of 3366 bp in length
155624 155723 gap of 100 bp
155724 158334 contig of 2611 bp in length
158335 158434 gap of 100 bp
160610 160509 contig of 2075 bp in length
160510 160609 gap of 100 bp
162343 contig of 1734 bp in length

175830 176905 contig of 1076 bp in length
177006 178431 contig of 1426 bp in length.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 41 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
13012 contig of 13012 bp in length
13113 13112 gap of 100 bp
13113 24677 contig of 11565 bp in length
24678 24777 gap of 100 bp
24778 34640 contig of 9863 bp in length
34641 34740 gap of 100 bp
34741 43196 contig of 8456 bp in length
43197 43296 gap of 100 bp
43297 50126 contig of 6830 bp in length
50127 50226 gap of 100 bp
50227 57725 contig of 7499 bp in length
57726 57825 gap of 100 bp
57826 64612 contig of 6787 bp in length
64613 64712 gap of 100 bp
64713 70999 contig of 6287 bp in length
71000 71099 gap of 100 bp
71100 76188 contig of 5089 bp in length
76189 76288 gap of 100 bp
76289 83580 contig of 7292 bp in length
83581 83680 gap of 100 bp
83681 90511 contig of 6831 bp in length
90512 90611 gap of 100 bp
90612 95493 contig of 4882 bp in length
95494 95594 gap of 100 bp
95594 102262 contig of 6669 bp in length
102263 102362 gap of 100 bp
102363 105866 contig of 3504 bp in length
105867 105966 gap of 100 bp
105967 111142 contig of 5176 bp in length
111143 11142 gap of 100 bp
111243 115923 contig of 4681 bp in length
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116024 121747 contig of 5724 bp in length
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121848 125532 contig of 3685 bp in length
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125633 127927 contig of 2295 bp in length
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131184 131184 contig of 3157 bp in length
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131285 132725 contig of 1441 bp in length
132726 132825 gap of 100 bp
132826 135566 contig of 2741 bp in length
135567 135666 gap of 100 bp
135667 138000 contig of 2334 bp in length
138001 138100 gap of 100 bp
138101 141194 contig of 3094 bp in length
141195 141294 gap of 100 bp
141295 143619 contig of 2325 bp in length
143620 143719 gap of 100 bp
143720 146448 contig of 2729 bp in length
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146549 149531 contig of 2983 bp in length
149532 149631 gap of 100 bp
149632 152157 contig of 2526 bp in length
152158 152257 gap of 100 bp
152258 155623 contig of 3366 bp in length
155624 155723 gap of 100 bp
155724 158334 contig of 2611 bp in length
158335 158434 gap of 100 bp
160509 contig of 2075 bp in length
160609 gap of 100 bp
162343 contig of 1734 bp in length

* 162344 162443: gap of 100 bp
* 162444 contig of 2366 bp in length
* 164809: gap of 100 bp
* 164910 contig of 2127 bp in length
* 167036: contig of 2127 bp in length
* 167136: gap of 100 bp
* 167037 contig of 2033 bp in length
* 169169: gap of 100 bp
* 169269: contig of 1783 bp in length
* 169170 contig of 1783 bp in length
* 171053 gap of 100 bp
* 171153 contig of 1781 bp in length
* 171153 contig of 1781 bp in length
* 172933: gap of 100 bp
* 173033: gap of 100 bp
* 173034 contig of 1147 bp in length
* 174180: gap of 100 bp
* 174181 contig of 1449 bp in length
* 174281 contig of 1449 bp in length
* 175729: gap of 100 bp
* 175730 contig of 1076 bp in length
* 175830 contig of 1076 bp in length
* 176906 gap of 100 bp
* 177005: gap of 100 bp
* 177006 contig of 1426 bp in length.

FEATURES

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1. 178431
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q24"
/clones="RP11-158J21"
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/note="assembly_fragment"
13113. 24677
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24778. 34640
/note="assembly_fragment"
34741. 43196
/note="assembly_fragment"
43297. 50126
/note="assembly_fragment"
50227. 57725
/note="assembly_fragment"
57826. 64612

Query Match 20.8%; Score 262; DB 2; Length 178431;

Best Local Similarity 99.7%; Pred. No. 4,1e-138;

Matches 382; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 49 GGGCGCAGTGGAGCTGGAGTTCGGGGTGGCGGGAGGCGACTCTCCGTGGTGTCTGA 108
Db 111412 GGGCGCAGTGGAGCTGGAGTTCGGGGTGGCGGGAGGCGACTCTCCGTGGTGTCTGA 111471
QY 109 GCAGCGCGAGAGCGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGT 168
Db 111472 GCAGCGCGAGAGCGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGT 111531
QY 169 GGGGTGCTTAGG-CCCAAGCCCCCACCAGGCTCCAAAGCTCCAGGCGCTCCCGCAG 227
Db 111532 GGGGTGCTTAGGCGCCCAAGCCCCCACCAGGCTCCAAAGCTCCAGGCGCTCCCGCAG 111591
QY 228 GCACCGTGTCTGCGCCCTCTCTCGGTGAGAACTGCCCTCGGGGCGAGTTCGTCCCA 287
Db 111592 GCACCGTGTCTGCGCCCTCTCTCGGTGAGAACTGCCCTCGGGGCGAGTTCGTCCCA 111651
QY 288 AAGGGTTTCCTCGAAAGAAATCTGAGAGGGGCGAGTTCCTGACCGAGGGAATCTCTGTG 347
Db 111652 AAGGGTTTCCTCGAAAGAAATCTGAGAGGGGCGAGTTCCTGACCGAGGGAATCTCTGTG 111711
QY 348 TAGCCTTGAAGCGCGCCAGCCCGAGAGATGCTGCTTCAATAGATGTTTCCCTCGGC 407
Db 111712 TAGCCTTGAAGCGCGCCAGCCCGAGAGATGCTGCTTCAATAGATGTTTCCCTCGGC 111771
QY 408 TTCTCTGCTTATCTACTGGG 430
Db 111772 TTCTCTGCTTATCTACTGGG 111794

RESULT 14
AC024604/c
LOCUS
DEFINITION
Homo sapiens chromosome Chromosome 10 clone RP11-331G19, WORKING
DRAFT SEQUENCE, 22 unordered pieces.
AC024604
AC024604.3 GI:8389428
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_CANCELLED.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Smith,D.R.
Genome Therapeutics Corporation Sequencing Center: Human Genome
Sequence Data
Unpublished
2 (bases 1 to 172546)
Smith,D.R.
Direct Submission
Submitted (01-MAR-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Walcham, MA 02453, USA
On Jun 9, 2000 this sequence version replaced gi:7549605.

Center: Genome Therapeutics Corporation
Center code: GTC
Web site: http://www.genomecorp.com/
Contact: gtc-seqcenter@genomecorp.com

Project Information
Center project name: Hg202

Summary Statistics
Sequencing vector: N/A
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 990315
Consensus quality: 152033 bases at least Q40
Consensus quality: 163535 bases at least Q30
Consensus quality: 165256 bases at least Q20
Insert size: 170446; sum-of-contigs
Quality coverage: 4.3x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1339: contig of 1339 bp in length
* 1340 1439: gap of unknown length
* 1440 2789: contig of 1350 bp in length
* 2790 2889: gap of unknown length
* 2890 4582: contig of 1673 bp in length
* 4583 4662: gap of unknown length
* 4663 6344: contig of 1682 bp in length
* 6345 6444: gap of unknown length
* 6445 9221: contig of 2777 bp in length
* 9222 9321: gap of unknown length
* 9321 11997: contig of 2676 bp in length
* 11998 12097: gap of unknown length
* 12098 14867: contig of 2770 bp in length
* 14868 14967: gap of unknown length
* 14968 19919: contig of 4952 bp in length
* 19920 20019: gap of unknown length
* 20020 24125: contig of 4106 bp in length
* 24126 24225: gap of unknown length
* 24226 29444: contig of 5219 bp in length
* 29445 29544: gap of unknown length
* 29545 34568: contig of 5024 bp in length
* 34569 39414: contig of 4746 bp in length
* 39415 39514: gap of unknown length
* 39515 45885: contig of 6371 bp in length

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* 45886 45985: gap of unknown length
* 45986 50997: contig of 5012 bp in length
* 50998 51917: gap of unknown length
* 51917 51943: contig of 8046 bp in length
* 51943 52943: gap of unknown length
* 52943 52944: contig of 8536 bp in length
* 52944 67779: gap of unknown length
* 67779 67879: gap of unknown length
* 67879 76429: contig of 8550 bp in length
* 76429 76529: gap of unknown length
* 76529 86704: contig of 10175 bp in length
* 86704 86805: gap of unknown length
* 86805 103147: contig of 16343 bp in length
* 103147 103248: gap of unknown length
* 103248 116343: contig of 13096 bp in length
* 116343 116344: gap of unknown length
* 116344 135318: contig of 18875 bp in length
* 135318 135319: gap of unknown length
* 135319 172546: contig of 37128 bp in length.
* 172546 172546: contig of 37128 bp in length.

FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="Chromosome 10"
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                     /clone_lib="RPC1-11"

ORIGIN
Query Match          17.9%; Score 226; DB 2; Length 172546;
Best Local Similarity 100.0%; Pred. No. 1.9e-117;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 595 ATTACGAGTATCGGAATGCCACACGAGGAGTGGAGAGCCCTTTACAGGGGCGCTGCAG 654
Db 54788 ATTTACGAGTATCGGAATGCCACACGAGGAGTGGAGAGCCCTTTACAGGGGCGCTGCAG 54729

QY 655 TCGAATGGCAGCAGGACCTCGCAGGACGTGTCATCAGTCTCAACGTCAGTCTGAAC 714
Db 54728 TCGAATGGCAGCAGGACCTCGCAGGACGTGTCATCAGTCTCAACGTCAGTCTGAAC 54669

QY 715 GACTCTGGGCTCTACACCTCGCAATGTGTCGGGAGTTTGAGTTTGAGGCGCATGGGCC 774
Db 54668 GACTCTGGGCTCTACACCTCGCAATGTGTCGGGAGTTTGAGTTTGAGGCGCATGGGCC 54609

QY 775 TTGTGAAGACAGCGGGTGTATCCCTTAAGAGTACCAGGAGG 820
Db 54608 TTGTGAAGACAGCGGGTGTATCCCTTAAGAGTACCAGGAGG 54563

RESULT 15
AB097521
LOCUS
DEFINITION
Macaca fascicularis brain cDNA clone:QmoA-13657, full insert
sequence.
AB097521
ACCESSION
AB097521.1 GI:26449236
VERSION
oligo capping; fls (full insert sequence).
KEYWORDS
Macaca fascicularis (crab-eating macaque)
SOURCE
Macaca fascicularis
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
REFERENCE
1
AUTHORS
Osada, N., Hida, M., Kusuda, J., Tanuma, R., Iseki, K., Hirata, M.,
Suto, Y., Hirai, M., Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K.
TITLE
Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
chromosomes.
JOURNAL
Gene 275 (1), 31-37 (2001)
MEDLINE
21458551
PUBMED
11574149
REFERENCE
2 (bases 1 to 3296)
AUTHORS
Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.
TITLE
Direct Submission
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Db	591		TCTGACTACCTTGCCATCCCATCTGAGAAACAGGAGAACTCTGCGGTACCAAGTGGAGAA	650
Qy	1021		TAGAACAGGAGCAGTGTGACATGAGGTGGCCTGAACACCTGAGGGACTGGACATCCCATG	1080
Db	651		TAGAACAGGAGCAGTGTGACATGAGGTGGCCTGAACACCTGAGGGACTGGACATCCCATG	710
Qy	1081		TTCAGCAATGTCAATGGCATCAGGAGG	1108
Db	711		TTCAGCAATGTCAATGGCATCAGGAGG	738

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 Job time : 5465 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 04:40:54 ; Search time 701 Seconds
(without alignments)
10648.779 Million cell updates/sec

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 10

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Minimum DB seq length: 0

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- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1261	100.0	1261	3 AAC67837	Aac67837 Human bet
2	1261	100.0	1261	10 ACF57870	Acf57870 Human SCN
3	1210	96.0	1261	10 ADB78651	Adb78651 Human ion
4	1104	87.5	4052	6 ABA93727	Aba93727 Human sig
5	860	68.2	1510	4 AAF84146	Aaf84146 Human nov
6	798	63.3	978	4 AAH98320	Aah98320 Human EST
7	798	63.3	978	13 ADS11487	Adsl1487 Human the
8	787	62.4	1045	4 AAK52345	Aak52345 Human pol
9	760	60.3	953	13 ADS10151	Adsl0151 Human the
10	396	31.4	1195	5 AAS86764	Aas86764 DNA encod
11	391	31.0	3531	5 AAS86763	Aas86763 DNA encod
12	324	25.7	471	2 AAV86895	Aav86895 EST clone
13	218	17.3	621	5 AAS86762	Aas86762 DNA encod
14	216	17.1	4625	4 AAL04971	Aal04971 Human rep
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16	91	7.2	407	4 ABA08942	Aba08942 Human vol
17	91	7.2	407	4 AAK53329	Aak53329 Human pol
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21	38	3.0	645	5 AAC90601	Aac90601 Rat sodiu
22	38	3.0	2220	3 AAC67836	Aac67836 Rat beta3
23	38	3.0	2632	5 AAC90602	Aac90602 Rat sodiu
24	38	3.0	3108	5 AAC90600	Aac90600 Rat sodiu
25	33	2.6	574	4 AAL01292	Aal01292 Human rep
26	33	2.6	574	4 ABL96750	Ab196750 Human tes
27	28	2.2	36	4 AAF84148	Aaf84148 Human nov
28	24	1.9	24	10 ADG19077	Adg19077 Voltage g
29	23	1.8	493	13 ADQ55080	Adq55080 Novel can
30	22	1.7	22	10 ADG19076	Adg19076 Voltage g
31	22	1.7	462	6 AAS05386	Aas05386 Human gen
32	21	1.7	1990	2 AAQ25816	Aaq25816 Villin ge
33	21	1.7	2152	13 ADR89479	Adr89479 Apoptosis
34	21	1.7	2352	4 AAK82355	Aak82355 Human imm
35	21	1.7	11122	6 ABX04611	Abx04611 Human end
36	20	1.6	420	3 AAA49871	Aaa49871 Mycobacte
37	20	1.6	627	13 ADQ56620	Adq56620 Novel can
38	20	1.6	628	5 AAH94296	Aah94296 Human foe
39	20	1.6	889	12 ADJ42665	Adj42665 Plant CDN
40	20	1.6	918	13 ADS49483	Ads49483 Bacterial
41	20	1.6	2514	8 ACA38647	Aca38647 Prokaryot
42	20	1.6	2517	4 AAH51950	Aah51950 Mycobacte
43	20	1.6	2517	8 ACA37596	Aca37596 Prokaryot
44	20	1.6	2517	8 ACA40274	Aca40274 Prokaryot
45	20	1.6	2547	8 ACA38177	Aca38177 Prokaryot

ALIGNMENTS

RESULT 1
AAC67837
ID AAC67837 standard; CDNA; 1261 BP.

AC AAC67837;

DT 15-FEB-2001 (first entry)

DE Human beta3 CDNA.

XX Human; beta sub-unit; beta3; analgesic; anticonvulsant;
KW cerebroprotective; vasotropic; cardiac; nootropic; cytostatic;
KW dermatological; gene therapy; voltage-gated sodium channel; pain;
KW epilepsy; stroke; ischaemia; heart disease; Jacobsen Syndrome;
KW familial nonchromaffin paraganglioma; phenylketonuria;
KW Charcot Marie Tooth disease; ss.

OS Homo sapiens.

PN WO200063367-A1.

PD 26-OCT-2000.

PF 24-FEB-2000; 2000WO-EP001783.

PR 15-APR-1999; 99US-0129473P.

PA (WARN) WARNER LAMBERT CO.

PI (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX Cox P, Dixon A, Jackson A, Morgan K;

DR WPI; 2000-665241/64.

DR P-PSDB; AAB36002.

XX Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium channel, and their corresponding polypeptides, useful for detecting and treating sodium channel-associated conditions, e.g. pain, epilepsy and stroke.

PS Claim 10; Page 70-71; 88pp; English.

XX The present sequence is given in the claims of a specification relating

CC to a novel family of beta sub-unit proteins from a voltage-gated sodium
CC channel. Human and rat beta sub-units, which have been collectively
CC identified as beta3, have been isolated. The polynucleotides and
CC polypeptides are useful for screening for agonists and antagonists of
CC sodium channels. The agonists, antagonists, proteins and nucleic acids
CC may be used diagnosing of treating diseases or conditions associated with
CC voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia,
CC heart disease, Jacobsen Syndrome, Familial Nonchromaffin Paraganglioma,
CC Phenylketonuria and Charcot Marie Tooth disease
XX
SQ Sequence 1261 BP; 263 A; 366 C; 372 G; 260 T; 0 U; 0 Other;

Query Match 100.0%; Score 1261; DB 3; Length 1261;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AAGCTGGAGTTCCGGGGTGGGGGAGGAGCGACTGTCCTGCTGTGAGCGCGCGCGAGA 120

QY 121 GCGGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGTCGCTTAG 180
DB 121 GCGGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGTCGCTTAG 180

QY 181 GGGCCAAAGCCCCACCGCGCTCCAAAGCTCCCGAGGGCTCCCGAGGACCGGTGCTCG 240
DB 181 GGGCCAAAGCCCCACCGCGCTCCAAAGCTCCCGAGGGCTCCCGAGGACCGGTGCTCG 240

QY 241 GCGCTTCCTTCGGTCAAGAGTGGCGCCCTGGGGGAGTGGTCCGCAAGGGTTTCCTCG 300
DB 241 GCGCTTCCTTCGGTCAAGAGTGGCGCCCTGGGGGAGTGGTCCGCAAGGGTTTCCTCG 300

QY 301 AAAGATCTGAGAGGGCGAGTCTTGGAGGGGAGTCTCTGTGTAGCTTGGAGG 360
DB 301 AAAGATCTGAGAGGGCGAGTCTTGGAGGGGAGTCTCTGTGTAGCTTGGAGG 360

QY 361 CGCCAGCCCGAGAGAGTGGCTGCTCAATAGATTGTTTCCCTGGCTTCTCTGTGCTT 420
DB 361 CGCCAGCCCGAGAGAGTGGCTGCTCAATAGATTGTTTCCCTGGCTTCTCTGTGCTT 420

QY 421 ATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCCTCGAGAGCGAGGCC 480
DB 421 ATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCCTCGAGAGCGAGGCC 480

QY 481 GTGCAGGGCAACCCCATGAGCTGCTGAGCGGGGAGTCTCTGTGTAGCTTGGAGG 540
DB 481 GTGCAGGGCAACCCCATGAGCTGCTGAGCGGGGAGTCTCTGTGTAGCTTGGAGG 540

QY 541 GGCACACCGGTGGTGAATGGTTTACAGGCGCGGAGGGCGGTAAGATTTCCTATTATAC 600
DB 541 GGCACACCGGTGGTGAATGGTTTACAGGCGCGGAGGGCGGTAAGATTTCCTATTATAC 600

QY 601 GAGTATCGGAATGGCCACAGAGAGTGGAGAGCCCTTTTCAGGGGCGCTGAGTGGAAAT 660
DB 601 GAGTATCGGAATGGCCACAGAGAGTGGAGAGCCCTTTTCAGGGGCGCTGAGTGGAAAT 660

QY 661 GGCAGCAAGGACTGCGAGAGCTGTCCATCATGTCATCTCAAGTCACTCTGAACGACTCT 720
DB 661 GGCAGCAAGGACTGCGAGAGCTGTCCATCATGTCATCTCAAGTCACTCTGAACGACTCT 720

QY 721 GGCCTCTACACCTGCAATGTGTCGGGAGTTGAGTTTGGCGCGCATCGGCCCTTTGTG 780
DB 721 GGCCTCTACACCTGCAATGTGTCGGGAGTTGAGTTTGGCGCGCATCGGCCCTTTGTG 780

QY 781 AAGACGACCGGCTGATCCCTCTAAGAGTCAACGAGAGGCTGGAGAGCTTACCTCT 840
DB 781 AAGACGACCGGCTGATCCCTCTAAGAGTCAACGAGAGGCTGGAGAGCTTACCTCT 840

QY 841 GTGGTCTCAGAAATCATGATGATACATCTTCTGCTTCTCCTCACCTTGGGCTGCTCATC 900

DB 841 GTGGTCTCAGAAATCATGATGATACATCTTCTGGTCTTCTCACCTTGGGCTGCTCATC 900
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QY 1021 TAGAACAGGACAGTGTGACATGAGTGGCTGAAACACCTGAGGGACTGGACATCCCATG 1080
DB 1021 TAGAACAGGACAGTGTGACATGAGTGGCTGAAACACCTGAGGGACTGGACATCCCATG 1080
QY 1081 TTCAGCAATGTCAATGGCATCAGAGGGGCGGCCCAAGGGCCCCCATCGCTTCCCTTCATGC 1140
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QY 1141 ATCCATTTGTTCTGTTCAATTCATTCATATCCATATCCATCCACCTGCTGTGAGCTTTCACCTCT 1200
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QY 1261 G 1261
DB 1261 G 1261

RESULT 2
ACF57870
ID ACF57870 standard; cDNA; 1261 BP.
XX ACF57870;
AC ACF57870;
XX DT 15-JAN-2004 (first entry)
XX Human SCN3B protein encoding cDNA.
DE DE
XX SCN3A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
KW neuroprotective; anesthetic; cytoskeletal; cerebroprotective; cardiant;
KW hypotensive; gene therapy; SCN3B; human; gene; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FT CDS 376..1023
FT /*tag= a
FT /product= "SCN3B"
XX WO2003072751-A2.
PN 04-SEP-2003.
XX 25-FEB-2003; 2003WO-US006010.
XX 25-FEB-2002; 2002US-0359382P.
XX (UYVA-) UNIV VANDERBILT.
XX George AL, Lossin C;
XX WPI: 2003-712725/67.
XX P-PSDB; ABR83183.
XX Recombinantly expressed sodium channel type 1 alpha subunit, useful in
XX screening for modulators, for treating e.g. epilepsy.
XX Disclosure; Page 145-147; 176pp; English.

The invention relates to a recombinantly expressed and isolated human SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally incorporated into a cell, is used to screen for specific modulators, potentially useful as anticonvulsant, antiepileptic, neuroprotective, analgesic and/or anesthetic agents, e.g. for treating severe myoclonic epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis, motor endplate diseases, hypertension, congestive heart failure and muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic and metastatic cancer cell lines). These activities can also be provided by gene therapy vectors that express (I) or the modulators. The modulators, also antibodies directed against (I), are used to detect SCN1A channel polypeptides. The present sequence represents a human SCN3B protein encoding cDNA

XX
SQ Sequence 1261 BP; 263 A; 366 C; 372 G; 260 T; 0 U; 0 Other;

Query Match 100.0%; Score 1261; DB 10; Length 1261;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTCCCTCCGAGCTGAGCTTACCTCGGCGCAACGACGAGGCGAGGGCGCGAGTGG 60
DB 1 CCCTCCCTCCGAGCTGAGCTTACCTCGGCGCAACGACGAGGCGAGGGCGCGAGTGG 60
QY 61 AAGCTGGAGTCCCGGGTGGCGGGAGGCGACTGTCCTGTCGTCGTCGTCGTCGTCGTCG 120
DB 61 AAGCTGGAGTCCCGGGTGGCGGGAGGCGACTGTCCTGTCGTCGTCGTCGTCGTCGTCG 120
QY 121 GCGGGCGCGAGGCGCTGAGTCGGCTCCCTGCAACTGGGAGGTCGAGTGGGGTGGCTTAG 180
DB 121 GCGGGCGCGAGGCGCTGAGTCGGCTCCCTGCAACTGGGAGGTCGAGTGGGGTGGCTTAG 180
QY 181 GGCCCAAGGCGCCACCCGCTCCAAAGCTCCAGGGCTCCCGAGGCGACCGGTGCTCG 240
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QY 361 CGCAGCGCCAGAGAGTGCCTGCTTCAATAGATGTTTCCCTCGCTCTCTCTGCTT 420
DB 361 CGCAGCGCCAGAGAGTGCCTGCTTCAATAGATGTTTCCCTCGCTCTCTCTGCTT 420
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DB 421 ATCTACTGGTTCAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCTCGGAGCGGAGGCC 480
QY 481 GTCCAGGGCAACCCATGAAGTCCGCTGATCTCTGCAATGAAGAGAGAGGAGTGGAG 540
DB 481 GTCCAGGGCAACCCATGAAGTCCGCTGATCTCTGCAATGAAGAGAGAGGAGTGGAG 540
QY 541 GCCACACCGTGTGGATGGTTCACAGGCGCGAGGGCGGTAAAGATTCCTTATTAC 600
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QY 601 GAGTATCGGAATGCCACAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTCGAGTGGAAAT 660
DB 601 GAGTATCGGAATGCCACAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTCGAGTGGAAAT 660
QY 661 GGAGCAGAGACCTGCGAGGAGTGTCCATCATCTGCTCAACGTCACTCTGAACGACTCT 720
DB 661 GGAGCAGAGACCTGCGAGGAGTGTCCATCATCTGCTCAACGTCACTCTGAACGACTCT 720
QY 721 GGCTCTTACACCTGCAATGTCCCGGAGTGTGAGTTTCAGGCGCATCGGCCCTTTGTG 780
DB 721 GGCTCTTACACCTGCAATGTCCCGGAGTGTGAGTTTCAGGCGCATCGGCCCTTTGTG 780
QY 781 AAGACGACGCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGGACTTTCACCTCT 840

781 AAGACGACGCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGGACTTTCACCTCT 840
QY 841 GTGGTCTCAGAATCATGATGATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
DB 841 GTGGTCTCAGAATCATGATGATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
QY 901 GAGATCATATATTTGCTTACAGAAAGGTCTCAAAAGCCGAAAGAGGAGGAGGAGGAGGAGG 960
DB 901 GAGATCATATATTTGCTTACAGAAAGGTCTCAAAAGCCGAAAGAGGAGGAGGAGGAGGAGG 960
QY 961 TCTGACTACTTGTGCCATCCCATCTGAGAACAGAGAGAACTCTTCCGGTATCCAGTGGAGAA 1020
DB 961 TCTGACTACTTGTGCCATCCCATCTGAGAACAGAGAGAACTCTTCCGGTATCCAGTGGAGAA 1020
QY 1021 TAGAACAGGAGGAGTGTGACATGAGTGGCTGAAACACCTTGAGGGAGTGGACATCCCATG 1080
DB 1021 TAGAACAGGAGGAGTGTGACATGAGTGGCTGAAACACCTTGAGGGAGTGGACATCCCATG 1080
QY 1081 TTGAGCAATGTCAATGGCATCAGGAGGCGGCCCAAGGGGCCCATCGCTTCCCTTTCATGC 1140
DB 1081 TTGAGCAATGTCAATGGCATCAGGAGGCGGCCCAAGGGGCCCATCGCTTCCCTTTCATGC 1140
QY 1141 ATCCATGTTCTGTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 1200
DB 1141 ATCCATGTTCTGTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1200
QY 1201 GACTCCCTTAACCTCAGACCTCTACGACCATTAAGACTCTGCCAGAACTGAGAGGCG 1260
DB 1201 GACTCCCTTAACCTCAGACCTCTACGACCATTAAGACTCTGCCAGAACTGAGAGGCG 1260
QY 1261 G 1261
DB 1261 G 1261

RESULT 3
ADB78651
ID ADB78651 standard; cDNA; 1261 BP.
XX
AC ADB78651;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human ion channel subunit cDNA mutant SCN1AR exon 1 SEQ ID NO:22.
XX
KW ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyrretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R.W.
XX
PI Mulvey JC, Harkin LA, Dibbans LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
XX

Identifying predisposition to an ion channel dysfunction, such as periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease, schizophrenia, anxiety and depression, by detecting encoding-gene mutation events.

Claim 6; SEQ ID NO 22; 106bp; English.

The invention relates to a novel method for identifying a subject predisposed to a disorder associated with ion channel dysfunction. The method comprises ascertaining if at least one of the genes encoding ion channel subunits (ICs) has undergone a mutation event so that a cDNA derived from the subject has any of 134 nucleotide sequences. The method of the invention has nootropic, neuroprotective, inotropic, antipyretic, antirhythmic, antimigraine, antidepressant, antiparkinsonian, neuroleptic, tranquiliser, analgesic, nephroretropic, antidiabetic, and ophthalmological activity. A polynucleotide of the invention acts as an ion channel agonist, or ion channel antagonist. The methods, isolated nucleic acids, polypeptides, antibody, selective agonist, antagonist or modulator of an ion channel, cells and genetically modified non-human animal, are useful for the diagnosis and treatment of epilepsy and/or a disorder associated with ion channel dysfunction, such as hyper- or hypokalemic periodic paralysis, myotonias, malignant hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety, depression, phobic obsessive symptoms, neuropathic pain, inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease, Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic fibrosis, congenital stationary night blindness and total colour blindness. The present sequence represents a mutant cDNA of the invention. The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

Sequence 1261 BP; 263 A; 365 C; 372 G; 261 T; 0 U; 0 Other;

Query Match 96.0%; Score 1210; DB 10; Length 1261;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CCCTCCCTCCGAGCTGAGCTTACCTGGCGCAACGAGCGAGGCGCGGAGTGG 60
1 CCCTCCCTCCGAGCTGAGCTTACCTGGCGCAACGAGCGAGGCGCGGAGTGG 60
61 AGCTGGAGTCCGGGTGGGAGGCGGAGTCTCGTGGTGTGAGCGCGCGGAGA 120
61 AGCTGGAGTCCGGGTGGGAGGCGGAGTCTCGTGGTGTGAGCGCGCGGAGA 120
121 GCGGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGCTCGCTTAG 180
121 GCGGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGCTCGCTTAG 180
181 GCGCCAAAGCCCCCAGCGGCTCCAAAGCTCCAGGGGCTCCCGAGGACCGGCTGCTG 240
181 GCGCCAAAGCCCCCAGCGGCTCCAAAGCTCCAGGGGCTCCCGAGGACCGGCTGCTG 240
241 GCGCTTCCTTCGGTCAAGAGTGGCGGCGGAGTTCGTCGCGGAGGCTTCCTCG 300
241 GCGCTTCCTTCGGTCAAGAGTGGCGGCGGAGTTCGTCGCGGAGGCTTCCTCG 300
301 AAAGAATCTGAGAGGCGGAGCTTCTTGACCGAGGGAATCTCTGTGTAGCTTGGAGG 360
301 AAAGAATCTGAGAGGCGGAGCTTCTTGACCGAGGGAATCTCTGTGTAGCTTGGAGG 360
361 CGCGAGCCCCAGAGATGCTGCTGCTTCAATAGATGTTTCCCTGCTGCTGCTGCTT 420
361 CGCGAGCCCCAGAGATGCTGCTGCTTCAATAGATGTTTCCCTGCTGCTGCTGCTT 420
421 ATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAGTCCCTCGGAGAGGAGGCC 480
421 ATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAGTCCCTCGGAGAGGAGGCC 480
481 GTGCGAGGCAACCCCATGAAGCTGCGCTGCATCTCTCGATGAAGAGAGAGGTGGAG 540

481 GTGCGAGGCAACCCCATGAAGCTGCGCTGCATCTCTCGATGAAGAGAGAGGTGGAG 540
541 GCCACACGCTGGTGGAAATGTTCTTACAGGCGCGGCGGTAAAGATTTCTTATTATAC 600
541 GCCACACGCTGGTGGAAATGTTCTTACAGGCGCGGCGGTAAAGATTTCTTATTATAC 600
601 GAGTATCGGAATGGCCACACGAGAGGTGGAGAGCCCTTTTCAGGGGCGCTGCAGTGGAA 660
601 GAGTATCGGAATGGCCACACGAGAGGTGGAGAGCCCTTTTCAGGGGCGCTGCAGTGGAA 660
661 GCGACCAAGGACCTTCAGAGAGCTGTCCATCACTGTGTCTCAAGCTCACTCTGAACGACTCT 720
661 GCGACCAAGGACCTTCAGAGAGCTGTCCATCACTGTGTCTCAAGCTCACTCTGAACGACTCT 720
721 GGCCTTACACTGCAATGTGTCCGGAGTGTGAGTTTGAAGGCGCATCGGCCCTTTGTG 780
721 GGCCTTACACTGCAATGTGTCCGGAGTGTGAGTTTGAAGGCGCATCGGCCCTTTGTG 780
781 AAGACGACGCGGCTGATCCCTCAAGAGTCAAGAGGAGGCTGGAGAGGACTTCACTCTCT 840
781 AAGACGACGCGGCTGATCCCTCAAGAGTCAAGAGGAGGCTGGAGAGGACTTCACTCTCT 840
841 GTGGTCTCAGAAATCATGATGTACATCTCTCTGTCTTCTCCTCACCTGTGGCTGCTCATC 900
841 GTGGTCTCAGAAATCATGATGTACATCTCTCTGTCTTCTCCTCACCTGTGGCTGCTCATC 900
901 GAGATGATATATTTGCTACAGAAAGTCTCAAAAGCGGAGGAGGAGCCCAAGAAACGGG 960
901 GAGATGATATATTTGCTACAGAAAGTCTCAAAAGCGGAGGAGGAGCCCAAGAAACGGG 960
961 TCTGACTACTTGGCTCCATCCCTCTGAGAAACAGGAGAACTCTGCGGTACCAGTGGAGAA 1020
961 TCTGACTACTTGGCTCCATCCCTCTGAGAAACAGGAGAACTCTGCGGTACCAGTGGAGAA 1020
1021 TAGAACAGGAGCAGTGTGACATGAGGTGGCTGTGAACACTCTGAGGGAGCTGGACATCCC 1080
1021 TAGAACAGGAGCAGTGTGACATGAGGTGGCTGTGAACACTCTGAGGGAGCTGGACATCCC 1080
1081 TTCAGCAATGTCATGGCATCAGAGGGGCGGCGGCGGAGGCGGCGGCGGCGGCGGCGG 1140
1081 TTCAGCAATGTCATGGCATCAGAGGGGCGGCGGCGGAGGCGGCGGCGGCGGCGGCGG 1140
1141 ATCCATGCTTCTGTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1200
1141 ATCCATGCTTCTGTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1200
1201 GACTCCCTTAACCTCCATCAGACCTTACGACCATTAAGACTCTGCGAGAACTGAGAGCGG 1260
1201 GACTCCCTTAACCTCCATCAGACCTTACGACCATTAAGACTCTGCGAGAACTGAGAGCGG 1260
1261 G 1261
1261 G 1261

RESULT 4
ABA93727

ID ABA93727 standard; cDNA; 4052 BP.

XX ABA93727;

DT 30-APR-2002 (first entry)

XX Human signal transduction cDNA clone amy2_2f18.

XX Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
XX gene therapy; ss.

XX Homo sapiens.

XX WO200198454-A2.

XX 27-DEC-2001.

XX 25-APR-2001; 2001WO-IB002050.
 PF XX
 XX 25-APR-2000; 2000US-0199380P.
 PR XX
 XX (GBHU-) GERMAN HUMAN GENOME PROJECT.
 PA XX
 XX Wiemann S;
 PI XX
 XX WPI: 2002-055860/07.
 DR P-PSDB; ABB05689.
 DR XX
 XX Human cDNA sequences and clones derived from human fetal brain, fetal
 PT kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
 PT screening and therapy.
 PT XX
 XX Claim 1; Page 174-175; 611pp; English.
 PS XX
 XX The present invention describes assemblages and computer readable media
 CC comprising novel human cDNA sequences and clones derived from human
 CC foetal brain, foetal kidney, melanoma, testis and amygdala cDNA
 CC libraries. ABA93702 to ABA93766 represent human cDNA sequences from the
 CC present invention which encode the proteins given in ABB05662 to
 CC ABB05729. The human cDNA sequences and clones can be used in gene
 CC therapy. The clones may be used in a variety of applications, for example
 CC they may be used in profiling assays, for providing large arrays of human
 CC genetic material for implementing large-scale screening strategies and
 CC for treating diseases via gene therapy procedures
 XX
 SQ Sequence 4052 BP; 994 A; 1033 C; 1036 G; 989 T; 0 U; 0 Other;
 Query Match 87.5%; Score 1104; DB 6; Length 4052;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1254; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 CTCCTTTCCGAGCTGAGCTTACCTCGGGCGCAACAGCGAGGCGAGGGCGCGAGTGGAA 62
 DB 431 CTCCTTTCCGAGCTGAGCTTACCTCGGGCGCAACAGCGAGGCGAGGGCGCGAGTGGAA 490
 QY 63 GCTGGAGTTCGGGGTGGGGGAGGCGAGCTGTCCTGTGTGCTGAGCGCGGGGAGAGC 122
 DB 491 GCTGGAGTTCGGGGTGGGGGAGGCGAGCTGTCCTGTGTGCTGAGCGCGGGGAGAGC 550
 QY 123 GGGCGGCGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCAGTGGGGTTCGCTTAGGG 182
 DB 551 GGGCGGCGAGCGGCTGATCAGCTCCCTCGAACTGGGAGGTCAGTGGGGTTCGCTTAGGG 610
 QY 183 CCCTTCTTCCGAGCTGAGCTTCCCTCGAAAGCTCCAGGGGCTCCCGAGGCGCGGCTCGGC 242
 DB 611 CCCTTCTTCCGAGCTGAGCTTCCCTCGAAAGCTCCAGGGGCTCCCGAGGCGCGGCTCGGC 670
 QY 243 CTTCTCTTCCGAGCTGAGCTTCCCTCGAAAGCTCCAGGGGCTCCCGAGGCGCGGCTCGGC 302
 DB 671 CTTCTCTTCCGAGCTGAGCTTCCCTCGAAAGCTCCAGGGGCTCCCGAGGCGCGGCTCGGC 730
 QY 303 AGAATCTGAGAGGCGGAGCTTCCCTCGAAAGCTCCAGGGGCTCCCGAGGCGCGGCTCGGC 362
 DB 731 AGAATCTGAGAGGCGGAGCTTCCCTCGAAAGCTCCAGGGGCTCCCGAGGCGCGGCTCGGC 790
 QY 363 CCAGCCCCCAGAGGATGCTGCTTCAATAGATTGTTTCCCTCGGCTTCTCTCGGCTTAT 422
 DB 791 CCAGCCCCCAGAGGATGCTGCTTCAATAGATTGTTTCCCTCGGCTTCTCTCGGCTTAT 850
 QY 423 CTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 482
 DB 851 CTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 910
 QY 483 GCAGGGCAACCCCATGAGCTGCGCTGCATCTCTGCTGATCAAGAGAGAGAGAGGTTGAGGC 542
 DB 911 GCAGGGCAACCCCATGAGCTGCGCTGCATCTCTGCTGATCAAGAGAGAGAGGTTGAGGC 970
 QY 543 CACCACGGTGGTGAATGGTTCTACAGCGCGGCGGCTGAAGATTCTTTATTACGA 602

DB 971 CACCACGGTGGTGAATGGTTCTACAGCCCGAGGGCGGTAAAGATTTCCTTTATTACGA 1030
 QY 603 GTATCGGAATGGCCACCAGAGGTTGGAGAGCCCTTTTCAGGGGCGCTTCGAGTGAATGG 662
 DB 1031 GTATCGGAATGGCCACCAGAGGTTGGAGAGCCCTTTTCAGGGGCGCTTCGAGTGAATGG 1090
 QY 663 CAGCAAGGACCTGCAGGACGTCCTGCTCAAGCTCACTGTGCTCAAGCTCACTGTGAGTCTGG 722
 DB 1091 CAGCAAGGACCTGCAGGACGTCCTGCTCAAGCTCACTGTGCTCAAGCTCACTGTGAGTCTGG 1150
 QY 723 CCTCTACACCTGCAATGTGTCCCGGAGTTTGAAGTGTGAGGCGCATCGGCCCTTTGTGAA 782
 DB 1151 CCTCTACACCTGCAATGTGTCCCGGAGTTTGAAGTGTGAGGCGCATCGGCCCTTTGTGAA 1210
 QY 783 GAGCAGCGGCTGATCCCTTAAGAGTCAAGAGGAGGCTGAGAGGAGCTTCACTCTGT 842
 DB 1211 GAGCAGCGGCTGATCCCTTAAGAGTCAAGAGGAGGCTGAGAGGAGCTTCACTCTGT 1270
 QY 843 GGTCTCAGAAATCATGATGTACATCTCTTGTGCTTCTCCTCACCTGTGGTGTCTCATCGA 902
 DB 1271 GGTCTCAGAAATCATGATGTACATCTCTTGTGCTTCTCCTCACCTGTGGTGTCTCATCGA 1330
 QY 903 GATGATATATGTGTACAGAAAGGTCTCAAAAGCGGAGAGGCGAGCCCAAGAAAACGGCTC 962
 DB 1331 GATGATATATGTGTACAGAAAGGTCTCAAAAGCGGAGAGGCGAGCCCAAGAAAACGGCTC 1390
 QY 963 TGACTACCTTGGCCATCCATCTGAGAACAGGAGAACTCTGCGGTACAGTGGAGGAAATA 1022
 DB 1391 TGACTACCTTGGCCATCCATCTGAGAACAGGAGAACTCTGCGGTACAGTGGAGGAAATA 1450
 QY 1023 GAACAGGAGCAGTGTGATGATGAGTGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 1082
 DB 1451 GAACAGGAGCAGTGTGATGATGAGTGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 1510
 QY 1083 CAGCAATGTCAATGGCATCAGAGGCGCGCCCAAGGCGCCCATCGCTTCCCTTTCATGAT 1142
 DB 1511 CAGCAATGTCAATGGCATCAGAGGCGCGCCCAAGGCGCCCATCGCTTCCCTTTCATGAT 1570
 QY 1143 CCATTGTTCTGTTTCACTTTCATTCATCATCATCATCATCATCATCATCATCATCATCATCATCTGA 1202
 DB 1571 CCATTGTTCTGTTTCACTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1630
 QY 1203 CTCCTTAACCTCCATCAGACCTTACGCAACCATTAAGACTCTGCCAGAACTGAGAGCC 1259
 DB 1631 CTCCTTAACCTCCATCAGACCTTACGCAACCATTAAGACTCTGCCAGAACTGAGAGCC 1687
 RESULT 5
 AAF84146
 ID AAF84146 standard; cDNA; 1510 BP.
 XX
 AC AAF84146;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human novel sodium channel betal-like subunit encoding cDNA.
 XX
 KW Sodium channel; sensory neurone specific channel; betal-like subunit;
 KW SNS; therapeutic; pain; analgesic; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 213..860
 FT /*tag= a
 FT /product= "sodium channel betal-like subunit"
 XX
 XX WO20014293-A2.
 XX
 XX 21-JUN-2001.
 XX
 XX 14-DEC-2000; 2000WO-GB004802.
 XX
 XX

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PR 17-DEC-1999; 99CB-00029970.
XX (GLAX ) GLAXO GROUP LTD.
PA Plumpton M, Powell AJ, Sanseau P;
PI WPI; 2001-398129/42.
XX P-PSDB; AAB85206.
DR Novel sub-unit for voltage-gated sodium channel proteins for producing
PT agents useful for treating pain.
XX Claim 4; Page 29-30; 31pp; English.
XX The invention provides a novel betal-like sub-unit for voltage-gated
CC sodium ion channel polypeptide, specifically a sensory neurone specific
CC channel (SNS) subunit. The novel betal-like subunit is useful for
CC producing a therapeutic agent which is useful treating pain in a patient.
CC The subunit can be expressed by standard recombinant methodology. The
CC present sequence represents a human novel sodium channel betal-like
CC subunit encoding cDNA
XX
SQ Sequence 1510 BP; 350 A; 410 C; 414 G; 336 T; 0 U; 0 Other;
Query Match 68.2%; Score 860; DB 4; Length 1510;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 910; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 349 AGCCTTGAAGCGCCGAGCCAGAGATGCTGCTTCAATAGATGTTTCCCTGGCT 408
DB 186 AGCCTTGAAGCGCCGAGCCAGAGATGCTGCTTCAATAGATGTTTCCCTGGCT 245
QY 409 TCTCTGCTTATCTACTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 468
DB 246 TCTCTGCTTATCTACTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 305
QY 469 GAGAGCGAGCGCTGAGCGGCAACCCATGAGTGGCTGCTGCTGCTGCTGCTGCTG 528
DB 306 GAGAGCGAGCGCTGAGCGGCAACCCATGAGTGGCTGCTGCTGCTGCTGCTGCTG 365
QY 529 GAGAGGCTGAGCGGCAACCCATGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588
DB 366 GAGAGGCTGAGCGGCAACCCATGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 425
QY 589 TTCCTTATTTACAGTATCGAATGCGCAACCGAGGCTGAGAGGCTGAGAGGCTG 648
DB 426 TTCCTTATTTACAGTATCGAATGCGCAACCGAGGCTGAGAGGCTGAGAGGCTG 485
QY 649 CTGCAGTGAATGGCAGCAAGGACCTGCGAGGAGCTGCTCCTCACTGCTCAACGTC 708
DB 486 CTGCAGTGAATGGCAGCAAGGACCTGCGAGGAGCTGCTCCTCACTGCTCAACGTC 545
QY 709 CTGAACGACTCTGGCTCTTACACCTGCAATGTGTCCTGGGAGTTTGAAGTTCAGG 768
DB 546 CTGAACGACTCTGGCTCTTACACCTGCAATGTGTCCTGGGAGTTTGAAGTTCAGG 605
QY 769 CGGCCCTTTGAGAGCAGCGGCTGTATCCCTTAAAGAGTCAACGAGAGGCTGAGAG 828
DB 606 CGGCCCTTTGAGAGCAGCGGCTGTATCCCTTAAAGAGTCAACGAGAGGCTGAGAG 665
QY 829 GACTTCACCTGTGTGCTCAGAAATCATGATGATCATCTTCTGTCTTCTCAACCTG 888
DB 666 GACTTCACCTGTGTGCTCAGAAATCATGATGATCATCTTCTGTCTTCTCAACCTG 725
QY 889 TGGCTGCTCATCGAGATGATATTTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCC 948
DB 726 TGGCTGCTCATCGAGATGATATTTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCC 785
QY 949 CAAGAAACCGCTGTGACTACCTTGGCATCCCATCTGAGAACAGAGAACTCTGGGTA 1008
DB 786 CAAGAAACCGCTGTGACTACCTTGGCATCCCATCTGAGAACAGAGAACTCTGGGTA 845
QY 1009 CCAGTGGAGGAATAGAACAGGAGCAGTGTGATGAGGTGGCTGCTGAACACCTGAGG 1068
DB 846 CCAGTGGAGGAATAGAACAGGAGCAGTGTGATGAGGTGGCTGCTGAACACCTGAGG 905
QY 1069 GGACATCCCATGTTTCAAGCAATGTCAATGGCATCAGAGGGCGCCCAAGGGCCCATCGC 1128
DB 906 GGACATCCCATGTTTCAAGCAATGTCAATGGCATCAGAGGGCGCCCAAGGGCCCATCGC 965
QY 1129 TTCCCTTCAATGATCCATGTTTCTTCAATTCATTCATTCATTCATTCATTCATTC 1188
DB 966 TTCCCTTCAATGATCCATGTTTCTTCAATTCATTCATTCATTCATTCATTCATTC 1025
QY 1189 GCTTTCACCTCTGACTCCCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1248
DB 1026 GCTTTCACCTCTGACTCCCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1085
QY 1249 ACTGAGAGGCC 1259
DB 1086 ACTGAGAGGCC 1096
RESULT 6
AAH98320
ID AAH98320 standard; cDNA; 978 BP.
XX
AC AAH98320;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST-derived coding sequence SEQ ID NO: 177.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002687.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI; 2001-476164/51.
XX
DR P-PSDB; AAM23661.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
PS Claim 1; Page 299-300; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention
XX
SQ Sequence 978 BP; 193 A; 283 C; 293 G; 209 T; 0 U; 0 Other;
Query Match 63.3%; Score 798; DB 4; Length 978;
```


QY 568 AGCCCGGCGGTAAGATTTCTTATTTACGATATCGGAATGGCCACGAGGAGTG 627
 Db 487 AGCCCGGCGGTAAGATTTCTTATTTACGATATCGGAATGGCCACGAGGAGTG 546
 QY 628 GAGAGCCCTTTTCAGGGGCGCTGCAAGTGAATGGCAGCAAGACCTGAGGACGTGTCC 687
 Db 547 GAGAGCCCTTTTCAGGGGCGCTGCAAGTGAATGGCAGCAAGACCTGAGGACGTGTCC 606
 QY 688 ATCACTGTGCTCAACTCTACTCTGAACGACTCTGGGCTCTACACCTGCAATGTCTCCCG 747
 Db 607 ATCACTGTGCTCAACTCTACTCTGAACGACTCTGGGCTCTACACCTGCAATGTCTCCCG 666
 QY 748 GAGTTTGAATGAGGCGGATCGCCCTTTGTGAAGACGAGCGGCTGATCCCTTAAGA 807
 Db 667 GAGTTTGAATGAGGCGGATCGCCCTTTGTGAAGACGAGCGGCTGATCCCTTAAGA 726
 QY 808 GTCAACGAGGAGGCTGAGAGGACTTCACTCTGTGTCTCAAAATCATGATGATCATC 867
 Db 727 GTCAACGAGGAGGCTGAGAGGACTTCACTCTGTGTCTCAAAATCATGATGATCATC 786
 QY 868 CTTCTGGTCTTCTCACC 885
 Db 787 CTTCTGGTCTTCTCACC 804

RESULT 8

AAK52345
 ID AAK52345 standard; cDNA; 1045 BP.
 AC AAK52345;
 XX
 DT 06-NOV-2001 (first entry)
 DE Human polynucleotide SEQ ID NO 890.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US004098.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 XX WPI; 2001-476283/51.
 DR P-PSDB; AAM79212.
 DR
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 XX
 PS Claim 1; Page 2934-2935; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the

CC encoded polypeptides' (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 SQ Sequence 1045 BP; 222 A; 289 C; 314 G; 220 T; 0 U; 0 Other;
 Query Match 62.4%; Score 787; DB 4; Length 1045;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 837; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 124 GCGCGGAGCGGCTGATCGGCTCCCTCGAATCGGGAGGTCAGTGGGTGCTTAGGGC 183
 Db 50 GCGCGGAGCGGCTGATCGGCTCCCTCGAATCGGGAGGTCAGTGGGTGCTTAGGGC 109
 QY 184 CCAAGAGCCGCCACCGGCTCCAAAAGCTCCCAAGGCTCCCAAGGACCGGTGCTCGGCC 243
 Db 110 CCAAGAGCCGCCACCGGCTCCAAAAGCTCCCAAGGCTCCCAAGGACCGGTGCTCGGCC 169
 QY 244 CTTCTTTCGGTCAGAAAGTGCCTCCCTGGGGCAGTTCGTCCCAAGGGTTTCTCGAAA 303
 Db 170 CTTCTTTCGGTCAGAAAGTGCCTCCCTGGGGCAGTTCGTCCCAAGGGTTTCTCGAAA 229
 QY 304 GAATCTGAGAGGGCGCAGTCTTGACCGAGGGAATCTCTGTGTAGCCTTGAAGCCGC 363
 Db 230 GAATCTGAGAGGGCGCAGTCTTGACCGAGGGAATCTCTGTGTAGCCTTGAAGCCGC 289
 QY 364 CAGCCCCAGAAGTGCCTTCAATAGATTTTCCCTGGCTTCTCTCGTGTATC 423
 Db 290 CAGCCCCAGAAGTGCCTTCAATAGATTTTCCCTGGCTTCTCTCGTGTATC 349
 QY 424 TACTGGGTGAGTGTCTGTCTTCCCTGTGTGGAAGTGCCTCGGAGACGAGGCGGTG 483
 Db 350 TACTGGGTGAGTGTCTGTCTTCCCTGTGTGGAAGTGCCTCGGAGACGAGGCGGTG 409
 QY 484 CAGGGCAACCCCATGAAGCTGCGTGCATCTCCTGCATGAGAGAGAGAGGAGTGGAGCC 543
 Db 410 CAGGGCAACCCCATGAAGCTGCGTGCATCTCCTGCATGAGAGAGAGAGTGGAGCC 469
 QY 544 ACCACGCTGGTGAATGGTTCTACAGGCGCGAGGCGGTAAAGATTTCTTATTTACGAG 603
 Db 470 ACCACGCTGGTGAATGGTTCTACAGGCGCGAGGCGGTAAAGATTTCTTATTTACGAG 529
 QY 604 TATCGAATGGCCACGAGAGGTGAGAGCCCTTTTCAGGGGCGCTGAGTGGGAATGCG 663
 Db 530 TATCGAATGGCCACGAGAGGTGAGAGCCCTTTTCAGGGGCGCTGAGTGGGAATGCG 589
 QY 664 AGCAGAGGAGTGCAGAGAGTGCATCTGCTGCTCAAGTGCATCTGCAACACTCTGCG 723
 Db 590 AGCAGAGGAGTGCAGAGAGTGCATCTGCTGCTCAAGTGCATCTGCAACACTCTGCG 649
 QY 724 CTTCTACCTGCAATGTGTCCCGGAGTTTGAAGTGAAGGCGCATCGGCCCTTTTGTGAAG 783
 Db 650 CTTCTACCTGCAATGTGTCCCGGAGTTTGAAGTGAAGGCGCATCGGCCCTTTTGTGAAG 709
 QY 784 ACGACGCGGCTGATCCCTCAAGAGTCAACGAGAGGCTGAGAGACTTCACTCTGTG 843
 Db 710 ACGACGCGGCTGATCCCTCAAGAGTCAACGAGAGGCTGAGAGACTTCACTCTGTG 769
 QY 844 GTCTCAGAAATCATGATGATCTTCTGCTTCTTCTCAACCTGCTGCTCATCGAG 903
 Db 770 GTCTCAGAAATCATGATGATGATCTTCTGCTTCTTCTCAACCTGCTGCTCATCGAG 829
 QY 904 ATGATATATTGTCACAGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACCGGT 961

Db 830 ATGATATATTCTACAGAAAGTCTCAAAGCCGAAGAGGAGCCCAAGAAACGGCT 887

RESULT 9

ADSL0151

ID ADS10151 standard; DNA; 953 BP.

XX AC

XX ADS10151;

XX

DT 16-DEC-2004 (first entry)

XX

DE Human therapeutic DNA - SEQ ID 388.

XX

XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;

KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;

KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.

XX

OS Homo sapiens.

XX

XX WO2004080148-A2.

XX

XX 23-SEP-2004.

XX

XX 30-SEP-2003; 2003WO-US030720.

XX

XX 02-OCT-2002; 2002US-0416186P.

XX

XX (NUVE-) NUVELO INC.

XX

PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;

PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;

XX

XX WPI; 2004-668857/65.

DR

DR P-PSDB; ADS10835.

XX

XX New polynucleotide, useful in preparing a composition for diagnosing or

PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,

PT aplastic anemia or cancer for promoting wound healing.

XX

PS Claim 1; SEQ ID NO 388; 718pp; English.

XX

CC The invention relates to a novel isolated polynucleotide and the encoded

CC polypeptide. The molecules of the invention demonstrate antiinflammatory,

CC neuroprotective, antianaemic, cytostatic and vulnery activities and may

CC be useful in preparing a composition for diagnosing or treating

CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell

CC disorders, such as aplastic anaemia or cancer, as well as for promoting

CC wound healing. The molecules may also be utilised during gene therapy

CC procedures. The current sequence is that of a human therapeutic DNA of

CC the invention. The current sequence is not shown explicitly within the

CC specification but can be accessed from the WIPO web-site.

XX

SQ Sequence 953 BP; 180 A; 279 C; 290 G; 204 T; 0 U; 0 Other;

Query Match 60.3%; Score 760; DB 13; Length 953;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 760; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 88 GCGGACTGTCGCTGCTGAGCGCCGCGGAGAGCGGCGGCGGCGGCTGATCGGCTCC 147

Db 39 GCGGACTGTCGCTGCTGAGCGCCGCGGAGAGCGGCGGCGGCTGATCGGCTCC 98

Qy 148 CTCGAATCGGGAGGTCAGTGCGGTCGTTAGGGCCCAAGCCGCCCGGCTCCAAA 207

Db 99 CTGNACTGGGAGGTCAGTGCGGTCGTTAGGGCCCAAGCCGCCCGGCTCCAAA 158

Qy 208 AGCTCCAGGCGCTCCCGGAGGTCGTTAGGGCCCGGCTCCCGGAGAGTCCGCC 267

Db 159 AGCTCCAGGCGCTCCCGGAGGTCGTTAGGGCCCGGCTCCCGGAGAGTCCGCC 218

Qy 268 CTTGGGGGCGATGCTGCTCCCAAGGTTTCTCGAAAGAAATCTGAGAGGCGGCTGCTG 327

Db 219 CTTGGGGGCGATGCTGCTCCCAAGGTTTCTCGAAAGAAATCTGAGAGGCGGCTGCTG 278

Qy 328 ACCGAGGGAATCTCTCTGTGTAGCTTTGGAAGCGCCAGCCAGAGAGATGCTGCGCTTC 387

Db 279 ACCGAGGGAATCTCTCTGTGTAGCTTTGGAAGCGCCAGCCAGAGAGATGCTGCGCTTC 338

Qy 388 AATAGATTGTTTCCCTGGCTTCTCTGCTTATCTACTTGGGTGAGTGTGCTGCTCCCT 447

Db 339 AATAGATTGTTTCCCTGGCTTCTCTGCTTATCTACTTGGGTGAGTGTGCTGCTCCCT 398

Qy 448 GTGTGTGTGAAGTGCCTCGGAGAGCGGCGCTGAGGGCAACCCCATGAAGCTGGC 507

Db 399 GTGTGTGTGAAGTGCCTCGGAGAGCGGCGCTGAGGGCAACCCCATGAAGCTGGC 458

Qy 508 TGCATCTCTCTGATGAAGAGAGAGGAGTGGAGGCCACACCGTGGTGGATGTTCTAC 567

Db 459 TGCATCTCTCTGATGAAGAGAGAGGAGTGGAGGCCACACCGTGGTGGATGTTCTAC 518

Qy 568 AGGCGCGAGGCGGTAAAGATTTCCTTATTAAGATTCGGAATGCGCAACCGAGAGGTG 627

Db 519 AGGCGCGAGGCGGTAAAGATTTCCTTATTAAGATTCGGAATGCGCAACCGAGAGGTG 578

Qy 628 GAGAGCCCTTTCAGGGCGCTGCGAGTGAAGTGGAGCAAGGACCTGCGAGGAGCTGCC 687

Db 579 GAGAGCCCTTTCAGGGCGCTGCGAGTGAAGTGGAGCAAGGACCTGCGAGGAGCTGCC 638

Qy 688 ATCACTGTGTCTCAACGTCACCTCTGAACGACTCTGGCCCTTACACCTGCAATGTGTCGG 747

Db 639 ATCACTGTGTCTCAACGTCACCTCTGAACGACTCTGGCCCTTACACCTGCAATGTGTCGG 698

Qy 748 GAGTTGAGTTTGAAGCGCATCGGCCCTTTGTGAAGACGACGCGGCTGATCCCTTAAGA 807

Db 699 GAGTTGAGTTTGAAGCGCATCGGCCCTTTGTGAAGACGACGCGGCTGATCCCTTAAGA 758

Qy 808 GTCAACGAGGAGGCTGAGAGGACTTCACTCTGTGCTCT 847

Db 759 GTCAACGAGGAGGCTGAGAGGACTTCACTCTGTGCTCT 798

RESULT 10

AAS86764

ID AAS86764 standard; cDNA; 1195 BP.

XX

XX AAS86764;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #22568.

XX

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Dmanac RT, Liu C, Tang YT;

XX

XX WPI; 2001-639362/73.

DR

DR P-PSDB; ABG22577.

XX

XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity.

QY 730 ACCTGCAATGTGTCCTGGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGAAGACGACG 789
Db 3259 ACCTGCAATGTGTCCTGGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGAAGACGACG 3318
QY 790 CGGCTGATCCCTTAAGAGTACCGAGGAGG 820
Db 3319 CGGCTGATCCCTTAAGAGTACCGAGGAGG 3349

RESULT 12
AAV86895
ID AAV86895 standard; cDNA; 471 BP.
XX AC AAV86895;
XX
DT 27-APR-1999 (first entry)
XX EST clone BM4.
XX
XX Expressed sequence tag; secreted protein; haematopoiesis regulator;
KW tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
KW chemotaxis; chemokines; haemostasis; gene therapy; thrombolysis;
KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
XX
OS Homo sapiens.
XX
XX WO9845435-A2.
XX
XX 15-OCT-1998.
XX
XX 10-APR-1998; 98WO-US006954.
XX
XX 10-APR-1997; 97US-00835913.
XX
XX (GEMY) GENETICS INST INC.
XX
XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Spaulding V, Agostino MJ;
XX WPI; 1999-070076/06.
XX
XX New polynucleotides encoding human secreted proteins - derived from e.g.
PT human blood, kidney, foetal lung, placenta, testes, brain, ovary,
PT pituitary, retina and colon cDNA libraries.
XX
XX Claim 1; Page 383-384; 633pp; English.

This sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic activity and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene therapy

Query Match 25.7%; Score 324; DB 2; Length 471;
Best Local Similarity 100.0%; Pred. No. 1e-146;
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 487 GGCAACCCCATGAAGTGCCTGCATCTCTGTCATGAAGAGAGAGGAGGCGGCACG 546
Db 139 GGCAACCCCATGAAGTGCCTGCATCTCTGTCATGAAGAGAGAGGAGGCGGCACG 198
QY 547 ACGGTGGTGAATGGTTCTACAGCCCGGAGCGGTAAGATTTCTTTATTACGAGTAT 606

Db 199 ACGGTGGTGAATGGTTCTACAGCCCGAGGGCGGTAAAGATTTCTTTATTACGAGTAT 258
QY 607 CGGAATGGCCACAGAGGTGGAGAGCCCTTTTCAGGGCGCCTGCAGTGGATGGCAGC 666
Db 259 CGGAATGGCCACAGAGGTGGAGAGCCCTTTTCAGGGCGCCTGCAGTGGATGGCAGC 318
QY 667 AAGGAGCTGCAGGACGTGTCCATCACTGTGTCTCAAGGTCACTCTGAACGACTCTGGGCTC 726
Db 319 AAGGAGCTGCAGGACGTGTCCATCACTGTGTCTCAAGGTCACTCTGAACGACTCTGGGCTC 378
QY 727 TACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGAAGACG 786
Db 379 TACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGAAGACG 438
QY 787 ACGCGCTGATCCCTTAAGAGTC 810
Db 439 ACGCGCTGATCCCTTAAGAGTC 462

RESULT 13
AAS86762
ID AAS86762 standard; cDNA; 621 BP.
XX AC AAS86762;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #22566.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
PI
XX WPI; 2001-639362/73.
DR P-PSDB; ABG22575.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 1; SEQ ID NO 22566; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have application in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 621 BP; 156 A; 155 C; 175 G; 135 T; 0 U; 0 Other;

Query Match 17.3%; Score 218; DB 5; Length 621;
 Best Local Similarity 100.0%; Pred. No. 3.1e-95;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 595 ATTACGATATCGGAATGCCACAGGAGGTGGAGAGCCCTTTTCAGGGGGCGCTGCAG 654

DB 58 ATTACGATATCGGAATGCCACAGGAGGTGGAGAGCCCTTTTCAGGGGGCGCTGCAG 117

OY 655 TCGAATGGCAGCAAGGACCTGCAGACGCTGCTCATCTGCTCAACGTCACCTCTGAAC 714

DB 118 TCGAATGGCAGCAAGGACCTGCAGACGCTGCTCATCTGCTCAACGTCACCTCTGAAC 177

OY 715 GACTCTGGCCTCTACACCTGCAGTAATGTCCCGGAGTTTGAGTTTGAGCGGCATCGGCC 774

DB 178 GACTCTGGCCTCTACACCTGCAGTAATGTCCCGGAGTTTGAGTTTGAGCGGCATCGGCC 237

OY 775 TTTGTGAGACACCGCGCTGATCCCTTAAGATCAC 812

DB 238 TTTGTGAGACACCGCGCTGATCCCTTAAGATCAC 275

RESULT 14

AAL04971

ID AAL04971 standard; DNA; 4625 BP.

XX AC AAL04971;

XX 21-NOV-2001 (first entry)

DE Human reproductive system related antigen DNA SEQ ID NO: 7659.

XX Human; reproductive system related antigen; reproductive system disorder;
 KW cancer; gene therapy; ds.

XX OS Homo sapiens.

XX PN WO200155320-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US001339.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 14-AUG-2000; 2000US-0225267P.
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 PR 20-OCT-2000; 2000US-0241828P.
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 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
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 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 XX WPI; 2001-465570/50.
 DR
 XX Isolated nucleic acid molecule encoding a reproductive system antigen is
 PT used in preventing, treating or ameliorating a medical condition.
 XX
 XX Disclosure; SEQ ID NO 7659; 1297pp + Sequence Listing; English.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of human reproductive system related antigens. These can be used
 CC in the prevention and treatment of reproductive system disorders,
 CC including cancer. The present sequence is a genomic sequence encoding a
 CC protein of the invention
 XX
 XX Sequence 4625 BP; 1222 A; 1130 C; 906 G; 1367 T; 0 U; 0 Other;
 SQ
 Query Match 17.1%; Score 216; DB 4; Length 4625;
 Best Local Similarity 100.0%; Pred. No. 2.8e-94;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1044 AGTGGCGCTGAACACCTGAGGAGCTGGACATCCCATGTTTCAGCAATGTCATGGCATCAG 1103
 DB 33 AGTGGCGCTGAACACCTGAGGAGCTGGACATCCCATGTTTCAGCAATGTCATGGCATCAG 92
 QY 1104 GAGGGGCCCCAGAGGCCCCCATGCTTCCTTCATGCATCATTTGTTCTTCATTCATT 1163
 DB 93 GAGGGGCCCCAGAGGCCCCCATGCTTCCTTCATGCATCATTTGTTCTTCATTCATT 152
 QY 1164 CATCCATACATCCACCTGCCTCTGAGCTTTTCAGCTCTGACTCCCTAACTCCATCAGACCT 1223

Db 153 CATCCATACATCCACCTGCCTCTGAGCTTTTCACCTCTGACTCCCTAACTCCATCAGACCT 212
 QY 1224 CTAGGCACCAATAAGACTCTGCCAGAACTGAGAAGCC 1259
 Db 213 CTAGGCACCAATAAGACTCTGCCAGAACTGAGAAGCC 248
 RESULT 15
 ABL97864
 ID ABL97864 standard; DNA; 4625 BP.
 XX
 AC ABL97864;
 DT 21-JUN-2002 (first entry)
 XX
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2516.
 XX
 KW Human; testicular antigen; testes; cancer; metastasis; immune disorder;
 KW reproductive system disorder; urinary system disorder; gene therapy;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disease; infection; cytostatic; gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200155317-A2.
 PN
 XX
 PD 02-AUG-2001.
 XX
 XX 17-JAN-2001; 2001WO-US001329.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
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 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
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PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
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PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
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PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
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PR 01-NOV-2000; 2000US-0244617P.
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PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483232/52.
DR
XX
PT Nucleic acids encoding 973 human testicular antigen polypeptides, useful
PT for preventing, diagnosing and/or treating testicular cancer.
XX
PS Disclosure; SEQ ID NO 2516; 766pp; English.
XX
CC The present invention provides the protein and coding sequences of 973
CC human testicular antigens, and fragments of their genomic sequences. The
CC sequences can be used in the treatment of cardiovascular, urinary system,
CC reproductive system, immune, respiratory, neurological and
CC gastrointestinal disorders, infections, and particularly cancer,
CC especially testicular cancers. The present sequence is a DNA encoding a
CC protein fragment of the invention
XX
SQ Sequence 4625 BP; 1222 A; 1130 C; 906 G; 1367 T; 0 U; 0 Other;
Query Match 17.1%; Score 216; DB 4; Length 4625;
Best Local Similarity 100.0%; Pred. No. 2.8e-94;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1044 AGGTGGCTGAACACCTGAGGACTGGACATCCCATGTTTCAGCAATGTCAATGGCATCAG 1103
DB 33 AGGTGGCTGAACACCTGAGGACTGGACATCCCATGTTTCAGCAATGTCAATGGCATCAG 92
QY 1104 GAGGGCGCCCAAGGGCCCATCGCTTCCTTCATGCAATCCATTGTTCTGTTTCATTCAAT 1163
DB 93 GAGGGCGCCCAAGGGCCCATCGCTTCCTTCATGCAATCCATTGTTCTGTTTCATTCAAT 152
QY 1164 CATCCATACATCCACCTGCCTCTGAGCTTCACCTGCTCCCTACCTCCCTAACTCCATCAGACCT 1223
DB 153 CATCCATACATCCACCTGCCTCTGAGCTTCACCTGCTCCCTACCTCCCTAACTCCATCAGACCT 212
QY 1224 CTACGCACCATTAAGACTCTGCCAGAACTGAGAAGCC 1259
DB 213 CTACGCACCATTAAGACTCTGCCAGAACTGAGAAGCC 248

Search completed: April 7, 2005, 06:13:24
Job time : 708 secs

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OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 05:56:24 ; Search time 254 Seconds
(without alignments)
8123.405 Million cell updates/sec

Title: US-09-977-579-4
Perfect score: 1261
Sequence: 1 cctcccttcgagctgagc.....tgccagaactgagaagccgg 1261

Scoring table: Oligo_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 10

Total number of hits satisfying chosen parameters: 578812

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCFUS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	24	1.9	601	4	US-09-949-016-26733, A
C 2	24	1.9	601	4	US-09-949-016-194175, A
C 3	24	1.9	137949	4	US-09-949-016-12196, A
C 4	24	1.9	137956	4	US-09-949-016-17260, A
C 5	20	1.6	1491	4	US-09-902-540-6997, Ap
C 6	20	1.6	4312	4	US-09-902-540-612, Ap
C 7	20	1.6	4403765	3	US-09-103-840A-2
C 8	20	1.6	4411529	3	US-09-103-840A-1
C 9	19	1.5	601	4	US-09-949-016-85015
C 10	19	1.5	601	4	US-09-949-016-85166
C 11	19	1.5	1626	1	US-08-381-433A-3
C 12	19	1.5	1626	4	US-09-799-978-17
C 13	19	1.5	1626	4	US-09-881-401-3
C 14	19	1.5	5895	4	US-09-902-540-792
C 15	19	1.5	109159	4	US-09-949-016-14169
C 16	19	1.5	109159	4	US-09-949-016-14170, A
C 17	18	1.4	344	3	US-09-157-177-128
C 18	18	1.4	344	4	US-09-541-210-128
C 19	18	1.4	466	3	US-09-280-116-14
C 20	18	1.4	570	4	US-09-621-976-1635
C 21	18	1.4	601	4	US-09-949-016-56070
C 22	18	1.4	601	4	US-09-949-016-122006
C 23	18	1.4	601	4	US-09-949-016-131295
C 24	18	1.4	601	4	US-09-949-016-131296
C 25	18	1.4	601	4	US-09-949-016-131297
C 26	18	1.4	601	4	US-09-949-016-134047
C 27	18	1.4	601	4	US-09-949-016-138018

ALIGNMENTS

RESULT 1

US-09-949-016-26733/c
; Sequence 26733, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26733
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-26733

Query Match 1.9%; Score 24; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1156	CATTCATTCATCCATCATCCACC	1179
Db	472	CATTCATTCATCCATCATCCACC	449

RESULT 2

US-09-949-016-194175/c
; Sequence 194175, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

Sequence 200562,
Sequence 200563,
Sequence 3370, Ap
Sequence 44, Appl
Sequence 9940, Ap
Sequence 10137, A
Sequence 27, Appl
Sequence 1, Appl
Sequence 1374, A
Sequence 1592, A
Sequence 1196, Ap
Sequence 5, Appl
Sequence 11893, A
Sequence 17007, A
Sequence 17389, A
Sequence 13375, A
Sequence 12748, A
Sequence 15165, A

US-09-949-016-200562
US-09-949-016-200563
US-09-902-540-3970
US-09-535-008-44
US-09-252-991A-9940
US-09-252-991A-10137
US-09-023-942A-27
US-08-178-257-1
US-09-949-016-13374
US-09-949-016-15592
US-09-902-540-1196
US-09-146-053-5
US-09-949-016-11893
US-09-949-016-17007
US-09-949-016-17389
US-09-949-016-13375
US-09-949-016-12748
US-09-949-016-15165

18 1.4 601 4
18 1.4 601 4
18 1.4 705 4
18 1.4 713 3
18 1.4 933 4
18 1.4 1023 4
18 1.4 3866 4
18 1.4 4506 4
18 1.4 16914 4
18 1.4 16963 4
18 1.4 18324 4
18 1.4 44533 3
18 1.4 45365 4
18 1.4 45456 4
18 1.4 55031 4
18 1.4 70262 4
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18 1.4 70947 4

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17260
; LENGTH: 137956
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
; ORGANISM: Human
; NAME/KEY: misc.feature
; LOCATION: (1)...(137956)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17260

Query Match
Best Local Similarity 100.0%; Score 24; DB 4; Length 137956;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1156 CATTTCATTCATCATCATCCACC 1179
Db 472 CATTTCATTCATCATCATCCACC 449

RESULT 3
US-09-949-016-12196
; Sequence 12196, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12196
; LENGTH: 137949
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
; ORGANISM: Human
; NAME/KEY: misc.feature
; LOCATION: (1)...(137949)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12196

Query Match
Best Local Similarity 100.0%; Score 24; DB 4; Length 137949;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1156 CATTTCATTCATCATCATCCACC 1179
Db 130759 CATTTCATTCATCATCATCCACC 130782

RESULT 4
US-09-949-016-17260
; Sequence 17260, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17260
; LENGTH: 137956
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
; ORGANISM: Human
; NAME/KEY: misc.feature
; LOCATION: (1)...(137956)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17260

Query Match
Best Local Similarity 100.0%; Score 24; DB 4; Length 137956;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1156 CATTTCATTCATCATCATCCACC 1179
Db 130759 CATTTCATTCATCATCATCCACC 130782

RESULT 5
US-09-902-540-6997
; Sequence 6997, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6997
; LENGTH: 1491
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; ORGANISM: Myxococcus xanthus
US-09-902-540-6997

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 1491;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 665 GCAAGGACCTGCAGGACGTG 684
Db 1205 GCAAGGACCTGCAGGACGTG 1224

RESULT 6
US-09-902-540-612/c
; Sequence 612, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 612
; LENGTH: 4312
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; ORGANISM: Myxococcus xanthus
US-09-902-540-612
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Query Match 1.6%; Score 20; DB 4; Length 4312;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 665 GCAAGGACCTGCAGGACGTG 684
DB 291 GCAAGGACCTGCAGGACGTG 272

RESULT 7
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: TUBERCULOSIS
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g

US-09-103-840A-2
Query Match 1.6%; Score 20; DB 3; Length 4403765;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 AGCTGCGCTCATCTCTGTC 519
DB 7383 AGCTGCGCTCATCTCTGTC 7364

RESULT 8
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: TUBERCULOSIS
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 1.6%; Score 20; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 AGCTGCGCTCATCTCTGTC 519

DB 7383 AGCTGCGCTCATCTCTGTC 7364

RESULT 9
US-09-949-016-85015
; Sequence 85015, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85015
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-85015

Query Match 1.5%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 TGTTCATTCATTCATCCAT 1170
DB 465 TGTTCATTCATTCATCCAT 483

RESULT 10
US-09-949-016-85166
; Sequence 85166, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85166
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-85166

Query Match 1.5%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 TGTTCATTCATTCATCCAT 1170
DB 465 TGTTCATTCATTCATCCAT 483

RESULT 11

US-08-381-433A-3
; Sequence 3, Application US/08381433A
; Patent No. 5786203
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy W.
; APPLICANT: Oltersdorf, Tilman
; APPLICANT: Liaw, Chen
; APPLICANT: Grigoriadis, Dimitri E.
; APPLICANT: DeSouza, Errol B.
; TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2
; TITLE OF INVENTION: RECEPTORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,433A
; FILING DATE: 31-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMaisters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 690068.401C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANDBERRY
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 216..1449
US-08-381-433A-3
Query Match 1.5%; Score 19; DB 1; Length 1626;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 72 CCGGGGTGGCGGGGAGGC 90
Db 95 CCGGGGTGGCGGGGAGGC 113
RESULT 12
US-09-799-978-17
; Sequence 17, Application US/09799978
; Patent No. 6670140
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09/799,978
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 1626

; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (216)..(1451)
US-09-799-978-17
Query Match 1.5%; Score 19; DB 4; Length 1626;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 72 CCGGGGTGGCGGGGAGGC 90
Db 95 CCGGGGTGGCGGGGAGGC 113
RESULT 13
US-09-881-401-3
; Sequence 3, Application US/09881401
; Patent No. 6723841
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy W.
; APPLICANT: Oltersdorf, Tilman
; APPLICANT: Liaw, Chen
; APPLICANT: Grigoriadis, Dimitri E.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: DeSouza, Errol B.
; TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2
; TITLE OF INVENTION: RECEPTORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,401
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 690068.401C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 216..1449
US-09-881-401-3
Query Match 1.5%; Score 19; DB 4; Length 1626;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 72 CCGGGGTGGCGGGGAGGC 90
Db 95 CCGGGGTGGCGGGGAGGC 113

RESULT 14

US-09-902-540-792
; Sequence 792, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 792
; LENGTH: 5895
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-792

Query Match 1.5%; Score 19; DB 4; Length 5895;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 GGGCGGTAAAGATTTCCTT 594

Db 5033 GGGCGGTAAAGATTTCCTT 5051

RESULT 15

US-09-949-016-14169
; Sequence 14169, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14169
; LENGTH: 109159
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14169

Query Match 1.5%; Score 19; DB 4; Length 109159;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 TGTTCATTCATTCATCCAT 1170

Db 50828 TGTTCATTCATTCATCCAT 50846

Search completed: April 7, 2005, 08:54:58
Job time : 266 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 06:02:29 ; Search time 6807 Seconds
(without alignments)
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Perfect score: 1261
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Gapop 60.0 , Gapext 60.0

Searched: 5615251 seqs, 3030001701 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	91	7.2	405	17	US-10-276-774-718
4	38	3.0	645	13	US-10-029-191-21
5	38	3.0	2220	11	US-09-977-579-3
6	38	3.0	2632	13	US-10-029-191-22
7	38	3.0	3108	13	US-10-029-191-1
8	33	2.6	574	10	US-09-764-891-1293
9	24	1.9	24	16	US-10-121-759-20
10	22	1.7	22	16	US-10-121-759-19
11	22	1.7	462	9	US-09-864-761-15643
Sequence 4, Appli					
Sequence 7659, Ap					
Sequence 718, Appl					
Sequence 21, Appl					
Sequence 3, Appli					
Sequence 22, Appl					
Sequence 1, Appli					
Sequence 1293, Ap					
Sequence 20, Appl					
Sequence 19, Appl					
Sequence 15643, A					

12	21	1.7	621	13	US-10-027-632-132914	Sequence 132914,
13	21	1.7	621	17	US-10-027-632-132914	Sequence 132914,
14	20	1.6	889	17	US-10-260-238-3665	Sequence 3665, Ap
15	20	1.6	918	17	US-10-369-493-27913	Sequence 27913, A
16	20	1.6	2514	17	US-10-282-122A-26517	Sequence 26517, A
17	20	1.6	2517	9	US-09-712-363-4	Sequence 4, Appli
18	20	1.6	2517	17	US-10-282-122A-25466	Sequence 25466, A
19	20	1.6	2517	17	US-10-282-122A-28144	Sequence 28144, A
20	20	1.6	2547	17	US-10-282-122A-26047	Sequence 26047, A
21	20	1.6	2884	14	US-10-219-219-3	Sequence 3, Appli
22	20	1.6	58922	18	US-10-322-281-526	Sequence 526, App
23	20	1.6	200418	13	US-10-087-192-568	Sequence 568, App
24	19	1.5	201	19	US-10-741-600-68354	Sequence 68354, A
25	19	1.5	376	18	US-10-425-115-74855	Sequence 74855, A
26	19	1.5	471	9	US-09-864-761-679	Sequence 679, App
27	19	1.5	625	13	US-10-027-632-86250	Sequence 86250, A
28	19	1.5	625	13	US-10-027-632-86251	Sequence 86251, A
29	19	1.5	625	17	US-10-027-632-86250	Sequence 86250, A
30	19	1.5	625	17	US-10-027-632-86251	Sequence 86251, A
31	19	1.5	637	13	US-10-027-632-217363	Sequence 217363,
32	19	1.5	637	17	US-10-027-632-217363	Sequence 217363,
33	19	1.5	688	18	US-10-767-701-8737	Sequence 8737, Ap
34	19	1.5	762	13	US-10-027-632-149779	Sequence 149779,
35	19	1.5	762	17	US-10-027-632-149779	Sequence 149779,
36	19	1.5	782	13	US-10-027-632-29933	Sequence 29933, A
37	19	1.5	782	17	US-10-027-632-29933	Sequence 29933, A
38	19	1.5	815	17	US-10-425-114-14905	Sequence 14905, A
39	19	1.5	1626	9	US-09-881-401-3	Sequence 3, Appli
40	19	1.5	1626	10	US-09-799-978-17	Sequence 17, Appl
41	19	1.5	1626	18	US-10-649-852-17	Sequence 17, Appl
42	19	1.5	1626	18	US-10-821-502-3	Sequence 3, Appli
43	19	1.5	1719	17	US-10-424-599-115665	Sequence 115665,
44	19	1.5	2024	18	US-10-425-115-77665	Sequence 77665, A
45	19	1.5	2166	17	US-10-425-114-18441	Sequence 18441, A

ALIGNMENTS

RESULT 1
US-09-977-579-4
; Sequence 4, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
; TITLE OF INVENTION: channel
; FILE REFERENCE: 674558-2001
; CURRENT FILING DATE: 2001-10-15
; CURRENT APPLICATION NUMBER: US/09/977,579
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-977-579-4

Query Match	100.0%	Score 1261;	DB 11;	Length 1261;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1261;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CCCTCCCTTCGAGCTGAGCTTACCTCGGCGCAACAGCAGCGAGCGCGCGAGTGG	60	
Db	1	CCCTCCCTTCGAGCTGAGCTTACCTCGGCGCAACAGCAGCGAGCGCGAGTGG	60	
Qy	61	AAGCTGAGTTCGCGGTGGCGGAGGCGACTGTCCGTGGTCTGAGCCCGCGGAGA	120	

Db 61 AAGCTGGAGTTCCGGGGTGGGGGAGGCGACTGTCGGTGGTGGCTGAGCGCGCGGAG 120
QY 121 GGGGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCTAGTGGGGTGGCTTAG 180
Db 121 GGGGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCTAGTGGGGTGGCTTAG 180
QY 181 GGGCCAAAGCCCCACCGGCTCCAAAGCTCCAGGGCTCCCAAGGACCGGTGCTCG 240
Db 181 GGGCCAAAGCCCCACCGGCTCCAAAGCTCCCAAGGCTCCCAAGGACCGGTGCTCG 240
QY 241 GCGCTTCCTTCGGTCAAGAAAGTCGCCCCCTGGGGGAGTTCGTCCTCAAGAGGTTTCCTCG 300
Db 241 GCGCTTCCTTCGGTCAAGAAAGTCGCCCCCTGGGGGAGTTCGTCCTCAAGAGGTTTCCTCG 300
QY 301 AAAGAACTCTGAGAGGCGGAGTCTTTGACCGGGAATCTCTCTGTGTAGCTTGAAGC 360
Db 301 AAAGAACTCTGAGAGGCGGAGTCTTTGACCGGGAATCTCTCTGTGTAGCTTGAAGC 360
QY 361 CGCCAGCCCCAGAAAGTCTGCTCAATAGATTGTTTCCCTGCTTCTCTGCTGCTT 420
Db 361 CGCCAGCCCCAGAAAGTCTGCTCAATAGATTGTTTCCCTGCTTCTCTGCTGCTT 420
QY 421 ATCTACTGGTCTAGTCTGCTTCCCTGTGTGTGAAAGTGCCTCGGAGACGAGGCC 480
Db 421 ATCTACTGGTCTAGTCTGCTTCCCTGTGTGTGAAAGTGCCTCGGAGACGAGGCC 480
QY 481 GTGACGGCAACCCCAATGAAGTGCCTGCATCTCTGTCATGAAGAGAGAGGAGTGGAG 540
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QY 541 GCCACACCGTGTGAATGGTCTACAGGCGGAGGCGGTAAAGTTTCCTATTATAC 600
Db 541 GCCACACCGTGTGAATGGTCTACAGGCGGAGGCGGTAAAGTTTCCTATTATAC 600
QY 601 GAGTATCGGAATGGCCACAGAGGTGGAGAGCCCTTTTCAGGGGCGCTCGAGTGGAA 660
Db 601 GAGTATCGGAATGGCCACAGAGGTGGAGAGCCCTTTTCAGGGGCGCTCGAGTGGAA 660
QY 661 GGCAGCAAGGACTGACAGAGGTCATCATCTGCTCAAGTCACTCTGAACGACTCT 720
Db 661 GGCAGCAAGGACTGACAGAGGTCATCATCTGCTCAAGTCACTCTGAACGACTCT 720
QY 721 GGCCTCTACCTGCAATGTGTCGGGAGTTTGAAGTTTGAAGCGCATCGGCCCTTTTG 780
Db 721 GGCCTCTACCTGCAATGTGTCGGGAGTTTGAAGTTTGAAGCGCATCGGCCCTTTTG 780
QY 781 AAGACGACGCGCTGATCCCTTAAGAGTCACCGAGGAGGCTGGAGAGACTTCACCTCT 840
Db 781 AAGACGACGCGCTGATCCCTTAAGAGTCACCGAGGAGGCTGGAGAGACTTCACCTCT 840
QY 841 GTGGTCTCAGAAATCATGATGTATCTTCTGGTCTTCTCACTACCTGTGGTGTCTATC 900
Db 841 GTGGTCTCAGAAATCATGATGTATCTTCTGGTCTTCTCACTACCTGTGGTGTCTATC 900
QY 901 GAGATCATATTTGCTACAGAAAGTCTCAAGCGGAGAGGCGACGCCCAAGAAACGCG 960
Db 901 GAGATCATATTTGCTACAGAAAGTCTCAAGCGGAGAGGCGACGCCCAAGAAACGCG 960
QY 961 TCTGACTTACTTGCATCCCATCTGAGAAACAGGAACTCTGCGGTACAGTGGAGGAA 1020
Db 961 TCTGACTTACTTGCATCCCATCTGAGAAACAGGAACTCTGCGGTACAGTGGAGGAA 1020
QY 1021 TAGAACAGAGCAGTGTGATGATGGTGGCTGAAACCTTGAGGAGCTGGACATCCCATG 1080
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QY 1081 TTCAGCAATGTCAATGGCATCAGAGGCGGCCCAAGGCGCCCTTCCTTCATGC 1140
Db 1081 TTCAGCAATGTCAATGGCATCAGAGGCGGCCCAAGGCGCCCTTCCTTCATGC 1140
QY 1141 ATCCATTGTTCTGTTCAATTCATTCATCCATACATCCACCTGCTCTGAGCTTTCACCTCT 1200
Db 1141 ATCCATTGTTCTGTTCAATTCATTCATCCATACATCCACCTGCTCTGAGCTTTCACCTCT 1200

QY 1201 GACTCCTTAATCCATCAGACCTCTAGCACCATAAGACTCTGCCAGAACTGAGAAGCCG 1260
Db 1201 GACTCCTTAATCCATCAGACCTCTAGCACCATAAGACTCTGCCAGAACTGAGAAGCCG 1260
QY 1261 G 1261
Db 1261 G 1261

RESULT 2

US-09-764-891-7659
; Sequence 7659, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7659
; LENGTH: 4625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7659

Query Match 17.1%; Score 216; DB 10; Length 4625;

Best Local Similarity 100.0%; Pred. No. 5.4e-107; Indels 0; Gaps 0;
Matches 216; Conservative 0; Mismatches 0;

QY 1044 AGGTGGCTTGAACACCTGAGGGACTGGACATCCCATGTTTCAGCAATGTCAATGGCATCAG 1103
Db 33 AGGTGGCTTGAACACCTGAGGGACTGGACATCCCATGTTTCAGCAATGTCAATGGCATCAG 92
QY 1104 GAGGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGCATCCATGTTTCTGTTTCATTCATT 1163
Db 93 GAGGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGCATCCATGTTTCTGTTTCATTCATT 152
QY 1164 CATCCATACATCCACTGCTCTGAGCTTTCACCTCTGACTCCCTAACTCCATCAGACCT 1223
Db 153 CATCCATACATCCACTGCTCTGAGCTTTCACCTCTGACTCCCTAACTCCATCAGACCT 212
QY 1224 CTACGCACCATAAAGACTCTGCCAGAACTGAGAAGCC 1259
Db 213 CTACGCACCATAAAGACTCTGCCAGAACTGAGAAGCC 248

RESULT 3

US-10-276-774-718/c
; Sequence 718, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20040053245A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 718
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-718

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Query Match      7.2%; Score 91; DB 17; Length 407;
Best Local Similarity 99.3%; Pred. No. 1.2e-38;
Matches 141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 820 GCTGGAGAGACTTCACCTCTGTGGTCTCAGAAATCATGATGATCATCTTCTGCTTC 879
Db 230 GCTGGAGAGACTTCACCTCTGTGGTCTCAGAAATCATGATGATCATCTTCTGCTTC 171

QY 880 CTCACCTGTGGCTGCTCATCGAGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAA 939
Db 170 CTCACCTGTGGCTGCTCATCGAGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAA 111

QY 940 GAGCGAGCCCAAGAAACGGGT 961
Db 110 GAGCGAGCCCAAGAAACGGGT 89

RESULT 4
US-10-029-191-21
; Sequence 21, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-21

Query Match      3.0%; Score 38; DB 13; Length 645;
Best Local Similarity 100.0%; Pred. No. 1e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 436 GTCTGCTTCCCTGTGTGTGGAGTGCCCTCGGAGAC 473
Db 61 GTCTGCTTCCCTGTGTGTGGAGTGCCCTCGGAGAC 98

RESULT 5
US-09-977-579-3
; Sequence 3, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodium channel
; TITLE OF INVENTION: channel
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977,579
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: rat
US-09-977-579-3
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Query Match      3.0%; Score 38; DB 11; Length 2220;
Best Local Similarity 100.0%; Pred. No. 9.6e-10;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 436 GTCTGCTTCCCTGTGTGTGGAGTGCCCTCGGAGAC 473
Db 423 GTCTGCTTCCCTGTGTGTGGAGTGCCCTCGGAGAC 460

RESULT 6
US-10-029-191-22
; Sequence 22, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2632
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-22

Query Match      3.0%; Score 38; DB 13; Length 2632;
Best Local Similarity 100.0%; Pred. No. 9.5e-10;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 436 GTCTGCTTCCCTGTGTGTGGAGTGCCCTCGGAGAC 473
Db 138 GTCTGCTTCCCTGTGTGTGGAGTGCCCTCGGAGAC 175

RESULT 7
US-10-029-191-1
; Sequence 1, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3108
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-1

Query Match      3.0%; Score 38; DB 13; Length 3108;
Best Local Similarity 100.0%; Pred. No. 9.4e-10;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 436 GTCTGCTTCCCTGTGTGTGGAGTGCCCTCGGAGAC 473
Db 138 GTCTGCTTCCCTGTGTGTGGAGTGCCCTCGGAGAC 175
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RESULT 8

US-09-764-891-1293
; Sequence 1293, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1293
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (517)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (540)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (556)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (564)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (571)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-891-1293

Query Match 2.6%; Score 33; DB 10; Length 574;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1227 CGCACCATAAGACTCTGCCAGAACTGAGAAGCC 1259

DB 2 CGCACCATAAGACTCTGCCAGAACTGAGAAGCC 34

RESULT 9

US-10-121-759-20/c
; Sequence 20, Application US/10121759
; Publication No. US20030194751A1
; GENERAL INFORMATION:
; APPLICANT: Dubin, Adrienne
; APPLICANT: Kaftan, Edward
; APPLICANT: Chaplan, Sandra
; APPLICANT: Brown, Sean
; TITLE OF INVENTION: Method For Identifying Modulators Of Ion Channels
; FILE REFERENCE: PRI-0007 (ORT 1534)
; CURRENT APPLICATION NUMBER: US/10/121,759
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer Oligonucleotide
US-10-121-759-20

Query Match 1.9%; Score 24; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1234 TAAGACTCTGCCAGAACTGAGAAG 1257

|||||

DB

24 TAAGACTCTGCCAGAACTGAGAAG 1

RESULT 10

US-10-121-759-19
; Sequence 19, Application US/10121759
; Publication No. US20030194751A1
; GENERAL INFORMATION:
; APPLICANT: Dubin, Adrienne
; APPLICANT: Kaftan, Edward
; APPLICANT: Chaplan, Sandra
; APPLICANT: Brown, Sean
; TITLE OF INVENTION: Method For Identifying Modulators Of Ion Channels
; FILE REFERENCE: PRI-0007 (ORT 1534)
; CURRENT APPLICATION NUMBER: US/10/121,759
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer Oligonucleotide
US-10-121-759-19

Query Match 1.7%; Score 22; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 963 TGACTACCTTGCCATCCCATCT 984

DB 1 TGACTACCTTGCCATCCCATCT 22

RESULT 11

US-09-864-761-15643/c
; Sequence 15643, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 15643
 ; LENGTH: 462
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AC011242.1
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
 US-09-864-761-15643

Query Match 1.7%; Score 22; DB 9; Length 462;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 TTCTGTTTCATTCATCCAT 1170
 Db 25 TTCTGTTTCATTCATCCAT 4

RESULT 12
 US-10-027-632-132914
 ; Sequence 132914, Application US/10027632
 ; Publication No. US20020198371A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 132914
 ; LENGTH: 621
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-132914

Query Match 1.7%; Score 21; DB 13; Length 621;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 TCTGTTTCATTCATCCAT 1170
 Db 194 TCTGTTTCATTCATCCAT 214

RESULT 13
 US-10-027-632-132914
 ; Sequence 132914, Application US/10027632
 ; Publication No. US20030204075A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 132914
 ; LENGTH: 621
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-132914

Query Match 1.7%; Score 21; DB 17; Length 621;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 TCTGTTTCATTCATCCAT 1170
 Db 194 TCTGTTTCATTCATCCAT 214

RESULT 14
 US-10-260-238-3665
 ; Sequence 3665, Application US/10260238
 ; Publication No. US20040016025A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Budworth, Paul R.
 ; APPLICANT: Moughamer, Todd G.
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Katagiri, Fumiyaki
 ; APPLICANT: Krepes, Joel
 ; APPLICANT: Provart, Nicholas
 ; APPLICANT: Ricke, Darrell
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 ; FILE REFERENCE: 60111-NP
 ; CURRENT APPLICATION NUMBER: US/10/260,238
 ; CURRENT FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,448
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,277
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/370,620
 ; PRIOR FILING DATE: 2002-04-04
 ; NUMBER OF SEQ ID NOS: 6077
 ; SEQ ID NO 3665
 ; LENGTH: 889
 ; TYPE: DNA

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; ORGANISM: Triticum aestivum
US-10-260-238-3665

Query Match      1.6%; Score 20; DB 17; Length 889;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GGAGCCGTGCAGGCAACC 493
Db 318 GGAGCCGTGCAGGCAACC 337

RESULT 15
US-10-369-493-27913/c
; Sequence 27913, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 27913
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-369-493-27913

Query Match      1.6%; Score 20; DB 17; Length 918;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 CGCCGGCGAGAGCGGCGCG 129
Db 148 CGCCGGCGAGAGCGGCGCG 129

Search completed: April 7, 2005, 10:53:58
Job time : 6808 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 05:56:04 ; Search time 3942 Seconds
(without alignments)
12176.318 Million cell updates/sec

Title: US-09-977-579-4
Perfect score: 1261
Sequence: 1 cctccctccgagctgagc.....tgccagaactgagaagccgg 1361

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 34239544 seqs, 190312134700 residues

Word size : 10

Total number of hits satisfying chosen parameters: 31203175

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1104	87.5	4052	3 HSM801563	AL136589 Homo sapi
2	860	68.2	2555	3 CR609664	CH609664 full-length
3	600	47.6	1062	5 BX420015	BX420015 BX420015
4	597	47.3	648	9 AY419145	AY419145 Homo sapi
5	499	39.6	582	5 BP200910	BP200910 BP200910
6	443	35.1	582	5 BP202832	BP202832 BP202832
7	437	34.7	584	5 BP361278	BP361278 BP361278
8	384	30.5	975	5 BX445002	BX445002 BX445002
9	381	30.2	582	5 BP311484	BP311484 BP311484
10	348	27.6	975	5 BX452112	BX452112 BX452112
11	288	22.8	1069	5 BM928131	BM928131 AGENCOURT
12	268	21.3	1078	1 AL534136	AL534136 AL534136
13	165	13.1	443	7 D44825	D44825 HUMSUPY279
14	158	12.5	584	9 AY419146	AY419146 Pan trogl
15	154	12.2	509	5 BX280396	BX280396 BX280396
16	109	8.6	972	5 BQ066875	BQ066875 AGENCOURT
c 17	70	5.6	926	5 BX411288	BX411288 BX411288
c 18	48	3.8	646	9 CE606396	CE606396 tigr-gss-
19	38	3.0	471	6 CB732717	CB732717 AMGNNUC:N
20	38	3.0	472	6 CB730533	CB730533 AMGNNUC:N
c 21	34	2.7	176	2 AW832826	AW832826 QW2-TT000
22	33	2.6	631	6 CB577357	CB577357 AMGNNUC:C
23	32	2.5	439	6 CB750230	CB750230 AMGNNUC:N
24	29	2.3	636	5 BM933157	BM933157 UI-M-BH3-

25	29	2.3	648	9	AY419147	AY419147 Mus muscu
26	29	2.3	652	2	BB652801	BB652801 BB652801
27	29	2.3	672	2	BB614118	BB614118 BB614118
28	29	2.3	700	4	BT739617	BT739617 603361873
29	29	2.3	705	6	CD349958	CD349958 UI-M-FY0-
30	29	2.3	714	7	CF531573	CF531573 UI-M-FY0-
31	29	2.3	723	6	CA749311	CA749311 UI-M-FY0-
32	29	2.3	742	6	CB526211	CB526211 UI-M-FY0-
33	29	2.3	750	6	CD349206	CD349206 UI-M-FY0-
34	29	2.3	780	5	BQ770528	BQ770528 UI-M-FY0-
35	29	2.3	825	5	BQ745919	BQ745919 UI-M-EXO-
36	29	2.3	845	6	CA327438	CA327438 UI-M-FY0-
37	29	2.3	846	6	CD355879	CD355879 UI-M-FY0-
38	29	2.3	927	5	BQ713131	BQ713131 AGENCOURT
39	29	2.3	950	4	BG294174	BG294174 602391245
40	29	2.3	1359	3	AK076466	AK076466 Mus muscu
41	29	2.3	3549	3	AK049747	AK049747 Mus muscu
42	29	2.3	4105	3	BC058083	BC058083 Mus muscu
43	29	2.3	4149	3	AK049286	AK049286 Mus muscu
44	28	2.2	712	6	CB526257	CB526257 UI-M-FY0-
45	26	2.1	734	7	CK367344	CK367344 AGENCOURT

ALIGNMENTS

RESULT 1
HSM801563
LOCUS Homo sapiens mRNA; cDNA DKFZp761F182 (from clone DKFZp761F182). linear HTC 22-SEP-2004
DEFINITION AL136589
ACCESSION AL136589.1 GI:13276680
VERSION
KEYWORDS HTC
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4052)
AUTHORS Ottenwagelder, B., Obermaier, B., Deutschenbaur, S., Schaidp, A.,
Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, N. and
Wiemann, S.
The German cDNA Consortium
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project.
This clone (DKFZp761F182) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp761F182
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES

source
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/organism="Homo sapiens"
/mol_type="mRNA"
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/db_xref="taxon:9606"
/clone="DKFZp761F182"
/tissue type="amygdala"
/clone_lib="761 (synonym: hamy2). Vector pSport1; host
DH10B; sites NotI + SalI"
/dev_stage="adult"
/notes="voltage-gated sodium channel beta-3 subunit"
1..4052
/gene="DKFZp761F182"
804..1451
/gene="DKFZp761F182"
/codon_start=1
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/protein_id="CAB66524.1"
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VSTLVNLVNLDSGLTCHVSRFEPEARHPFKVTRLLIPLRVTEBAGDFISVSEI
MMYILLVFLTMLLLEMIYCYRKVSKAEBAENASDYLAIPTSENKENSAPVPE"
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ORIGIN

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Query Match      87.5%; Score 1104; DB 3; Length 4052;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1254; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CTCCTTCCGAGCTGAGCTTACCTCGGCGCAAAACGAGGAGCAGCGGCGCGAGTGGAA 62
DB 431 CTCCTTCCGAGCTGAGCTTACCTCGGCGCAAAACGAGGAGCAGCGGCGCGAGTGGAA 490

QY 63 GCTGGAGTTCGGGGTGGGGGGGAGCGACTGTCTCGTGTGTGAGCGCGCGGAGGC 122
DB 491 GCTGGAGTTCGGGGTGGGGGGGAGCGACTGTCTCGTGTGTGAGCGCGCGGAGGC 550

QY 123 GGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCAGTGGGTCGCTTAGGG 182
DB 551 GGGCGCGAGCGGCTGATCAGCTCCCTCGAACTGGGGAGGTCAGTGGGTCGCTTAGGG 610

QY 183 CCAAGGCCCCCAGCGCTCCAAAGCTCCAGGCGCTCCCGAGCAACCGGTGCTCGGC 242
DB 611 CCAAGGCCCCCAGCGCTCCAAAGCTCCAGGCGCTCCCGAGCAACCGGTGCTCGGC 670

QY 243 CTTCTCTTGGTCCAGAAAGTCGCGCCCTGGGGCAGTTCGTCCCAAGGGTTTCCTCGAA 302
DB 671 CTTCTCTTGGTCCAGAAAGTCGCGCCCTGGGGCAGTTCGTCCCAAGGGTTTCCTCGAA 730

QY 303 AGAATCTGAGAGGCGCAGTCCCTTGACCGAGGGAATCTCTGTGTAGCTTGGAAAGCG 362
DB 731 AGAATCTGAGAGGCGCAGTCCCTTGACCGAGGGAATCTCTGTGTAGCTTGGAAAGCG 790

QY 363 CAGCCCCAGAAAGATCGCTCCCTTAATAGATTGTTTCCCTCGGCTTCTCTGTGTTAT 422
DB 791 CAGCCCCAGAAAGATCGCTCCCTTAATAGATTGTTTCCCTCGGCTTCTCTGTGTTAT 850

QY 423 CTACTGGGTGAGTGTCTGCTTCCCTCTGTGTGTGGAGTGCCTCGAGACGAGGCGCT 482
DB 851 CTACTGGGTGAGTGTCTGCTTCCCTCTGTGTGTGGAGTGCCTCGAGACGAGGCGCT 910

QY 483 GCAGGCAACCCCATGAAGCTGCGCTGCATCTCTGCATGAAGAGAGAGGTGAGGC 542
DB 911 GCAGGCAACCCCATGAAGCTGCGCTGCATCTCTGCATGAAGAGAGAGGTGAGGC 970

QY 543 CACACGGTGGTGAATGTTTACAGGCCGAGGCGGTAAAGATTCTCTTATTTACGA 602
DB 971 CACACGGTGGTGAATGTTTACAGGCCGAGGCGGTAAAGATTCTCTTATTTACGA 1030

QY 603 GTATCGGAATGCCACAGAGGTGAGAGCCCTTTTCAGGGCGCTCGAGTGAATGG 662
DB 1031 GTATCGGAATGCCACAGAGGTGAGAGCCCTTTTCAGGGCGCTCGAGTGAATGG 1090

QY 663 CACAGAGGACCTCAGAGAGTGTCCATCACTGTGCTCAACGTCACCTCTGAAAGACTCTGG 722
DB 1091 CACAGAGGACCTCAGAGAGTGTCCATCACTGTGCTCAACGTCACCTCTGAAAGACTCTGG 1150

QY 723 CTTCTACCTGCAATGTGTCCGGGAGTTTGAAGTTGAGGCGCATCGGCCCTTTGTGAA 782
DB 1151 CTTCTACCTGCAATGTGTCCGGGAGTTTGAAGTTGAGGCGCATCGGCCCTTTGTGAA 1210

QY 783 GAGCAGCGGCTGATCCCTTAAGAGTCAACGAGGAGGTGGAGAGACTTACCTCTGT 842
DB 1211 GAGCAGCGGCTGATCCCTTAAGAGTCAACGAGGAGGTGGAGAGACTTACCTCTGT 1270

QY 843 GGTCTCAGAAATCATGATGATCATCTTCTGTGCTTTCCTCACCTGTGGCTGCTCATCGA 902
DB 1271 GGTCTCAGAAATCATGATGATCATCTTCTGTGCTTTCCTCACCTGTGGCTGCTCATCGA 1330
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QY 903 GATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAGAGGAGGCCCAAGAAAACCGCTC 962
DB 1331 GATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAGAGGAGGCCCAAGAAAACCGCTC 1390

QY 963 TGACTACCTTGGCATTCCCATCTGAGAAACAGAGAACTCTGCGGTACCACTGGAGGAATA 1022
DB 1391 TGACTACCTTGGCATTCCCATCTGAGAAACAGAGAACTCTGCGGTACCACTGGAGGAATA 1450

QY 1023 GAACGAGGACAGTGTGACATGAGGTGGCTGAACACCTGAGGAGCTTGGACATCCCATGTT 1082
DB 1451 GAACGAGGACAGTGTGACATGAGGTGGCTGAACACCTGAGGAGCTTGGACATCCCATGTT 1510

QY 1083 CAGCAATGTAATGGCATCAGGAGGCGGCCCAAGGCGCCCATCGCTTCCCTTCATGCAT 1142
DB 1511 CAGCAATGTAATGGCATCAGGAGGCGGCCCAAGGCGCCCATCGCTTCCCTTCATGCAT 1570

QY 1143 CCATTGTTCTGTTTCAATTCATTCATCATCATCCACCTGCTGAGCTTTCACCTCTGA 1202
DB 1571 CCATTGTTCTGTTTCAATTCATTCATCATCATCCACCTGCTGAGCTTTCACCTCTGA 1630

QY 1203 CTCCTTAATCCATCAGACCTCTAGCCACCAAGAATCTGCGCAAACTGAGAAGCC 1259
DB 1631 CTCCTTAATCCATCAGACCTCTAGCCACCAAGAATCTGCGCAAACTGAGAAGCC 1687

RESULT 2
CR609664 2555 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DF023YA09 of Fetal brain of Homo sapiens
(human).
ACCESSION CR609664
VERSION CR609664.1 GI:50490471
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2555)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 2555)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES             Location/Qualifiers
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     1..2555
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         /mol_type="mRNA"
         /db_xref="taxon:9606"
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ORIGIN
Query Match      68.2%; Score 860; DB 3; Length 2555;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 910; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 349 AGCCTTGGAGCGCGCAGCCCGAGAGATGCTGCTCAATAGATTGTTCCCTGGCT 408
DB 208 AGCCTTGGAGCGCGCAGCCCGAGAGATGCTGCTCAATAGATTGTTCCCTGGCT 267
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Qy	409	TCTCTGCTGCTTATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAGTGCCTCG	468
Db	268	TCTCTGCTGCTTATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAGTGCCTCG	327
Qy	469	GAGACGAGGCGGTGCGAGGCAACCCCATGAAGCTGGCTGCATCTCTGCATGAAGAGA	528
Db	328	GAGACGAGGCGGTGCGAGGCAACCCCATGAAGCTGGCTGCATCTCTGCATGAAGAGA	387
Qy	529	GAGGAGTGGAGGCCACACGCTGGTGAATGGTTCTACAGGCCGAGGGCGGTAAAGAT	588
Db	388	GAGGAGTGGAGGCCACACGCTGGTGAATGGTTCTACAGGCCGAGGGCGGTAAAGAT	447
Qy	589	TTCTCTTATTTACGAGTATCGGAATGGCCACAGAGGTGGAGAGCCCTTTTCAGGGGCGC	648
Db	448	TTCTCTTATTTACGAGTATCGGAATGGCCACAGAGGTGGAGAGCCCTTTTCAGGGGCGC	507
Qy	649	CTGCAGTGGAAATGGCAGAGGACCTGCGAGCATGTGCTCAACGTCACCT	708
Db	508	CTGCAGTGGAAATGGCAGAGGACCTGCGAGCATGTGCTCAACGTCACCT	567
Qy	709	CTGAACGACTCTGSCCTCTACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAGGGCGAT	768
Db	568	CTGAACGACTCTGSCCTCTACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAGGGCGAT	627
Qy	769	CGGCCCCCTTGTGAAGACGACGCGGCTGATCCCCCTAAGAGTCAACGAGGAGGCTGGAGAG	828
Db	628	CGGCCCCCTTGTGAAGACGACGCGGCTGATCCCCCTAAGAGTCAACGAGGAGGCTGGAGAG	687
Qy	829	GACTTCACTCTGTGGTCTCAGAAATCATGATGATGATCTTCTGTGCTTCTTCCACCTG	888
Db	688	GACTTCACTCTGTGGTCTCAGAAATCATGATGATGATCTTCTGTGCTTCTTCCACCTG	747
Qy	889	TGCTGCTCATCGAGATGATATTTGCTACAGAAAGTCTCAAAAGCCGAGGCGAGCC	948
Db	748	TGCTGCTCATCGAGATGATATTTGCTACAGAAAGTCTCAAAAGCCGAGGCGAGCC	807
Qy	949	CAAGAAAACCGCTCTGACTACTCTGCTTCCATCCATCTCAGAAACAGGAGAACTCTGCGGTA	1008
Db	808	CAAGAAAACCGCTCTGACTACTCTGCTTCCATCCATCTCAGAAACAGGAGAACTCTGCGGTA	867
Qy	1009	CCAGTGGAGAAATAGAACAGAGCAGTGTGACATGAGTGGCTGGCTGAACACCTGAGGACT	1068
Db	868	CCAGTGGAGAAATAGAACAGAGCAGTGTGACATGAGTGGCTGGCTGAACACCTGAGGACT	927
Qy	1069	GGACATCCCATGTTTACGAATGCAATGGCATCAGGAGGCGCCCAAGGGCCCCATCGC	1128
Db	928	GGACATCCCATGTTTACGAATGCAATGGCATCAGGAGGCGCCCAAGGGCCCCATCGC	987
Qy	1129	TTCCCTTCATGCTATTCATTTCTGTTTCAATTCATTCATCATCATCATCTGCTCTGA	1188
Db	988	TTCCCTTCATGCTATTCATTTCTGTTTCAATTCATTCATCATCATCATCTGCTCTGA	1047
Qy	1189	GCTTTTCACTCTGACTCCCTTAACTCCATCAGACTCTTACGACCATGAAGACTCTGCGAGA	1248
Db	1048	GCTTTTCACTCTGACTCCCTTAACTCCATCAGACTCTTACGACCATGAAGACTCTGCGAGA	1107
Qy	1249	ACTGAGAGCC	1259
Db	1108	ACTGAGAGCC	1118
RESULT 3			
BX420015			
LOCUS			
DEFINITION BX420015 Homo sapiens FETAL BRAIN Homo sapiens cdna clone EST 01-MAY-2004			
CS0DF023YA09 5-PRIME, mRNA sequence.			
ACCESSION BX420015			
VERSION BX420015.2 GI:46929710			
KEYWORDS EST.			
SOURCE Homo sapiens (human)			
ORGANISM Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 1062)

Li, W. B., Gruber, C., Jessee, J., and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 13, 2003 this sequence version replaced gi:30646738.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 6147.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DF023YA09&l=6147.r.

Location/Qualifiers

1. .1062

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DF023YA09"

/tissue_type="FETAL BRAIN"

/dev_stage="fetal"

/clone_lib="Homo sapiens FETAL BRAIN"

/note="Organ: brain; vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime and

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

Query Match 47.8%; Score 600; DB 5; Length 1062;

Best Local Similarity 99.7%; Pred. No. 1.3e-302;

Matches 700; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 349 AGCTTTGGAAGCCGCGAGAGAGTCCCTGCTTCAATAGATTGTTTCCCTCGCT 408

Db 207 AGCTTTGGAAGCCGCGAGAGAGTCCCTGCTTCAATAGATTGTTTCCCTCGCT 266

Qy 409 TCTCTGCTGCTTATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCTCG 468

Db 267 TCTCTGCTGCTTATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCTCG 326

Qy 469 GAGACGAGGCGCTGCGAGGCAACCCCATGAAGCTGGCTGCATCTCTGCATGAAGAGA 528

Db 327 GAGACGAGGCGCTGCGAGGCAACCCCATGAAGCTGGCTGCATCTCTGCATGAAGAGA 386

Qy 529 GAGGAGTGGAGGCCACCGTGGTGGATGTTCTACAGGCCCGAGGGCGGTAAAGAT 588

Db 387 GAGGAGTGGAGGCCACCGTGGTGGATGTTCTACAGGCCCGAGGGCGGTAAAGAT 446

Qy 589 TTCTCTTATTTACGAGTATCGGAATGGCCACAGGAGGTGGAGAGCCCTTTTCAGGGGCGC 648

Db 447 TTCTCTTATTTACGAGTATCGGAATGGCCACAGGAGGTGGAGAGCCCTTTTCAGGGGCGC 506

Qy 649 CTGCAGTGGAAATGGCAGAGGACCTGCGAGCATGTGCTCAACGTCACCT 708

Db 507 CTGCAGTGGAAATGGCAGAGGACCTGCGAGCATGTGCTCAACGTCACCT 566

Qy 709 CTGAACGACTCTGSCCTCTACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAGGGCGAT 768

Db 567 CTGAACGACTCTGSCCTCTACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAGGGCGAT 626

Qy 769 CGGCCCCCTTGTGAAGACGACGCGGCTGATCCCCCTAAGAGTCAACGAGGAGGCTGGAGAG 828

Db 627 CGGCCCCCTTGTGAAGACGACGCGGCTGATCCCCCTAAGAGTCAACGAGGAGGCTGGAGAG 686

Qy 829 GACTTCACTCTGTGGTCTCAGAAATCATGATGATGATCTTCTGTGCTTCTTCCACCTG 888

Db 687 GACTTCACTCTGTGGTCTCAGAAATCATGATGATGATCTTCTGTGCTTCTTCCACCTG 746

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QY 889 TGCTGCTCATCGAGATGATATATTCTACAGAAAGGTCTCAAAAGCCGGAAGAGGAGCC 948
Db 747 TGCTGCTCATCGAGATGATATATTCTACAGAAAGGTCTCAAAAGCCGGAAGAGGAGCC 806
QY 949 CAAGAAAACGGCTGCTGACTACCTTGCATCCATCTGAGAACAAAGAGAACTCTGCGGTA 1008
Db 807 CAAGAAAACGGCTGCTGACTACCTTGCATCCATCTGAGAACAAAGAGAACTCTGCGGTA 866
QY 1009 CCAGTGGAGGAATAGAACAGGAGCAGTGTGACATGAGGTGGC 1050
Db 867 CCAGTGGAGGAATAGAACAGGAGCAGTGTGACATGAGGTGGC 908

RESULT 4
AY419145
LOCUS
DEFINITION Homo sapiens HCM6793 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY419145
VERSION AY419145.1 GI:39775105
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 648)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 648)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
These sequences were made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..648
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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ORIGIN
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Best Local Similarity 99.8%; Pred. No. 4.8e-301; Indels 0; Gaps 0;
Matches 647; Conservative 0; Mismatches 1;

QY 376 ATGCTGCTTCAATAGATTGTTCCCTGGCTTCTCTGCTTATCTACTGGGTGAGT 435
Db 1 ATGCTGCTTCAATAGATTGTTCCCTGGCTTCTCTGCTTATCTACTGGGTGAGT 60
QY 436 GTCTGCTTCCCTGTGTGTGGAGTGCCTCGAGACGAGGCCCTGAGGGCAACCCC 495
Db 61 GTCTGCTTCCCTGTGTGTGGAGTGCCTCGAGACGAGGCCCTGAGGGCAACCCC 120
QY 496 ATGAAGCTGGCTGATCTCTCATGAAGAGAGAGGTGGAGGCCACCGGTGGTG 555
Db 121 ATGAAGCTGGCTGATCTCTCATGAAGAGAGAGGTGGAGGCCACCGGTGGTG 180
QY 556 GAATGTTCTTACAGGCCCGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGCC 615
Db 181 GAATGTTCTTACAGGCCCGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGCC 240

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QY 616 CACCAGGAGGTGGAGAGCCCTTTTCAGGGGCGCCTGAGTGGAATGGCAGCAAGGACCTG 675
Db 241 CACCAGGAGGTGGAGAGCCCTTTTCAGGGGCGCCTGAGTGGAATGGCAGCAAGGACCTG 300
QY 676 CAGGACGTGTCCATCAGTGTGCTCAACGTCACCTGTAACGACTCTGGCCCTCTACACCTGC 735
Db 301 CAGGACGTGTCCATCAGTGTGCTCAACGTCACCTGTAACGACTCTGGCCCTCTACACCTGC 360
QY 736 AATGTGTCCCGGAGTGTGAGTTTGAGGCGCATCGGCCCTTTTGTGAAGACGACGCGGCTG 795
Db 361 AATGTGTCCCGGAGTGTGAGTTTGAGGCGCATCGGCCCTTTTGTGAAGACGACGCGGCTG 420
QY 796 ATCCCTTAAGAGTCAACGAGGAGGCTGAGAGGACTTCACCTCTGTGTCTCAGAAATC 855
Db 421 ATCCCTTAAGAGTCAACGAGGAGGCTGAGAGGACTTCACCTCTGTGTCTCAGAAATC 480
QY 856 ATGATGTACATCTTCTGCTCTTCTCACCCTGTGGCTCTCATCGAGATGATATATTC 915
Db 481 ATGATGTACATCTTCTGCTCTTCTCACCCTGTGGCTCTCATCGAGATGATATATTC 540
QY 916 TACAGAAAGGTCTCAAAAGCCGAGAGGAGGCCCAAGAAAACGCGTCTGACTACCTTGC 975
Db 541 TACAGAAAGGTCTCAAAAGCCGAGAGGAGGCCCAAGAAAACGCGTCTGACTACCTTGC 600
QY 976 ATCCATCTGAGAACAGAGAGAACTCTGGGTACAGTGGAGGAATAG 1023
Db 601 ATCCATCTGAGAACAGAGAGAACTCTGGGTACAGTGGAGGAATAG 648

RESULT 5
BP200910
LOCUS
DEFINITION BP200910 Sugano cDNA library, amygdala Homo sapiens cDNA clone
AMR03894, mRNA sequence.
ACCESSION BP200910
VERSION BP200910.1 GI:52050356
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
Suzuki, Y., Yanashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
source
1..582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="AMR03894"
/tissue_type="amygdala"
/clone_lib="Sugano cDNA library, amygdala"

ORIGIN
Query Match 39.6%; Score 499; DB 5; Length 582;
Best Local Similarity 100.0%; Pred. No. 1.1e-249;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 378 GCTCGCTTCAATAGATTGTTCCCTGGCTTCTCTGCTTATCTACTGGGTGAGTGT 437
Db 33 GCTCGCTTCAATAGATTGTTCCCTGGCTTCTCTGCTTATCTACTGGGTGAGTGT 92
QY 438 CTGCTTCCCTGTGTGTGGAGTGCCTCGAGAGCGGAGCGCGTGCAGGGCAACCCAT 497

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QY 411 TCTCGTCTTATCTAGTGGTCTAGTCTGCTCTTCCCTGTGTGTGTGTGGAAGTGCCTCGGA 470
Db 157 TCTCGTCTTATCTAGTGGTCTAGTCTGCTCTTCCCTGTGTGTGTGTGGAAGTGCCTCGGA 216
QY 471 GACGAGGCGCTGACGGCAACCCATGAAGCTGCGCTGCATCTCTGTCATGAAGAGAGA 530
Db 217 GACGAGGCGCTGACGGCAACCCATGAAGCTGCGCTGCATCTCTGTCATGAAGAGAGA 276
QY 531 GGAGGTGGAGGCCACCAACCGTGTGTGAATGTTCTACAGSCCGAGGCGGTAAAGATT 590
Db 277 GGAGGTGGAGGCCACCAACCGTGTGTGAATGTTCTACAGSCCGAGGCGGTAAAGATT 336
QY 591 CCTATTATTACGAGTATCGAATCGCCACACGAGAGGTGAGAGCCCTTTTCAGSGGCGCCT 650
Db 337 CCTATTATTACGAGTATCGAATCGCCACACGAGAGGTGAGAGCCCTTTTCAGSGGCGCCT 396
QY 651 GCAGTGGATGGCAGCAAGACCTGCAGGACGTGCTCATCTGCTCTCAACGTCACTCT 710
Db 397 GCAGTGGATGGCAGCAAGACCTGCAGGACGTGCTCATCTGCTCTCAACGTCACTCT 456
QY 711 GAACGACTCTGGCTCTACACCTGCAATGTGTCCCGGAGTTTGAAGTTCAGGCGCATCG 770
Db 457 GAACGACTCTGGCTCTACACCTGCAATGTGTCCCGGAGTTTGAAGTTCAGGCGCATCG 516
QY 771 GCCCTTTGTGAACACGACGCGCTGATCCCTTAAGAGTCAACGAGAGGCTGGAGAGA 830
Db 517 GCCCTTTGTGAACACGACGCGCTGATCCCTTAAGAGTCAACGAGAGGCTGGAGAGA 576
QY 831 CTTCACT 838
Db 577 CTTCACT 584

RESULT 8
BX445002
LOCUS BX445002 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF023YA09 5-PRIME, mRNA sequence.
ACCESSION BX445002
VERSION BX445002.2 GI:47009181
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT On May 15, 2003 this sequence version replaced gi:30782286.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 6147.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS1AF006Z050P1sc=6147.r.
FEATURES
source
1. .975
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/mol_type="mRNA"
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was primed with a NotI-oligo(dT) primer. Five prime end
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ORIGIN
Query Match 30.5%; Score 384; DB 5; Length 975;
Best Local Similarity 100.0%; Pred. No. 2.3e-189; Indels 0; Gaps 0;
Matches 384; Conservative 0; Mismatches 0;

QY 349 AGCCTTGGAGCGCCAGCCAGAGATGCCCTTCAATAGATTGTTTCCCTGGCT 408
Db 208 AGCCTTGGAGCGCCAGCCAGAGATGCCCTTCAATAGATTGTTTCCCTGGCT 267
QY 409 TCTCTCGTCTTATCTAGTGGTCTAGTCTGCTTCCCTGTGTGTGTGGAAGTGCCTCG 468
Db 268 TCTCTCGTCTTATCTAGTGGTCTAGTCTGCTTCCCTGTGTGTGTGGAAGTGCCTCG 327
QY 469 GAGACGGAGGCGCTGCAGGCGCAACCCATGAAGCTGCGCTGCATCTCCTGCATGAAGAGA 528
Db 328 GAGACGGAGGCGCTGCAGGCGCAACCCATGAAGCTGCGCTGCATCTCCTGCATGAAGAGA 387
QY 529 GAGGAGGTGGAGGCCACCAACCGTGTGTGAATGTTCTACAGGCGCCGAGGCGGTAAAGAT 588
Db 388 GAGGAGGTGGAGGCCACCAACCGTGTGTGAATGTTCTACAGGCGCCGAGGCGGTAAAGAT 447
QY 589 TTCCTTATTTACGAGTATCGAATGSCCAACGAGGAGGTGGAGAGCCCTTTTCAGGGGCGC 648
Db 448 TTCCTTATTTACGAGTATCGAATGSCCAACGAGGAGGTGGAGAGCCCTTTTCAGGGGCGC 507
QY 649 CTGCAGTGAATGGCAGCAAGGACCTGCAGGAGCTGCTCCATCTGCTCAACGTCAC 708
Db 508 CTGCAGTGAATGGCAGCAAGGACCTGCAGGAGCTGCTCCATCTGCTCAACGTCAC 567
QY 709 CTGAACGACTCTGGCTCTTACACC 732
Db 568 CTGAACGACTCTGGCTCTTACACC 591

RESULT 9
BX311484
LOCUS BP311484 Sugano cDNA library, brain Homo sapiens cDNA clone
DEFINITION NRR06134, mRNA sequence.
ACCESSION BP311484
VERSION BP311484.1 GI:52240459
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
JOURNAL Mizushima-Sugano, J., Nakai, K. and Sugano, S.
COMMENT Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
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1. .582
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NRR06134"
/tissue_type="brain"
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ORIGIN
Query Match 30.2%; Score 381; DB 5; Length 582;
Best Local Similarity 100.0%; Pred. No. 8.4e-188;
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enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

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ORIGIN
Query Match      22.8%; Score 288; DB 5; Length 1069;
Best Local Similarity 100.0%; Pred. No. 4.9e-139;
Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 AGCCTTGGAGCGCCAGCCAGAGATGCTGCTTCAATAGATTGTTCCCTGGCT 408
DB 355 AGCCTTGGAGCGCCAGCCAGAGATGCTGCTTCAATAGATTGTTCCCTGGCT 414
QY 409 TCTCTGCTTATCTACTTGGGTGAGTCTGCTTCCCTGTGTGTGGAAGTGCCTCG 468
DB 415 TCTCTGCTTATCTACTTGGGTGAGTCTGCTTCCCTGTGTGTGGAAGTGCCTCG 474
QY 469 GAGACGAGCGCGTGAGGGCAACCCATGAAGTGCCTGTCATCTCTGCATGAAGAGA 528
DB 475 GAGACGAGCGCGTGAGGGCAACCCATGAAGTGCCTGTCATCTCTGCATGAAGAGA 534
QY 529 GAGGAGTGGAGCCACACGCTGGTGGTGAATGGTTCTACAGCCCGAGGCGGTAAAGAT 588
DB 535 GAGGAGTGGAGCCACACGCTGGTGGTGAATGGTTCTACAGCCCGAGGCGGTAAAGAT 594
QY 589 TTCTTTATTTAGAGTATCGGAATGCCACAGGAGGTGGAGAGCCCC 636
DB 595 TTCTTTATTTAGAGTATCGGAATGCCACAGGAGGTGGAGAGCCCC 642

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RESULT 12
LOCUS      AL5341136      1078 bp      mRNA      linear      EST 24-MAR-2004
DEFINITION AL5341136 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CS0DF005Y102 5-PRIME, mRNA sequence.
ACCESSION  AL5341136
VERSION     AL5341136.3 GI:45709952
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL     Full-length cDNA libraries and normalization
COMMENT     Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pcMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 6147.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?8-CS0DF005BB01QP1&c=6147.r.
Location/Qualifiers
1. .1078
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/clone="CS0DF005Y102"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/notes="Organ: Brain; Vector: pcMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and

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FEATURES
source

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ORIGIN
Query Match      21.3%; Score 268; DB 1; Length 1078;
Best Local Similarity 99.7%; Pred. No. 1.5e-128;
Matches 388; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 134 GGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGTGCTTAGGSCCCCAAGCCCC 193
DB 521 GGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGTGCTTAGGSCCCCAAGCCCC 580
QY 194 CACCGGCTCAGAAAGTCCAGAGGCTCCCGAGGACCGGTGCTCGGCCCTTCTTCGG 253
DB 581 CACCGGCTCAGAAAGTCCCGAGGCTCCCGAGGACCGGTGCTCGGCCCTTCTTCGG 640
QY 254 TCAGAAAGTCCGCCCTCGGGGACGTTGCTGCCAAAGGGTTTCTCGAAAGAAATCTGAGA 313
DB 641 TCAGAAAGTCCGCCCTCGGGGACGTTGCTGCCAAAGGGTTTCTCGAAAGAAATCTGAGA 700
QY 314 GGGCGCAGTCTCTGACCGAGGGAATCTCTGTGTAGCTTCGAAAGCCCGAGCCCCAGA 373
DB 701 GGGCGCA-TCTCTGACCGAGGGAATCTCTGTGTAGCTTCGAAAGCCCGAGCCCCAGA 759
QY 374 AGATCGCTGCTTCAATAGATTGTTCCCTGGCTTCTCGTGTATCTACTGGGTCA 433
DB 760 AGATCGCTGCTTCAATAGATTGTTCCCTGGCTTCTCGTGTATCTACTGGGTCA 819
QY 434 GTGTCTGCTTCCCTGTGTGGAAGTCCCTCGAGACGAGGCGGTGCGAGGCAACC 493
DB 820 GTGTCTGCTTCCCTGTGTGGAAGTCCCTCGAGACGAGGCGGTGCGAGGCAACC 879
QY 494 CCATGAAGTGGCTGCATCTCTCGATG 522
DB 880 CCATGAAGTGGCTGCATCTCTCGATG 908

RESULT 13
LOCUS      D44825      443 bp      mRNA      linear      EST 20-FEB-1998
DEFINITION HUMSUP279 Human brain cDNA Homo sapiens cDNA clone NF220-K, mRNA
sequence.
ACCESSION  D44825
VERSION     D44825.1 GI:1572300
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       Hadano, S., Ishida, Y., Tomiyasu, H., Yamamoto, K., Bates, G.P. and
JOURNAL     Ikeda, J.
COMMENT     Transcript map of the human chromosome 4p16.3 consisting of 627
cDNA clones derived from 1 Mb of the Huntington's disease locus
DNA Res. 3 (4), 239-255 (1996)
MEDLINE     97101646
PUBMED      8946164
Contact: Shinji Hadano
Japan Science and Technology Corporation, NeuroGenes Project, ICORP
Univ. of Tokai School of Med.
Bohseidai, Isehara, Kanagawa 259-1193, Japan
Tel: 81-463-91-5095
Fax: 81-463-91-4993
Email: shinji@ng.med.u-tokai.ac.jp.
Location/Qualifiers
1. .443
/organism="Homo sapiens"
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Matches 215; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1044 AGGTGGCTGAACACCTGAGGAGTGGACATCCCATGTTTCAGCAATGTCATGCAATGCATCAG 1103
DB 33 AGGTGGCTGAACACCTGAGGAGTGGACATCCCATGTTTCAGCAATGTCATGCAATGCATCAG 92

QY 1104 GAGGGCCCCCAAGGGCCCCCATGCTTCCCTTCATGATCCATGTTCTGTTCAATTCATT 1163
DB 93 GAGGGCCCCCAAGGGCCCCCATGCTTCCCTTCATGATCCATGTTCTGTTCAATTCATT 152

QY 1164 CATCATATACATCCACATGCTGCTCTGAGCTTTTCCCTTCACTGACTCCCTAACTCCATCAGACCT 1223
DB 153 CATCATATACATCCACATGCTGCTCTGAGCTTTTCCCTTCACTGACTCCCTAACTCCATCAGACCT 212

QY 1224 CTAGGCACCATAGACTCTGCGCAGAACTGAGAGCC 1259
DB 213 CTAGGCACCATAGACTCTGCGCAGAACTGAGAGCC 248

RESULT 14
AY419146
LOCUS
DEFINITION      Pan troglodytes HCM6793 gene, VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION      AY419146
VERSION        AY419146.1 GI:39775106
KEYWORDS
SOURCE
ORGANISM      Pan troglodytes (chimpanzee)
REFERENCE
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 584)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
PUBMED      Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 584)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
These sequences were made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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DB 1 ATGCCTGCCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTCTATCTACTGGGTCACT 60

QY 436 GTCTGCTTCCCTGTGTGTGGAGTGCCTTCGAGACGGAGCCGTCGAGGGCAACCC 495
DB 61 GTCTGCTTCCCTGTGTGTGGAGTGCCTTCGAGACGGAGCCGTCGAGGGCAACCC 120
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DB 121 ATGAAGCTGGCTGATCTCTCTCATGAAGAGAGGGA 158

RESULT 15
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LOCUS
DEFINITION      BX280396 NIH_MGC_121 Homo sapiens cDNA clone IMAGE9998F0412832;
IMAGE:5769987, mRNA sequence.
ACCESSION      BX280396
VERSION        BX280396.1 GI:28612393
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
REFERENCE
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 509)
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD: IMAGP998F0412832
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13u, Primer sequence: CGTTGTAAACGACGCGCCAGT.
FEATURES
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Site 2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."
ORIGIN
Query Match      12.2%; Score 154; DB 5; Length 509;
Best Local Similarity 100.0%; Pred. No. 8.6e-69;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 356 AGCCTTGGAGCCGCCAGCCAGAGATGCTTCAATAGATTGTTTCCCTGGCT 415

QY 409 TCTCTCGTGTCTTACTACTGGGTCACTGTCTGCTTCCCTGTGTGTGGAAGTCCCTCG 468
DB 416 TCTCTCGTGTCTTACTACTGGGTCACTGTCTGCTTCCCTGTGTGTGGAAGTCCCTCG 475

QY 469 GAGACGGAGCCGCTGCGAGGCAACCCCATGAAGC 502
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Db 476 GAGACGGAGCGCGTCAGGGCAACCCCATGAAGC 509

Search completed: April 7, 2005, 08:50:28
Job time : 3950 secs